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Table 430

	NT2RP2003506	18.91	15.11	21.41	10.64	13.4	7.04	4.15	4.83	3.94	*	**	-	-
	NT2RP2003511	12.05	3.9	4.64	8.42	8.48	3	2.22	2.49	1.23			-	-
5	NT2RP2003513	5.02	4.48	4.09	4.53	1.64	2.04	2.58	1.55	3.7	*		-	-
	NT2RP2003517	3.09	1.94	2.24	4.01	1.27	1.81	1.81	0.62	1.53			-	-
	NT2RP2003522	5.79	5.52	8.11	4.61	3.87	1.76	1.31	4.96	5.44			-	-
	NT2RP2003525	12.34	13.08	16.44	6.02	5.34	4.08	6.04	6.6	5.02	**	**	-	-
	NT2RP2003533	88.01	167.21	169.95	95.54	157.31	89.62	178.62	120.18	151.89			-	-
	NT2RP2003541	3.67	3.34	5.25	3.35	1.69	1.26	1.11	0.78	0.47	**		-	-
10	NT2RP2003543	6.02	7.31	6.9	4.81	3.89	1.42	3.96	1.71	3.06	*	**	-	-
	NT2RP2003545	16.66	28.91	37	10.57	5.83	7.38	9	7.02	10.57	*	*	-	-
	NT2RP2003559	24.73	30.59	37.42	18.05	13.28	13.04	17.81	5.8	6.39	*	*	-	-
	NT2RP2003564	4.21	3.5	2.84	5.11	2.21	2.76	1.47	1.11	1.54	**		-	-
	NT2RP2003565	5.56	6.05	9.75	8.3	2.97	4.12	3.13	4.62	3.34			-	-
15	NT2RP2003567	52.47	49.61	31.71	25.62	16.56	16.12	8.17	19.23	14.83	*	*	-	-
	NT2RP2003575	228.18	422	264.34	79.35	234.74	114.07	248.45	399.29	319.2			-	-
	NT2RP2003576	12.51	13.48	14.93	11.41	10.35	7.47	9.35	12.38	11.58	*		-	-
	NT2RP2003579	6.35	14.72	8.69	5.77	5	3.85	5.14	3.96	3.9			-	-
	NT2RP2003581	5.18	8.39	5.74	5.34	1.72	1.57	1.66	0.89	1.73	**		-	-
	NT2RP2003587	5.23	4.31	3.93	4.85	1.48	2.81	2.91	3.12	2.6	*		-	-
20	NT2RP2003590	10.26	7.56	7.31	8.22	4.4	10.25	8.81	5.02	6.24			-	-
	NT2RP2003593	30.36	26.83	29	16.89	17.04	17.86	10.43	21.71	15.35	**	*	-	-
	NT2RP2003596	9.32	8.79	11.25	13.55	9.73	9.49	8.79	14.74	9.47			-	-
	NT2RP2003599	23.27	13.17	35	8.05	27.81	6.94	3.86	4	10.53			-	-
	NT2RP2003600	19.86	30.4	31.86	22.5	9.14	19.7	15.99	13.53	9.08	*		-	-
	NT2RP2003604	5.88	9.89	7.47	5.4	1.89	1.85	3.39	3.16	2.76	*	*	-	-
25	NT2RP2003629	8.19	7.7	5.26	5.58	3.64	2.51	3.1	3.51	2.87	*		-	-
	NT2RP2003630	4.6	3.1	1.8	4.67	0.47	1.48	1.43	1.9	2.02			-	-
	NT2RP2003643	14.26	14.44	12.75	14.01	7.67	9.12	19.42	10.04	13.07			-	-
	NT2RP2003655	7.62	6.24	7.73	7.33	2.44	6.8	2.97	5.19	4.57	*		-	-
	NT2RP2003664	8.96	13.57	11.03	11.23	17.02	7.98	3.52	3.83	3.73	**		-	-
	NT2RP2003668	5.83	2.7	3.35	6.14	1.92	4.61	2.43	9.15	4.25			-	-
30	NT2RP2003687	2.45	2.75	3.32	4.63	0.64	2.77	0.71	2.3	0.91			-	-
	NT2RP2003691	2.86	0.41	1.55	4.29	1.06	2.07	1.69	2.35	1.51			-	-
	NT2RP2003702	7.99	4.44	8.03	9.77	1.89	6.56	5.26	5.52	3.42			-	-
	NT2RP2003704	6.11	9.87	8.33	7.33	6.55	3.79	6.43	2.95	5.24			-	-
	NT2RP2003706	7.36	9.13	9.09	6.95	3.88	3.8	6.16	3.16	4.56	*	*	-	-
35	NT2RP2003713	10.55	5.71	14.4	8.75	4.92	4.56	5.34	3.61	4.08			-	-
	NT2RP2003714	8.27	4.37	12.63	8.63	2.38	6.34	8.02	5.56	6.23			-	-
	NT2RP2003727	13.72	9.91	16.65	14.5	8.49	5.28	4.4	3.92	5.54	*		-	-
	NT2RP2003737	5.45	5.17	12.85	7.76	3.42	3.25	3.61	5.76	7.42			-	-
	NT2RP2003751	4.58	1.12	4.62	4.58	0.42	0.71	2.16	1.87	0.69			-	-
	NT2RP2003760	5.71	6.37	7.89	7.16	2.44	3.65	5.58	4.39	4.01			-	-
40	NT2RP2003764	4.38	3.82	3.93	5.42	1.13	2.52	3.39	1.74	2.45	*		-	-
	NT2RP2003769	20.81	10.06	18.85	16.88	9.37	7.83	5.73	10.32	7.17			-	-
	NT2RP2003770	46.73	23.49	36.27	27.58	17.68	15.16	13.53	17.82	25.92			-	-
	NT2RP2003777	15.17	10.4	15.63	9.4	5.35	5.3	5.51	8.22	8.17	*	*	-	-
	NT2RP2003781	85.09	53.2	80.23	44.9	32.89	44.6	88.34	75.84	75.38	*		-	-
	NT2RP2003785	11.62	18.04	20.61	13.78	15.2	6.96	6.32	9.84	5.9	*		-	-
45	NT2RP2003793	16.4	16.91	28.84	17.84	16.4	19.5	8.6	5.86	10.58	*		-	-
	NT2RP2003806	22.61	30.87	30.72	19.98	15.24	17.95	21.46	20.85	31.8	*		-	-
	NT2RP2003825	121.72	69.01	127.36	108.65	103.08	122.02	106.86	101.92	114.26			-	-
	NT2RP2003840	11.66	9.2	14.49	9.94	6.01	4.99	5.06	8.29	6.32	*		-	-
	NT2RP2003857	12.37	17.33	20.12	13.2	12.38	5.39	3.92	13.14	19.37			-	-
	NT2RP2003859	19.27	8.66	21.11	12.54	7.05	8.25	8.14	9.73	13.41			-	-
50	NT2RP2003871	24.21	21.74	19.35	11.95	9.6	10.67	5.81	8.41	8.75	**	**	-	-
	NT2RP2003876	10.53	11.98	18.66	19.02	25.1	11.05	7.68	10.36	8.8			-	-
	NT2RP2003878	8.32	9.1	10.32	8.36	3.76	3.6	4.02	3.95	3.32	**		-	-
	NT2RP2003885	6.08	8.46	6.77	5.72	4.33	2.2	4.11	3.32	4.21	*		-	-
	NT2RP2003888	16.47	22.78	20.73	12.55	8.77	11.94	7.99	8.27	7.33	*	**	-	-
	NT2RP2003902	21.99	10.54	20.36	16.59	8	10.58	8.28	15.68	15.89			-	-
55	NT2RP2003912	35.16	73.65	32.26	21.86	23.82	12.49	13.87	18.46	19.33			-	-
	NT2RP2003931	16.31	15.84	40.63	15.98	12.61	14.09	15.19	20.43	45.95			-	-
	NT2RP2003940	26.29	28.19	28.81	19.73	11.64	14	20.12	28.2	22.66	**		-	-
	NT2RP2003950	10.42	7.47	13.08	10.4	5.75	5.62	6.83	8.37	6.11			-	-

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Table 431

	NT2RP2003952	8.61	6.4	10.47	5.99	3.42	3.14	3.11	4	4.05	*	*	-	-
	NT2RP2003968	14.45	22.39	24.81	11.6	25.12	6.38	6.57	9.01	14.39	*	*	-	-
5	NT2RP2003976	33.5	36.02	32.11	28.15	26.29	22.25	25.49	23.11	18.45	*	**	-	-
	NT2RP2003981	10.38	7.73	15.47	7.98	3.66	7.9	3.93	9.3	6.45				
	NT2RP2003984	21.86	17.33	21.82	17.29	10	7.7	4.79	10.99	18.59				
	NT2RP2003986	29.04	20.99	42.5	17.22	10.08	14.95	20.31	27.16	19.47				
	NT2RP2003988	17.98	13.61	22.96	15.07	9.71	10.14	10.31	12.25	15.8				
	NT2RP2004013	76.9	66.49	68.74	48.94	44.57	34.09	28.41	25.31	32.75	**	**	-	-
10	NT2RP2004014	12.05	10.78	9.86	7.34	4.69	5.32	4.75	6.66	7.06	**	**	-	-
	NT2RP2004036	38.11	34.32	48.47	33.97	30.52	34.54	23.89	26.94	32.83				
	NT2RP2004041	15.68	9.6	13.65	12.24	6.88	6.29	9.46	7.39	4.47				
	NT2RP2004042	10.47	6.9	14.24	8.26	4.18	4.2	3.12	8.29	6.46				
	NT2RP2004049	50.08	29.35	58.86	54.03	47.21	47.08	23.48	30.4	35.04				
	NT2RP2004060	14.43	11.83	19.24	13.07	7.66	8.82	6.25	9.01	6.7	*	*	-	-
15	NT2RP2004066	9.22	7.65	15.12	7.14	3.11	3.37	2.62	3.51	3.15	*	*	-	-
	NT2RP2004069	13.07	11	19.34	9.29	5.59	3.82	4.85	6.14	4.78	*	*	-	-
	NT2RP2004076	7.23	8.97	8.94	6.15	5.2	2.62	3.55	3.66	4.01	*	*	-	-
	NT2RP2004080	16.76	19.32	21.22	10.81	7.94	4.93	7.71	6.49	6.54	**	**	-	-
	NT2RP2004081	12.13	9.06	12.95	7.67	4.89	5.2	4.76	5.29	3.41	*	**	-	-
20	NT2RP2004098	14.04	9.1	18.6	7.17	4.55	6.94	5.74	6.96	7.08				
	NT2RP2004108	15	13.48	22.62	10.06	6.21	6.99	5.4	7.73	10.17	*	*	-	-
	NT2RP2004124	8.21	9.75	17.19	8.66	5.64	4.42	4.13	6.1	2.63				
	NT2RP2004130	14.54	18.18	16.71	14.91	10.54	10.38	6.64	6.32	8.03	**	*	-	-
	NT2RP2004133	9.17	7.74	14.55	6.02	4.47	1.66	3.8	2.83	1.86	*	*	-	-
	NT2RP2004141	13.91	6.7	8.65	9.25	5.97	4.12	2.68	2.87	3.2	*	*	-	-
25	NT2RP2004142	20.24	20.66	23.15	12.58	8.99	0.11	7.76	8.1	8.83	*	**	-	-
	NT2RP2004152	12.94	17.34	28.22	13.04	12.79	7.85	8.66	8.13	4.02				
	NT2RP2004165	23.06	20.1	27.11	14.41	8.19	16.16	10.91	12.82	15.14	*	*	-	-
	NT2RP2004170	14.84	22.1	21.27	11.56	5.42	12.52	7.64	14.97	10.1	*	*	-	-
	NT2RP2004172	11.82	8.43	19.13	9.78	6.86	6.4	5.08	5.49	3.29				
30	NT2RP2004176	16.04	24.68	27.17	14.08	13.85	12.56	15.42	21.18	13.53				
	NT2RP2004179	11.06	11.88	18.99	6.12	3.68	3.62	3.12	4.46	3.04	*	*	-	-
	NT2RP2004187	10.62	14.3	17.05	10.83	6.49	6	6.3	3.3	5.65	*	*	-	-
	NT2RP2004190	11.44	13.08	11.65	11.65	16.98	5.99	14.27	4.91	8.09				
	NT2RP2004194	34.23	32.85	35.34	19.96	14.64	15.16	22.5	12.25	14.92	**	**	-	-
	NT2RP2004196	30.83	39.33	27.33	12.84	5.98	11.23	10.98	13.1	14.08	**	**	-	-
35	NT2RP2004205	29.01	29.84	37.62	20.1	10.4	15.74	17.25	16.98	24.08	*	*	-	-
	NT2RP2004207	8.99	13.88	16.49	8.05	7.02	4.72	8.6	7.78	25.16				
	NT2RP2004226	17.66	11.75	16.67	11.25	9.6	5.13	9.93	6.52	8.04	*	*	-	-
	NT2RP2004232	9.38	7.39	12.33	6.45	7.37	3.57	6.49	3.42	8.98				
	NT2RP2004239	9.12	12.33	10.22	7.52	5.19	3.55	2.71	5.07	3.29	*	**	-	-
	NT2RP2004240	34.67	45.84	33.56	20.39	18.64	6.67	14.35	6.97	4.81	*	**	-	-
40	NT2RP2004242	15.64	15.83	16.65	14.76	9.29	9.76	10.22	6.01	6.98	**	*	-	-
	NT2RP2004245	7.49	8.21	10.79	7.33	2.04	4.45	4.33	4.59	4.95	*	*	-	-
	NT2RP2004270	62.73	47.21	68.41	46.4	33.04	45.75	50.52	75.49	70.49				
	NT2RP2004300	12.51	8.53	13.1	8.54	9.07	5.04	6.79	9.38	7.79				
	NT2RP2004304	16.04	25.81	28.38	10.74	8.89	6.86	7.57	8.7	9.4	*	*	-	-
	NT2RP2004313	5.32	5.55	8.05	4.79	1.11	1.27	2.98	2.46	2.35	*	*	-	-
45	NT2RP2004316	7.59	19.66	19.22	7.37	4.16	2.63	3.4	2.3	5.68	*	*	-	-
	NT2RP2004321	11.35	10.01	12.72	6.18	1.74	2.16	3.62	2.37	4.34	**	**	-	-
	NT2RP2004336	6.56	6.01	5.01	7.15	3.83	3.55	3.86	1.85	3.64	*	*	-	-
	NT2RP2004339	86.87	54.65	64.97	50.21	27.02	70.75	73.53	111.22	98.32				
	NT2RP2004347	9.56	12.29	15.81	9.78	3.94	5.75	4.47	6.18	9.27				
50	NT2RP2004365	17.82	15.18	19.5	11.98	7.62	12.3	9.63	15.21	13.78	*	*	-	-
	NT2RP2004366	16.43	16.15	23.6	8.67	8.61	4.88	6.23	5.81	4.59	*	**	-	-
	NT2RP2004373	6.71	10.58	9.59	7.66	3.53	5.17	5.46	3.22	3.29	*	*	-	-
	NT2RP2004375	12.26	11.21	11.74	7.26	2.71	4.58	3.35	3.56	4.51	**	**	-	-
	NT2RP2004389	63.47	77.52	81.72	36.96	16.48	21.89	34.46	29.81	18.56	**	**	-	-
	NT2RP2004392	11.31	16.36	12.26	9.91	2.21	4.95	5.82	4.38	4.02	*	**	-	-
55	NT2RP2004396	57.13	31.73	43.78	20.38	16.25	19.24	10.86	16.27	14.58	*	*	-	-
	NT2RP2004399	13.42	9.2	11.06	9.69	3.89	7.39	5.67	7.43	7.76	*	*	-	-
	NT2RP2004400	25.77	19.74	26.11	15.91	12.56	15.11	9.21	12.21	10.01	*	**	-	-
	NT2RP2004404	10.29	9.25	9.33	9.9	4.17	8.44	7.31	8.61	9.43	*	*	-	-
	NT2RP2004404	142.91	126.47	123.47	87.01	85.43	109.26	171.94	127.81	174.94	*	*	-	-

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Table 432

	NT2RP2004410	39.53	65.74	46.52	39.11	16.74	16.36	21.28	23.23	25.45	*	-
	NT2RP2004412	14.74	10.36	20.72	26.06	1.96	8.17	8.89	4.91	6.36		
5	NT2RP2004414	8.26	7	7.21	7.75	3.36	2.32	8.71	6.3	5.47		
	NT2RP2004425	10.2	6.28	19.09	7.43	2.9	4.39	7.1	5.14	4.24		
	NT2RP2004447	7.9	4.2	15.6	7.23	1.76	4.51	4.43	8.04	6.17		
	NT2RP2004463	53.44	48.94	45.23	51.07	39.96	24.66	38.74	19.02	17.11	*	-
	NT2RP2004476	18.45	12.59	23.94	14.93	16.73	11.7	16.21	16.49	14.59		
	NT2RP2004488	10.21	10.37	13.58	8.53	5.46	7.65	8.97	6.18	4.15	*	*
10	NT2RP2004490	6.88	9.48	11.96	10.41	4.06	3.06	6.4	5.15	3.37		
	NT2RP2004495	59.84	40.86	52.11	47.08	29.44	39.52	53.9	45.74	40.44		
	NT2RP2004512	17.42	8.07	18.38	11.03	4.08	6.19	1.75	5.77	3.87	*	-
	NT2RP2004523	26.61	22.99	26.09	20.55	9.56	18.73	12.96	22.93	30.09		
	NT2RP2004524	21.22	18.85	29.36	17.14	12.55	10.77	11.27	10.59	14.51	*	-
	NT2RP2004535	39.58	17.04	37.57	26.29	26.05	14.38	14.91	28.86	19.32		
15	NT2RP2004538	145.51	113.79	134.59	95.27	89.81	81.41	118.33	103.7	132.33	*	-
	NT2RP2004548	21.33	25.87	20.88	16.6	11.36	9.17	14.62	15.2	15	*	**
	NT2RP2004551	8.55	11.05	18.95	8.38	5.63	4.59	5.77	5.04	6.54		
	NT2RP2004556	107.44	116.09	115.34	100.64	83.01	68.21	138.61	66.34	73.2	*	-
	NT2RP2004568	25.54	15.99	32.04	18.77	7.42	18.63	9.21	19.06	44.48		
20	NT2RP2004580	28.48	22.84	30.46	23.04	12.01	15.3	24.34	30.63	24.49		
	NT2RP2004585	104.19	75.97	102.59	102.16	96.71	82.97	64.51	65.78	63.06	*	-
	NT2RP2004587	7.64	7.71	10.73	6.38	2.94	4.03	2.08	3.66	11.64	*	-
	NT2RP2004594	9.49	13.7	13.53	10.94	10.06	5.96	7.18	7.17	14.25		
	NT2RP2004600	11.79	11.86	12.42	9.8	6.39	8.89	9.84	7.14	9.81	*	*
	NT2RP2004602	16.85	24.33	21.89	13.29	12.49	8.02	12.27	7.59	7.04	*	*
25	NT2RP2004606	282.85	252.35	268.41	181.43	249.55	245.26	257.06	189.04	158.13		
	NT2RP2004614	9.31	7.04	11.06	6.07	2.67	4.48	3.52	3.61	6.4	*	*
	NT2RP2004648	12.5	37.87	41.62	14.38	8.31	11.65	10.13	8.24	22.59		
	NT2RP2004655	27.02	40.5	41.28	26.01	23.69	13	4.9	10	13.87	**	-
	NT2RP2004664	12.3	12.14	15.06	9.64	6.17	5.52	2.65	4.39	2.54	*	**
	NT2RP2004670	9.81	11.79	9.6	6.17	5.86	2.45	3.26	4.14	2.42	*	**
30	NT2RP2004675	22.26	31.4	25.45	19.55	10.99	11.73	17.4	17	31.58	*	-
	NT2RP2004681	11.82	17.49	14.89	8.26	5.82	3.58	5.62	7.61	5.68	*	**
	NT2RP2004689	5.34	26.14	16.38	15.38	9.9	10.44	10.84	15.98	14.64		
	NT2RP2004709	38.28	22.19	35.75	22.32	11.28	19.42	7.33	20.31	16.27		
	NT2RP2004710	23.78	32.41	33.69	19.19	16.47	14	10.16	17.13	21.44	*	*
35	NT2RP2004721	16.3	9.83	18.51	7.64	2.48	4.31	3.84	6.3	2.86	*	*
	NT2RP2004736	12.51	12.2	14.69	12.94	8.12	6.27	5.93	10.36	6.34	*	-
	NT2RP2004743	18.86	18.19	16.11	11.52	9.54	6.56	6.31	8.72	9.61	**	**
	NT2RP2004750	59.2	56.12	53.52	47.6	43.74	38.38	59.22	63.07	62.81	**	-
	NT2RP2004755	27.3	33.26	34.09	17.59	21.76	19.12	17.05	12.23	8.96	**	**
	NT2RP2004767	16.81	19.28	18.07	14.61	10.15	10.32	11.83	8.67	9.96	*	**
	NT2RP2004768	39.27	17.22	28.44	49.02	23.23	30.46	23.63	20.93	17.76		
40	NT2RP2004775	10.4	6.35	15.81	7.59	3.37	4.94	1.86	3.35	3.03	*	-
	NT2RP2004791	35.3	37.93	43.25	33.95	20.1	16.04	17.4	29.11	27.1	*	-
	NT2RP2004794	54.46	52.25	59.56	37.23	24.39	18.04	14.21	17.04	17.83	*	-
	NT2RP2004795	16.82	13.04	16.28	12.97	8.52	3.96	6.33	6.26	8.64	**	-
	NT2RP2004799	16.76	14.17	14.52	9.03	7.47	5.55	2.73	2.76	3.58	**	**
45	NT2RP2004802	42.99	46.43	41.16	46.78	39.32	30.76	28.53	29.92	38.26	*	-
	NT2RP2004810	18.3	18.68	17.35	9.03	6.57	4.19	8.85	4.21	4.39	**	**
	NT2RP2004816	30.61	34.82	43.2	16.85	15.68	3.1	5.7	11.84	0.57	*	**
	NT2RP2004837	55.01	32.88	59.21	31.78	19.82	27.08	12.99	11.53	9.41	*	-
	NT2RP2004841	12.28	19.6	17.04	13.83	8.03	5.66	4.26	5.92	8.44	*	-
	NT2RP2004847	56	45.24	59.59	31.54	30.59	31.44	43.02	39.63	29.66	**	-
50	NT2RP2004861	6.61	6.78	10.74	6.21	2.52	2.33	3.42	5.23	3.33		
	NT2RP2004897	8.06	8.52	10.02	7.86	4.8	3.34	2.33	3.07	4.66	**	-
	NT2RP2004932	11.96	10.46	13.81	9.34	4.73	6.48	4.87	3.86	6	*	**
	NT2RP2004933	6.78	7.42	14.62	6.21	3.1	2.23	3.41	1.97	1.54	*	-
	NT2RP2004936	9.66	18.67	21.72	10.34	4.39	7.29	2.62	3.9	3.25	*	-
55	NT2RP2004951	8.57	7.11	15.72	9.26	2.32	5.42	3.11	6.13	4.04		
	NT2RP2004958	12.5	13.69	22.18	6.53	5.09	6.63	3.92	5.67	5.43	*	*
	NT2RP2004961	15.97	14.64	23.99	12.05	7.35	8.71	10.28	8.72	8.04	*	-
	NT2RP2004962	15.99	15.58	20.13	13.9	10.21	9.93	9.78	10.66	9.69	*	-
	NT2RP2004966	6.94	8.72	7.55	5.31	3.88	2.7	4.34	2.81	2.89	*	**

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Table 433

	NT2RP2004967	18.8	14.08	15.99	13.12	5.04	9.98	11.43	12.91	9.85	*	-
	NT2RP2004974	8.02	8.78	7.74	5.74	3.27	3.73	5.44	2.35	2.1	**	*
	NT2RP2004978	14.12	27.31	13.7	11.96	4.65	6.79	4.16	9.57	4.35	*	-
5	NT2RP2004982	4.88	6.54	10.22	4.28	1.48	0.85	1.99	1	1.83	*	-
	NT2RP2004985	209.85	195.75	215.75	166.58	153.94	208.41	198.37	224.84	192.82		
	NT2RP2004999	16.04	12.97	26.42	17.44	8.41	10.32	9.65	18.31	9.11		
	NT2RP2005000	9.18	10.25	11.07	6.99	2.87	3.26	5.46	4.95	3.42	*	**
	NT2RP2005001	18.08	20.79	40.06	15.62	11.69	13.08	12.25	15.19	13.27		
10	NT2RP2005003	15.88	14.42	15.05	11.32	5.53	6.52	11.83	11.19	8.75	*	*
	NT2RP2005012	40.61	57.66	43.61	20.05	11.76	16.65	21.02	13.16	20.53	**	**
	NT2RP2005018	6.29	10.32	12.32	7.2	3.34	4.91	3.54	5.22	4.18	*	-
	NT2RP2005020	138.98	109.02	105.29	97.72	59.61	79.54	117.66	175.16	138.64		
	NT2RP2005022	8.77	8.01	12.34	8.19	7.74	5.07	4.96	7.16	9.74		
	NT2RP2005027	53.46	62.9	51.33	58.43	50.24	56.5	33.74	38.11	31.82	**	-
15	NT2RP2005031	6.85	8.81	9.58	5.73	4.02	3.36	3.46	3.48	3.14	*	**
	NT2RP2005037	16.82	18.46	19.47	6.47	4.36	2.93	2.65	3.66	6.14	**	**
	NT2RP2005038	6.96	8.98	11.09	7.2	2.46	3.49	4.34	2.45	1.1	*	-
	NT2RP2005043	39.21	28.46	29.89	31.24	22.21	43.14	32.34	46.11	37.29		
	NT2RP2005069	79.3	47.14	64.37	36.64	18.08	20.34	23.96	33.08	29.72	*	*
	NT2RP2005073	67.78	54.66	62.54	70.16	48.08	81.7	55.95	55.76	57.19		
20	NT2RP2005097	10.25	7.51	14.59	6.49	1.21	4.7	3.75	2.8	2.35	*	-
	NT2RP2005108	13.57	11.63	13.11	6.87	5.69	6.68	5.31	6.56	5.73	**	**
	NT2RP2005116	11.75	10.87	12.14	10.24	4.17	4.29	7.43	5.88	6.2	**	-
	NT2RP2005126	21.43	28.84	28.25	14.77	6.89	5.64	7.77	5.68	5.93	*	**
	NT2RP2005135	10.21	11.92	11.29	12.06	3.02	7.4	9.29	7.72	6.92	*	-
25	NT2RP2005139	4.47	5.9	6.41	6.94	3.02	9.46	4.16	4.52	4.09		
	NT2RP2005140	10.93	7.52	7.44	7.58	3.55	5.44	3	4.22	2.26	*	-
	NT2RP2005144	13.73	10.54	13.89	8.29	4.49	7.83	1.84	3.98	2.4	*	**
	NT2RP2005147	22.69	15.06	21.74	11.07	5.61	11.36	5.53	13.64	8.82	*	*
	NT2RP2005148	19.34	14.98	12.3	16.32	7.5	14.47	18.68	18.99	24		
	NT2RP2005159	9.52	7.06	9.83	13.34	5.14	7.92	4.36	3.56	6.05	*	-
30	NT2RP2005162	14.54	12.5	16.31	14.53	7.94	8	8.72	9.34	7.02	**	-
	NT2RP2005163	25.5	37.52	33.86	15.82	13.92	18.66	24.95	23.28	21.32	*	-
	NT2RP2005168	10.58	6.62	14.16	11.05	6.89	4.43	4.83	6.74	4.36		
	NT2RP2005181	4.05	2.99	8.75	6.74	2.11	1.29	1.74	3.19	2.03		
	NT2RP2005204	14.87	10.24	20.73	15.12	7.06	10.51	11.01	6.88	10.24		
	NT2RP2005219	24.24	19.15	32.19	26.01	12.29	15.28	21.03	18.69	23.06		
35	NT2RP2005227	12.24	9.75	17.91	17.67	5.27	7.45	11.51	12.06	11.25		
	NT2RP2005237	103.35	89.54	103.29	128.64	70.44	96.83	81.16	75.94	83.42	*	-
	NT2RP2005239	4.86	6.22	9.52	8.57	2.23	3.55	3.5	4.01	4.35		
	NT2RP2005247	22.45	26.01	32.27	32.43	14.24	19.04	34.79	31.96	33.52		
	NT2RP2005254	36.5	15.86	25.1	17.04	11.36	15.24	5.51	13.65	13.69		
40	NT2RP2005270	25.5	13.21	29.5	13.51	9.93	13.53	11.24	14.21	22.67		
	NT2RP2005276	40.6	21.43	40.17	20.18	14.43	16.86	10.58	8.43	8.36	*	-
	NT2RP2005287	16.9	10.22	25.14	13.6	9.12	7.29	8.33	9.76	8.8		
	NT2RP2005288	6.35	8.09	8.85	7.18	3.2	3.43	4.54	4.39	3.3	*	-
	NT2RP2005289	19.76	15.26	21.43	14.2	10.57	10.92	15.53	14.93	15.73	*	-
	NT2RP2005293	9.79	11.07	10.95	8.57	5.47	3.14	6.98	5.79	5.74	*	**
45	NT2RP2005315	15.84	21	21.65	20.97	8.72	12.4	13.48	9.21	11.44	*	-
	NT2RP2005322	33.55	31.7	65.28	25.82	25.53	26.43	14.38	22.11	31.46		
	NT2RP2005325	54.2	44	55.99	38.68	30.92	29.07	18.94	27.07	30.65	*	**
	NT2RP2005336	20.36	12.98	27.96	11.35	7.87	9.01	10.99	13.9	14.17		
	NT2RP2005343	12.61	22.98	14.15	9.9	5.77	8.7	7.81	10.19	10.12		
50	NT2RP2005344	6.04	8.8	10.41	8.82	3.18	3.71	4.76	3.86	3.88	*	-
	NT2RP2005347	7.59	13.3	8.99	7.33	4.35	4.03	4.9	3.27	3.77	*	-
	NT2RP2005354	41.58	40.59	43.7	31.3	21.57	29.41	26.2	24.6	22.64	**	**
	NT2RP2005358	43.39	32.77	43.03	61.06	32.41	50.49	63.9	54.2	58.54	*	+
	NT2RP2005360	11.79	10	18.74	11.01	6.71	7.24	3.72	6.21	9.76		
	NT2RP2005378	29.24	21.46	29.8	11.99	9.12	7.48	6.73	9.68	15.33	**	*
	NT2RP2005391	8.87	18.64	25.48	15.21	9.76	9	4.05	7.34	6.04		
55	NT2RP2005393	18.88	11.72	17.99	12.44	7.52	10.75	12.61	18.43	12.16		
	NT2RP2005407	7.79	10.99	12.03	9.14	5.76	6.4	4.56	6.12	6.26	*	-
	NT2RP2005419	14.03	13.17	13.95	13.78	13.3	12.37	11.42	9.28	10.02	**	-
	NT2RP2005425	22.13	23.63	29.77	16.49	17.86	16.5	26.07	23.18	23.95	*	-

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Table 434

	NT2RP2005429	20.77	21.25	24.75	28.87	19.9	22.9	31.5	41.11	27.5			
	NT2RP2005436	21.72	21.01	36.27	15.82	10.49	11.17	6.19	10.76	15.31			
	NT2RP2005441	12.34	10.42	16.43	6.82	3.95	2.88	3.88	5.58	7.88	*	*	-
5	NT2RP2005442	100.99	76.34	97.05	85.22	107.34	64.16	56.06	96.44	76.81			
	NT2RP2005444	44.56	42.84	50.52	45	41.48	37.39	33.32	34.33	40.3	*	*	-
	NT2RP2005453	6.3	5.27	7.3	6.26	2.81	2.81	2.27	2.79	2.65	**	*	-
	NT2RP2005457	65.08	106.4	103.3	51.25	79.76	59.93	40.37	56.9	47.82	*	*	-
	NT2RP2005458	19.63	18.76	13.48	12.24	12.61	6.33	8.23	12.39	11.01	*	*	-
10	NT2RP2005463	26.71	23.66	25.36	21.35	13.39	12.75	11.08	11.67	8.93	*	**	-
	NT2RP2005464	28.8	25.9	35.07	16.26	12.23	8.38	4.05	11.36	13.81	**	**	-
	NT2RP2005465	8.44	13.41	18.06	10.55	9.11	6.34	5.69	6.77	5.88			
	NT2RP2005472	156.47	127.25	179.85	146.2	122.26	139.88	141.98	194.05	159			
	NT2RP2005476	18.49	17.23	18.61	16.08	8.51	7.62	10.76	9.58	6.82	**	*	-
	NT2RP2005490	38.19	48.01	41.98	41.4	60.4	46.27	36.8	25.85	27.98	*	*	-
15	NT2RP2005491	79.97	62.21	87.46	43.7	46.69	33.15	42.26	41.55	39.38	*	**	-
	NT2RP2005495	8.67	12.67	12.73	8.05	5.23	3.12	3.29	2.22	4.63	*	**	-
	NT2RP2005496	40.82	33.68	40.13	35.53	16.36	22.99	49.27	41.88	52.93			
	NT2RP2005498	14.64	10.07	20.28	8.15	3.71	0.94	3.15	5.06	7.24	*	*	-
	NT2RP2005501	15.01	11.26	15.06	10.4	6.02	5.78	5.37	7.88	6.8	*	**	-
20	NT2RP2005506	385.46	291.76	402.21	469.63	426.17	208.66	248.04	333.44	241.6			
	NT2RP2005509	12.93	15.67	24.29	8.78	9.8	9.01	11.69	14.68	14.73			
	NT2RP2005514	15.12	18.77	16.43	9.09	7.1	7.44	5.07	6.13	3.95	**	**	-
	NT2RP2005520	125.71	88	119.54	107.31	84.59	104.73	102.45	122.23	104.75			
	NT2RP2005525	11.61	19.18	16.45	11.91	8.22	5.77	3.77	4.63	4.84	**	*	-
	NT2RP2005531	6.49	2.54	4.37	5.65	2.65	0.74	1.72	1.38	1.4			
25	NT2RP2005535	28.78	24.33	27.3	18.42	7.97	16.95	13.78	20.87	16.38	*	*	-
	NT2RP2005539	7.33	11.94	18.75	8.51	6.39	4.26	3.51	3.63	4.88			
	NT2RP2005540	16.33	11.75	18.94	9.77	17.11	5.41	9.79	8.14	4.41	*	*	-
	NT2RP2005541	14.69	11.15	19.91	13.02	7.16	8.12	7.95	8.57	7	*	*	-
	NT2RP2005549	11.12	11.63	18.04	9.08	7.83	5.49	4.23	4.44	5.21	*	*	-
	NT2RP2005555	16.74	21.24	18.63	10.59	10.43	7.67	9.05	5.08	3.67	**	**	-
30	NT2RP2005557	15.1	14.02	12.36	10.06	7.31	4.94	4.63	4.36	4.73	*	**	-
	NT2RP2005581	28.08	26.29	29.21	26.59	10.92	19.41	31.86	21.24	23.29			
	NT2RP2005586	16.13	21.05	17.82	8.84	4.94	6.39	4.6	7.07	6.9	**	**	-
	NT2RP2005597	6.89	6.97	9.77	7.01	1.89	3.66	2.71	4.02	1.82	*	*	-
	NT2RP2005600	10.61	7.34	12.5	8.41	8.29	5.16	5.14	5.97	3.47	*	*	-
35	NT2RP2005605	53.68	52.91	55.5	30.27	27.97	29.06	25.09	21.21	26.25	**	**	-
	NT2RP2005614	9.49	10.07	16.9	6.5	3.69	4.19	2.85	3.64	2.63	*	*	-
	NT2RP2005620	17.66	10.99	8.05	7.1	2.87	3.18	7.89	3.09	3.37			
	NT2RP2005622	16.16	16.55	15.71	9.98	5.85	5.98	5.01	2.43	3.54	**	**	-
	NT2RP2005632	24.79	21.59	16.99	24.01	11.37	16.72	22.78	10.85	12.69			
	NT2RP2005635	41.82	31.3	47.35	47.22	30.84	66.01	30.58	31.82	30.82			
40	NT2RP2005637	8.32	23.19	12.21	8.57	5.9	4.47	3.6	7.75	5.54			
	NT2RP2005640	15.46	12.6	16.31	14.33	9.36	13.4	14.45	17.32	12.67			
	NT2RP2005645	23.93	18.08	21.54	10.6	8.02	9.84	11.24	9.09	9.16	**	**	-
	NT2RP2005651	27.47	30.93	34.21	15.98	10.8	18.12	23.48	20.74	24.88	**	*	-
	NT2RP2005654	13.13	10.24	14.43	6.36	4.26	2.41	3.56	3.27	5.28	**	**	-
	NT2RP2005666	12.61	72.48	13.27	7.56	5.9	4.42	7.43	6.32	9.59			
45	NT2RP2005669	15.23	15	15.44	12.86	8.17	11.55	8.81	7.49	8.17	*	**	-
	NT2RP2005670	7.59	11.17	16.69	7.09	6.37	6.24	3.98	5.41	8.38			
	NT2RP2005671	8.66	9.38	12.5	6.17	4.27	6.41	3.39	7.42	4.35	*	*	-
	NT2RP2005675	53.41	58.69	56.21	73.47	47.08	88.08	46.13	47.46	45.27	**	*	-
	NT2RP2005683	12.5	14.86	22.54	12.03	8.9	11.13	12.51	11.13	11			
	NT2RP2005690	7.16	9.78	9.15	7.31	2.58	3.76	6.01	4.75	5.81	*	*	-
50	NT2RP2005694	13.45	13.78	12.27	8.68	4.9	4.46	6.63	6.81	8.01	**	**	-
	NT2RP2005701	21.29	27.54	24.8	13.54	7.14	7.23	9.96	8.67	7.38	**	**	-
	NT2RP2005712	5.67	6.5	6.73	7.41	2.31	3.04	4.59	2.86	2.66	*	*	-
	NT2RP2005719	17.92	12.64	12.02	8.92	5.92	13.08	4.64	11.29	9.06			
	NT2RP2005722	24.17	15.94	25.68	22.5	8.47	9.89	8.38	12.95	9.48	*	*	-
	NT2RP2005723	11.76	19.91	11.37	8.9	4.43	7.12	5.8	6.31	6.59	*	*	-
55	NT2RP2005726	13.16	8.51	18.51	13.17	7.93	10.58	7.85	8.96	10.35			
	NT2RP2005729	20.35	17.21	20.34	11.64	9.52	5.78	12.25	8.44	10.44	**	**	-
	NT2RP2005731	4.25	2.53	4.11	5.17	0	0.69	1.06	1.65	0.86	*	*	-
	NT2RP2005732	54.72	53.14	65.72	91.69	67.12	83.97	67.17	50.47	67.53	*	+	-

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Table 435

	NT2RP2005737	61.08	46.51	54.73	57.66	30.52	54.91	80.55	70.19	69.81	*	+
	NT2RP2005741	8.17	4.22	11.68	8.13	3	5.42	3.62	4.85	3.95		
	NT2RP2005748	8.36	5.27	13.52	8.19	3.71	6.33	3.46	4.51	7.44		
5	NT2RP2005752	31.75	22.62	38.43	14.99	13.75	18.04	15.51	16.74	18.45	*	*
	NT2RP2005753	34.44	30.95	46.77	33.24	26.02	18.11	26.19	25.32	15.55		
	NT2RP2005763	8.78	7.62	12.88	6.76	3.85	3.68	4.32	5.6	4.17	*	-
	NT2RP2005767	8.89	8.69	15.86	7.42	5.16	5.67	6.13	4.89	5.16		
	NT2RP2005773	53.73	61.68	69.19	40.66	32.98	33.21	37.38	30.92	21.66	**	**
10	NT2RP2005774	13.75	12.5	18.48	16.31	7.06	7.63	18.33	17.56	17.06		
	NT2RP2005775	12.13	7.53	22.24	13.73	4.82	6.66	4.04	6.6	5.74		
	NT2RP2005781	39.68	23.61	38.05	24.73	22.45	22.65	9.91	16.91	23.06		
	NT2RP2005784	30.34	20	41.77	17.54	13.38	14.34	11.13	13.26	15.12		
	NT2RP2005789	16.92	16.55	24.71	17.16	13.64	7.39	8.95	14.02	9.78		
	NT2RP2005799	11.23	8.75	9.48	10.01	3.28	4.24	3.37	6.03	3.88	**	-
15	NT2RP2005804	106.7	97.93	105.55	76.62	70.98	67.98	110.4	84.7	108.91	**	-
	NT2RP2005812	6.56	9.52	8.36	6.62	4.2	4.89	5.32	2.9	2.58	*	-
	NT2RP2005815	2.76	4.98	5.71	6.34	2.94	2.66	4.39	4.52	4.97		
	NT2RP2005835	26.87	25.04	37.02	18.31	16.79	16.79	10.34	14.43	39.55	*	-
	NT2RP2005841	22.25	27.56	27.52	20.49	14.43	16.92	11.4	11.65	19.51	*	-
20	NT2RP2005853	18.13	15.89	21.67	12.41	10.18	1.04	9.88	13.51	11.3	*	-
	NT2RP2005857	11.03	8.75	10.83	7.42	4.51	1.32	4.21	5.92	5.5	*	**
	NT2RP2005859	12.15	11.97	15.23	11.24	7.93	4.86	8.29	8.94	6.43	*	-
	NT2RP2005860	0.96	5.77	2.68	4.74	2.31	1.31	1.34	1.77	1.13		
	NT2RP2005863	8.01	8.99	7.06	7.45	6.66	5.32	7.67	5.36	4.12		
	NT2RP2005868	5.66	10.09	8.76	11.28	4.39	6.75	7.63	5.42	5.14		
25	NT2RP2005876	29.94	9.36	44.21	25.04	19.27	15.81	14.52	17.33	37.26		
	NT2RP2005878	17.4	21.07	28.07	15.86	10.5	10.77	9.96	17.05	21.58		
	NT2RP2005883	9.58	9.62	13.3	8.93	6.54	7.61	3.43	11.45	8.28		
	NT2RP2005886	109.48	86.27	131.02	108.7	95.74	145.77	77.39	72	86.69		
	NT2RP2005887	12.65	18.34	15.15	9.59	5.47	2.19	3.8	5.68	5.07	*	**
	NT2RP2005890	11.6	13.15	14.84	6.76	5.32	5.53	4.7	5.77	4.32	**	**
30	NT2RP2005901	11.96	15.27	14.95	10.18	6.55	8.12	6.42	5	5.8	*	**
	NT2RP2005902	4.82	5.49	5.62	9.24	3.69	5.72	4.9	8.33	5.18		
	NT2RP2005908	24.41	23.56	59.06	23.37	17.17	15.35	18.41	25.09	27.9		
	NT2RP2005927	7.88	6.48	15.44	8.31	4.33	4.46	3.45	5.76	4.29		
	NT2RP2005933	14.92	15.67	28.13	12.37	6.74	6	4	6.32	4.28	*	-
	NT2RP2005941	10.69	8.58	13.22	7.84	3.9	3.96	2.9	4.82	2.65	*	**
35	NT2RP2005942	10.35	10.52	11.7	8.52	4	3.46	3.66	4.6	2.9	*	**
	NT2RP2005946	8.12	19.6	14.91	5.77	6.58	2.97	4.94	4.86	6.09		
	NT2RP2005970	73.5	72.19	81.01	50.77	49.15	40.53	67.44	62.72	62.64	**	*
	NT2RP2005980	7.01	5.07	5.9	6.68	2.11	2.14	3.31	3.86	4.51	*	-
	NT2RP2005994	12.99	9.14	13.53	7.59	4.09	0.3	2.32	3.71	4.52	*	**
40	NT2RP2006004	7.54	4.47	13.06	6.53	2.59	2.1	2.72	2.9	3.13		
	NT2RP2006013	11.06	6.58	20.3	11.12	5.96	2.47	2.76	11.94	3.04		
	NT2RP2006023	79.4	60.83	74.67	51.53	34.64	38.07	64.39	76.12	79.93	*	-
	NT2RP2006028	23.13	26.87	22.92	16.89	12.58	6.73	6.52	8.45	15.41	*	**
	NT2RP2006038	4.35	4.75	6.83	4.07	1.31	0.83	1.09	0.16	1.4	*	**
	NT2RP2006042	15.45	13.74	13.53	9.24	8.86	3.55	5.34	6.22	7.22	*	**
45	NT2RP2006043	17.81	13.76	15.29	13.7	7.47	8.55	9.41	5.9	6.89	**	-
	NT2RP2006052	12.36	8.55	16.5	5.69	3	4.31	2.78	3.7	3.31	*	-
	NT2RP2006057	7	6.58	13.05	6.99	3.77	3.67	1.75	3.57	2.95	*	-
	NT2RP2006064	31.45	32.66	33.8	25.4	15.66	8.71	6.36	7.35	7.36	*	**
	NT2RP2006068	7.85	6.5	16.27	7.3	3.64	3.64	2.88	4.02	3.43		
	NT2RP2006069	10.49	8.04	9.64	6.75	2.89	1.65	2.28	1.16	1.94	*	**
50	NT2RP2006071	12.09	22.31	12.61	10.26	7.27	0.85	3.44	3.17	3.04	*	-
	NT2RP2006090	10.61	10.59	22.59	7.62	4.75	0.57	5.24	4.28	5.3		
	NT2RP2006092	15.25	7.07	12.08	13.1	8.69	10.62	13.15	8.79	8.66		
	NT2RP2006097	52.21	101.2	64.35	48.63	48.31	38.97	25.59	53.43	52.7		
	NT2RP2006098	13.67	12.41	21.3	14.85	6.15	8.49	5.13	8.68	3.6	*	-
55	NT2RP2006099	65.92	60.33	80.23	76.5	49.76	0.24	73.49	73.17	78.2		
	NT2RP2006100	14.09	12.17	17.63	9.6	8.02	0.77	4.01	5.07	4.89	**	-
	NT2RP2006103	6.26	4.22	7.72	5.83	3.58	2.06	2.74	2.72	2.55	*	-
	NT2RP2006106	48	36	55.68	34.38	35.82	35.56	24.01	21.59	18.79	*	-
	NT2RP2006127	6.5	4.86	5.96	5.76	1.93	3.45	3.78	1.37	2.06	*	-

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	NT2RP2006134	9.57	6.53	12.45	11.76	2.26	6.54	9.28	6.55	5.96			
	NT2RP2006141	13.6	10.51	20.75	11.91	8.44	5.24	5.17	8.6	15.73			
5	NT2RP2006166	43.39	37.58	47.62	23.75	15.94	0.88	44.65	56.53	70.7	*	-	
	NT2RP2006176	17.92	13.68	20.98	13.87	7.31	8.84	7.42	10.41	8.82	*	-	
	NT2RP2006181	4.75	8.83	6.23	3.92	1.81	1.35	3.97	2.81	2.8	*	-	
	NT2RP2006184	64.52	54.32	63.63	42.14	32.28	42.22	63.72	47.39	43.75	**	-	
	NT2RP2006186	8.19	11.92	9.4	6.19	2.49	2.83	2.18	2.13	1.87	*	**	-
	NT2RP2006196	22.53	23.16	21.9	14.52	7.82	10.37	16.26	11.79	10.32	**	**	-
10	NT2RP2006199	9.01	9.11	8.26	8.72	4.43	4.65	6.19	4.21	5.05	**	-	
	NT2RP2006200	7.28	4.32	9.53	5.05	3.47	3.37	3.59	4.46	2.65			
	NT2RP2006210	90.78	69.8	53.22	55.44	37.83	25.49	20.22	40.51	30.76	*	-	
	NT2RP2006219	11.28	20.39	17.51	8.1	14.35	6.63	11.34	9.44	19.6			
	NT2RP2006224	12.75	19.13	21.38	12.72	10.81	3.64	17.87	16.61	1.85			
	NT2RP2006237	7.47	20.77	9.96	5.08	2.48	0.88	3	2.56	0.6			
15	NT2RP2006238	10.52	14.31	12.03	6.19	1.38	2.03	2.55	2.62	2.66	**	**	-
	NT2RP2006258	10.05	20.38	11.9	6.71	3.4	2.58	5.8	4.54	6.64	*	-	
	NT2RP2006261	8.38	9.18	5.31	9.6	2.51	4.78	2.42	4.07	4.58	*	-	
	NT2RP2006269	17.03	14.29	15.32	11	5.59	7.26	3.86	12.06	5.85	*	*	-
	NT2RP2006275	46.12	39	46.05	70.83	38.96	80.2	37.5	48.02	38.3	*	*	-
20	NT2RP2006282	18.4	26.43	24.55	13.47	12.52	6.62	5.66	6.21	6.64	*	**	-
	NT2RP2006302	17.18	26.6	32.5	13.26	6.56	8.01	5.28	4.17	5.65	*	*	-
	NT2RP2006312	31.59	23.04	41.51	9.42	5.96	4.21	6.1	4.79	7.53	*	**	-
	NT2RP2006320	41.28	41.71	36.93	24.86	13.12	15.23	28.98	37.1	32.63	**	-	
	NT2RP2006321	10.41	8.33	12.86	10.26	2.43	5.6	7.6	9.6	8.78			
	NT2RP2006323	7.58	5.4	4.29	6.62	1.35	3.01	7.41	4.95	4.91			
25	NT2RP2006333	5.03	7.52	4.99	6.18	1.44	5.34	2.1	4.81	3.82			
	NT2RP2006334	7.94	8.71	7.64	8.5	4.46	6.47	2.3	4.34	3.32	**	-	
	NT2RP2006338	12.7	9.34	36.56	7.32	2.93	4.16	2.16	2.04	3.64			
	NT2RP2006339	6.41	4.31	4.61	6.37	3.36	3.67	2.31	2.9	2.66	*	-	
	NT2RP2006355	6.78	12.38	3.94	6.81	1.66	2.59	2.74	4.14	2.84			
	NT2RP2006365	5.27	2.38	4.32	5.39	0.85	1.53	2.13	3.92	2.48			
30	NT2RP2006374	123.01	124.5	151.43	183.62	144.52	148.4	137.08	112.64	166.86			
	NT2RP2006393	22.69	18.53	23.1	17.79	6.84	13.61	27.67	23.54	25.74			
	NT2RP2006394	15.6	11.55	17.73	16.97	12.66	13.34	9.59	13.69	11.86			
	NT2RP2006400	8.82	4.99	12	10.48	4.15	11.24	9.88	11.64	10.5			
	NT2RP2006411	4.42	4.9	11.08	5.28	2.3	3.07	2.25	3.04	3.21			
35	NT2RP2006429	2.69	1.8	8.38	6.1	1.17	1.68	2.03	2.68	1.46			
	NT2RP2006435	1.14	1.44	3.96	3.86	0	1.28	1.25	0.25	0.25			
	NT2RP2006436	18.89	25.65	29.36	23.03	10	15.2	18.88	16.71	17.66			
	NT2RP2006441	3.24	5.37	8.45	6.78	2.17	3.47	5.5	2.69	1.87			
	NT2RP2006447	19.2	14.3	18.35	21.17	15.45	16.45	6.09	13.77	11.65			
	NT2RP2006454	8.01	2.56	13.95	6.26	3.2	3.65	3.95	4.09	2.96			
40	NT2RP2006455	37.87	46.16	39.71	20.34	20.45	22.87	31.23	29.73	37.11	**	-	
	NT2RP2006456	12.66	10.34	20.88	11.22	5.29	5.49	7.54	4.09	3.92			
	NT2RP2006464	49.31	38.6	70.84	30.42	38.8	32.65	22.89	19.33	15.74	*	-	
	NT2RP2006467	7.41	7.72	13.37	8.13	6.48	4.56	10.4	4.81	8.63			
	NT2RP2006472	17.27	35.33	39.96	36.59	25.1	29.12	15.84	31.69	29.65			
	NT2RP2006474	5.31	10.55	8.31	9.45	5.79	7.02	7.91	11.16	8.64			
45	NT2RP2006475	14.67	7.33	18.42	13.4	5.52	5.53	5.81	10.03	7.38			
	NT2RP2006476	21.17	14.25	23.98	17.93	10.29	15.83	16.59	21.36	17.75			
	NT2RP2006501	80.64	47.79	67.54	47.86	36.74	36.28	29.87	41.76	52.91			
	NT2RP2006512	10.73	9.4	12.56	6.68	7.05	5.5	3.87	4.91	5.32	*	**	-
	NT2RP2006526	12.09	17.75	22.2	19.62	16.43	13.33	17.31	20.34	13.23			
	NT2RP2006527	4.41	6.17	7.16	7.48	1.84	1.55	3.51	2.56	2.84	*	-	
50	NT2RP2006534	4.37	9.41	7.99	5.05	4.19	2.96	4.68	2.83	2.5			
	NT2RP2006537	5.9	9.98	11.68	11.28	5.12	7.83	10.34	5.58	8.5			
	NT2RP2006543	12.11	8.37	13.04	12.23	3.26	11.04	6.8	5.53	9.23			
	NT2RP2006554	7.01	5.37	13.82	7.47	2.64	2.23	3.56	4.89	9.98			
	NT2RP2006565	14.34	12.69	22.07	6.94	4.33	4.74	3.36	7.61	8.3	*	*	-
55	NT2RP2006571	65.34	49.49	69.38	45.6	41.55	34.63	47.98	65.86	43.88	*	-	
	NT2RP2006573	12.86	9.58	16.76	8.82	7.97	5.87	5.7	4.86	5.46	*	-	
	NT2RP2006598	5.92	15.24	10.14	5.39	4.48	3.2	2.52	3.49	4.84			
	NT2RP2006601	5.82	8.92	7.57	6.45	4.69	2.53	4.15	3.79	3.98	*	-	
	NT2RP3000002	17.28	31.41	14.62	22.94	26.64	18.92	27.08	23.91	17.49			

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	NT2RP3000011	14.9	6	15.29	9.33	4.35	7.79	4.33	10.84	6.28				
	NT2RP3000014	108.09	109.54	95.92	98.76	68.18	81.91	47.71	112.2	132.8				
5	NT2RP3000016	14.35	13.63	24.71	7.65	8.46	5.45	3.86	7.49	4.11	*	*	-	-
	NT2RP3000022	7.65	10.24	13.67	9.49	4.92	2.16	2.89	2.32	2.03	*		-	-
	NT2RP3000024	12.64	12.37	14.37	11.32	5.72	6.81	6.24	6.05	6.52	*	**	-	-
	NT2RP3000031	77.24	79.76	145.67	144.42	128.63	86.96	77.23	69.72	83.66				
	NT2RP3000034	6.27	6.62	8.74	6.38	3.4	3.43	4.64	3.79	2.96	*		-	-
	NT2RP3000037	17.58	19.44	20.81	11.72	11.55	13.9	18.45	10.67	14.15	**		-	-
10	NT2RP3000040	27.59	16.23	24.01	13.53	7.79	10.55	2.51	8.1	6.81	*	*	-	-
	NT2RP3000041	5.08	4.46	12.76	6.9	3.15	3.65	6.44	3	1.87			-	-
	NT2RP3000046	7.63	5.75	15.27	8.29	3.02	2.83	2.71	4.54	5.05			-	-
	NT2RP3000047	5.93	4.81	14.06	5.49	2.34	2.87	0.9	3.18	1.51			-	-
	NT2RP3000049	6.45	8.2	10.35	6.13	1.6	1.78	2.62	3.99	1.9	*		-	-
	NT2RP3000050	11.72	13.02	12.95	7.97	7.04	4.74	3.27	4.45	3.93	**	**	-	-
15	NT2RP3000051	20.55	9.33	16.87	14.09	17.37	4.84	3.99	4.5	4.21	*		-	-
	NT2RP3000054	6.46	5.61	6.8	6.67	3.52	2.38	1.52	2.23	2.77	**		-	-
	NT2RP3000055	18.47	13.61	17.33	12.33	8.89	12.37	7.71	11.31	9.35	*	*	-	-
	NT2RP3000056	1.67	2.36	8.51	3.35	1.42	1.09	0.81	1.36	0.36			-	-
	NT2RP3000059	7.89	7.9	22.29	10.9	7.16	5.13	2.59	4.88	2.31			-	-
20	NT2RP3000063	1.84	4.14	7.63	4.56	1.09	0.43	0.47	0.97	0			-	-
	NT2RP3000068	6.17	8.89	16.21	5.26	4.81	2.29	6.13	4.42	2.89			-	-
	NT2RP3000069	9.15	8.31	8.75	6.58	4.56	4.92	4.17	3.76	6.03	**	**	-	-
	NT2RP3000072	32.05	40.26	39.15	31.11	26.2	25.34	26.47	26.26	26.37	*	*	-	-
	NT2RP3000080	25.2	23.2	22.56	18.48	15.63	13.5	21.79	14.38	13.52	**		-	-
	NT2RP3000085	67.96	43.89	70.79	53.46	33.71	65.94	52.26	69.62	62.27			-	-
25	NT2RP3000087	111.9	96.79	117.72	81.88	54.53	62.52	49.82	71.54	66.46	*	**	-	-
	NT2RP3000092	9.87	12.43	24.83	8.97	4.39	4.92	2.95	7.36	3.67			-	-
	NT2RP3000109	10.57	9.88	12.54	8.31	8.64	5.99	6.65	6.37	5.22	*	**	-	-
	NT2RP3000119	8.08	6.85	10.03	6.29	4.73	2.45	4.69	3.89	2.89	*		-	-
	NT2RP3000125	6.75	8.13	6.71	5.47	2.88	2.09	0.61	2.51	2.19	*	**	-	-
	NT2RP3000131	13.6	16.29	13.49	12.52	5.73	6.16	5.37	4.48	4.22	**	**	-	-
30	NT2RP3000134	18.43	21.97	18.23	9.28	9.9	8.55	6.96	2.89	3.6	**	**	-	-
	NT2RP3000137	10.23	18.11	17.39	15.98	4.55	11.71	4.48	6.98	5.44	*		-	-
	NT2RP3000142	35.53	27.58	35.61	21.77	15.45	19.48	21.05	30.25	26.9	*		-	-
	NT2RP3000148	26.32	39.38	34.66	19.53	19	15.35	18.54	17.46	14.71	*	*	-	-
	NT2RP3000149	32.9	38.63	27.1	14.1	20.26	8.54	10.04	7.73	9.34	*	**	-	-
35	NT2RP3000163	8.85	9.04	13.21	8.67	3.56	5.95	3.7	3.77	3.35	**		-	-
	NT2RP3000168	15.39	20.39	19.23	9.48	11.8	5.55	7.63	15.26	9.88	*		-	-
	NT2RP3000169	15.25	12.33	13.06	7.58	7.27	4.09	8.07	3.27	4.36	**	**	-	-
	NT2RP3000171	6.75	12.8	10.62	11.26	6.03	4.95	8.98	2.23	5.04			-	-
	NT2RP3000172	40.04	25.12	32.12	25.17	9.97	24.6	26.83	33.18	37.52			-	-
	NT2RP3000186	16.1	16.13	19.67	12.39	6.63	8.09	5.65	10.05	10.55	*	*	-	-
40	NT2RP3000197	50.94	62.27	70	34.47	33.63	20.62	34.62	48.18	55.04	*		-	-
	NT2RP3000201	14.53	11.88	22.5	7.11	4.59	3.11	5.14	5.79	5.41	*	*	-	-
	NT2RP3000204	4.16	4.96	6.59	4.48	1.18	2.3	2.66	1.7	2.27	*		-	-
	NT2RP3000207	95.59	249.91	234.63	30.21	59.19	29.76	35.62	12.46	31.91	*	*	-	-
	NT2RP3000216	7.95	7.31	6.95	6.17	2.69	2.5	2.94	3.29	3.98	*	**	-	-
	NT2RP3000220	22.18	29.86	28.92	10.43	5.88	15.01	13.77	5.33	14.12	**	*	-	-
45	NT2RP3000221	10.31	9.17	11.73	12.25	5.03	10.36	5.52	10.77	5.91			-	-
	NT2RP3000232	46.66	42.43	53.26	15.69	8.2	7.9	5.53	11.37	6.25	**	**	-	-
	NT2RP3000233	8.3	12.35	2.97	7.16	16.65	2.19	9.24	3.42	2.51			-	-
	NT2RP3000234	3.63	3.88	5.88	5.35	3.32	2.04	1.6	2.52	2.2	*		-	-
	NT2RP3000235	9.35	15.39	13.27	13.07	5.58	8.43	10.72	9.32	10.97			-	-
	NT2RP3000239	18.63	25.23	22.23	15.58	11.06	7.77	9.06	9.28	12.71	*	**	-	-
50	NT2RP3000247	32.06	44.16	41.62	22.89	17.24	20.67	24.3	20.29	19.85	**	*	-	-
	NT2RP3000251	44.56	41.2	38.69	25.94	14.62	23.41	43.42	39.09	44.51	**		-	-
	NT2RP3000252	21.9	16.55	21.84	18.88	16.64	19.17	13.44	23.92	18.04			-	-
	NT2RP3000255	18.67	16.02	17.43	18.73	10.56	14.35	9.36	10.73	8.47	**		-	-
	NT2RP3000262	17.74	15.84	18.49	25.1	16.29	24.75	12.36	12.76	13.36	**		-	-
	NT2RP3000265	37.8	22.61	54.63	46.91	29.06	37.64	30.75	39.28	44.8			-	-
55	NT2RP3000267	5.43	5.61	4.39	6.25	5.05	2.74	3.18	2.68	2.59	**		-	-
	NT2RP3000271	4.92	10.2	10.62	7.08	4.11	3.49	3.88	5.36	2.72			-	-
	NT2RP3000278	6.77	11.93	8.85	9.67	5.55	4.79	8.29	7.56	5.48			-	-
	NT2RP3000281	32.19	29.94	32.48	16.28	8.76	14.6	16.94	10.41	13.64	**	**	-	-

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Table 438

	NT2RP3000292	73.41	53.56	62.96	43.77	42.72	40.98	49.91	45.23	84.29	*	-
	NT2RP3000299	6.1	3.92	13.07	7.5	3.65	4.11	4.21	4.47	3.64	*	-
5	NT2RP3000304	25.73	24.35	31.49	22.39	17.08	15.95	20.38	9.68	10.08	*	-
	NT2RP3000310	21.09	16.82	33.26	14.15	13.15	10.27	8.12	6.37	6.54	*	-
	NT2RP3000312	0.99	6.75	7.52	6.17	1.98	0.95	3.63	3.7	0.46	*	-
	NT2RP3000320	11.54	11.91	24.03	15.6	10.14	7.39	6.78	13.07	6.3	*	-
	NT2RP3000322	6.3	10.23	13.74	8.18	5.89	5.4	11.65	9.13	4.6	*	-
	NT2RP3000324	3.35	4.35	17.76	5.33	3.9	3.91	1.03	4.83	1.94	*	-
10	NT2RP3000326	64.19	41.44	38.83	20.52	19.15	16.6	15.62	30.96	63.08	*	-
	NT2RP3000329	11.55	11.02	22.98	13.53	7.92	12.17	10.06	11.03	12.62	*	-
	NT2RP3000330	7.65	5.98	10.92	7.41	2.84	4.65	3.07	4.04	3.9	*	-
	NT2RP3000333	5.32	5.01	9.94	8.43	4.88	3.17	4.98	3.48	4.27	*	-
	NT2RP3000341	13.68	14.31	17.57	13.78	9.61	9.9	9.7	9.67	11.82	*	-
15	NT2RP3000344	45.81	52.79	53.7	28.28	29.87	22.15	36.08	31.27	32.79	**	-
	NT2RP3000345	9.05	22.29	17.79	14.81	9.64	10.42	11.7	5.94	6.21	*	-
	NT2RP3000348	152.75	76.47	143.51	181.96	103.16	145.4	96.65	108.56	99.33	*	-
	NT2RP3000350	14.44	9.79	17.94	12.6	7.91	9.69	10.66	15.9	13.61	*	-
	NT2RP3000359	12.38	12.66	23.75	11.88	10.77	13.58	14.05	17.04	16.51	*	-
	NT2RP3000361	30.21	20.92	25.69	12.5	10.99	10.9	7.28	12.88	9.35	**	-
20	NT2RP3000366	69.71	53.96	58.74	44.82	38.68	40.33	27.58	41.09	30.61	*	-
	NT2RP3000378	5.8	12.66	6.1	6.74	3.98	3.58	4.72	5.63	5.68	*	-
	NT2RP3000384	26.45	19.42	18.46	13.21	9.98	7.79	8.34	6.32	5.93	*	-
	NT2RP3000389	22.1	25.13	28.16	17.61	19.95	18.45	23.81	18.85	25.81	*	-
	NT2RP3000393	33.85	14.06	19.19	10.32	8.44	17.76	6.01	7.4	12.32	*	-
	NT2RP3000395	24.46	28.99	21.1	13.42	10.29	14.47	9.05	14.21	24.87	**	-
25	NT2RP3000397	24.89	21.35	36.91	14.31	14.82	16.14	17.25	23.74	23.2	*	-
	NT2RP3000398	9.55	10.75	17.31	7.25	6.82	4.6	4.16	4.17	3.99	*	-
	NT2RP3000403	93.32	64.65	56.89	57.84	43.74	45.93	35.74	40.63	30.88	*	-
	NT2RP3000418	14.37	22.01	20.2	11.88	12.29	11.51	7.67	14.89	12.11	*	-
	NT2RP3000424	40.86	56.6	51.72	39.57	32.99	30.24	31.05	29.26	23.73	*	-
30	NT2RP3000427	19.59	24.95	16.59	14.3	10.74	15.64	9.16	9.9	12.52	*	-
	NT2RP3000431	16.18	14.67	25.82	11.73	10.4	20.33	8.15	16.47	13.08	*	-
	NT2RP3000433	25.31	54.08	36.8	35.67	31.56	27.85	24.04	39.4	34.85	*	-
	NT2RP3000436	9.62	10.09	16.49	6.56	4.89	5.29	2.88	5.01	2.75	*	-
	NT2RP3000439	44.72	47.78	44.4	50.96	50.94	30.43	33.38	44	42.05	*	-
	NT2RP3000441	10.82	8.95	14.82	10.83	6.19	5.02	6.65	8.63	7.39	*	-
35	NT2RP3000444	17.45	14.75	26.3	14.55	11.35	9.32	12.21	11.85	12.68	*	-
	NT2RP3000448	6.61	7.47	11.97	6.37	5.01	4.15	4.85	3.6	5.55	*	-
	NT2RP3000449	17.38	26.19	23.45	8.67	7.34	7.86	3.61	4.2	2.92	**	-
	NT2RP3000451	31.29	40.71	35.46	10.79	20.02	15.29	13.25	22.78	15.67	**	-
	NT2RP3000456	6.24	4.2	13.64	8.03	3.84	0	2.84	3.63	2.55	*	-
	NT2RP3000460	10.33	10.39	17.07	7.27	4.9	3.93	5.19	5.56	4.78	*	-
40	NT2RP3000471	11.88	7.85	23.63	10.17	6.71	3.54	3.68	5.28	5.09	*	-
	NT2RP3000477	49.73	54.72	58.77	38.09	33.62	22.58	25.2	26.62	28.76	*	-
	NT2RP3000478	6.95	4.02	8.07	5.51	2.95	1.38	1.83	1.8	1.91	*	-
	NT2RP3000481	11.03	7.58	11.93	11.71	8.13	6.39	6.65	9.77	6.96	*	-
	NT2RP3000484	25.46	33.21	34.57	19.56	15.47	13.67	14.97	11.89	12.9	*	-
	NT2RP3000487	21.14	29.38	33.76	13.62	12.2	14.9	5.33	12.46	12.14	*	-
45	NT2RP3000512	12.44	14.88	14.98	11.55	7.87	5.16	5.05	7.04	5.14	*	-
	NT2RP3000523	93.94	104.88	80.32	71.64	44.61	35.48	20.12	30.84	18.85	*	-
	NT2RP3000526	7.94	7.79	12.87	7.19	2.92	3.56	4	5.42	4.09	*	-
	NT2RP3000527	42.97	38.74	42.72	25	28.15	22.19	19.81	21.07	11.92	**	-
	NT2RP3000531	20.64	13.92	14.48	12.89	10.75	4.81	8.04	4.79	4.56	*	-
	NT2RP3000532	5.33	6.65	5.17	4.82	3.38	2.17	2.24	1.62	4.13	*	-
50	NT2RP3000542	21.28	18.32	16.2	8.3	8.11	6.12	3.53	3.83	3.8	**	-
	NT2RP3000554	11.71	17.67	14.03	9.45	3.02	6.99	4.57	4.9	5.09	*	-
	NT2RP3000561	21.04	16.88	23.96	14.27	9.57	9.4	4.67	15.18	7.79	*	-
	NT2RP3000562	56.42	51.6	61.28	47.36	46.18	42.62	32.74	44.25	48.68	*	-
	NT2RP3000578	19.29	21.22	25	14.6	13.72	9.4	9.07	9.7	10.06	*	-
	NT2RP3000582	9.4	7.64	13.09	8.29	5.67	6.43	5.12	6.71	5.65	*	-
55	NT2RP3000584	22.71	44.85	35.97	15.47	26.23	10.78	9.11	11.41	6.79	*	-
	NT2RP3000586	8.23	4.88	7.14	6.37	3.31	2.97	3.91	1.9	2.63	*	-
	NT2RP3000590	7.21	5.97	5.97	5.32	2.92	1.94	4.92	2.84	1.77	*	-
	NT2RP3000592	69.63	37.92	90.02	128.75	103.66	125.15	70.02	69.72	60.26	*	+

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Table 439

	NT2RP3000596	8.71	11.87	13.23	5.92	4.35	3.28	4.65	3.35	4	*	**	-	-
	NT2RP3000599	39.3	60.28	67.05	35.1	44.12	24.38	35.82	36.31	35.96	*	*	-	-
	NT2RP3000603	69.47	91.4	87.14	91.5	86.56	93.49	64.94	61.32	72.5	**	*	-	-
5	NT2RP3000605	22.45	27.45	25.73	13.14	8.89	13.46	17.63	11.14	9.76	*	*	-	-
	NT2RP3000607	10.48	11.53	16.41	10.77	7.11	9.56	5.29	9.79	8.32	*	*	-	-
	NT2RP3000616	11.96	13.13	17.29	7.98	6.33	4.22	6.69	4.25	4.27	*	**	-	-
	NT2RP3000621	218.49	188.17	246.49	222.59	168.47	221.1	202.08	168.53	186.24	*	*	-	-
	NT2RP3000622	11.99	8.26	9.27	9.15	3.89	5.28	6.73	6.59	3.57	*	*	-	-
10	NT2RP3000624	27.07	18.6	22.96	16.72	12.03	13.8	17.33	23.33	18.89	*	*	-	-
	NT2RP3000628	27.69	34.41	73.45	22.73	20.51	22.18	15.98	19.75	18.56	*	*	-	-
	NT2RP3000631	6.03	12.91	11.07	11.79	9.91	5.14	4.52	6.12	7.95	*	*	-	-
	NT2RP3000632	16.5	21.72	26.01	18.26	13.03	16.89	15.73	14.14	13.67	*	*	-	-
	NT2RP3000638	31.94	42.93	38.07	22.76	17	20.23	24.56	32.44	30.42	**	*	-	-
	NT2RP3000644	26.66	26.83	24.84	16.68	14.97	15.79	28.13	27.03	30.11	**	*	-	-
15	NT2RP3000645	12.37	13.95	21.96	14.87	10.1	8.68	7	6.44	7.2	*	*	-	-
	NT2RP3000652	20.17	23.26	25.45	12.67	9.39	13.26	9.11	9.19	15.37	**	*	-	-
	NT2RP3000658	6.96	4.69	8.52	6.05	2.7	4.41	2.15	3.59	3.85	*	*	-	-
	NT2RP3000660	21.94	12.21	11.63	11.36	9.42	9.56	9.02	8.73	8.05	*	*	-	-
	NT2RP3000661	15.39	18.23	27.58	11.62	4.78	9.25	6.26	7.03	6.07	*	*	-	-
	NT2RP3000665	34.94	43.07	59.18	27.69	16.86	21.15	16.2	20.9	14.32	*	*	-	-
20	NT2RP3000676	11.53	4.79	8.95	6.6	4.34	2.4	4.94	2.78	3.68	*	*	-	-
	NT2RP3000677	12.19	14.6	7.18	13.97	4.51	9.55	9.82	11.58	12.06	*	**	-	-
	NT2RP3000681	7.72	7.98	7.04	6.12	2.54	4.33	4.62	3.23	3.26	*	*	-	-
	NT2RP3000683	16.43	8.63	13.69	14.68	12.94	13.49	5.83	9.27	7.59	*	*	-	-
	NT2RP3000685	8.41	6.46	7.19	10.24	3.04	4.6	5.55	3.8	3.45	*	*	-	-
	NT2RP3000690	11.52	7.55	10.23	15.03	9.13	13.25	14.85	17.96	14.92	*	*	-	-
25	NT2RP3000698	6.94	6.35	7.8	8.41	2.13	5.63	3.39	7.51	5.51	*	*	-	-
	NT2RP3000708	9.74	10.33	12.77	11.25	8.14	10.39	9.73	10.17	12.86	*	*	-	-
	NT2RP3000719	9.86	16.24	14.31	8.23	2.38	5.7	5.89	3.68	4.39	*	*	-	-
	NT2RP3000721	8.23	3.7	5.33	7.95	1.94	5.33	6.54	5.47	6.13	*	*	-	-
	NT2RP3000728	4.68	4.59	4.86	7.19	1.44	3.15	5.16	3.82	3.57	*	*	-	-
30	NT2RP3000730	14.89	15.22	17.78	16.76	11.05	11.99	16.08	10.04	9.6	*	*	-	-
	NT2RP3000733	62.46	50.63	81.88	55.7	39.3	45.85	39.59	39.01	40.88	*	*	-	-
	NT2RP3000735	4.91	3.22	9.89	6.52	1.99	3.91	2.03	3.65	2.09	*	*	-	-
	NT2RP3000736	6.36	3.45	10.98	8.89	2.09	4.31	3.75	3.03	2.56	*	*	-	-
	NT2RP3000739	40.42	44.03	40.83	24.77	27.39	34.23	25.37	20.3	32.14	*	*	-	-
	NT2RP3000742	4.84	6.47	8.58	7.03	4.15	2.9	3.28	5.74	3.55	*	*	-	-
35	NT2RP3000753	8.3	6.8	12.66	10.6	4.35	5.47	5.99	5.75	7.45	*	*	-	-
	NT2RP3000759	36.84	70.63	56.01	36.02	19.41	27.88	8.09	6.25	5.44	**	*	-	-
	NT2RP3000789	45.54	27.39	34.07	33.12	27.39	34.54	20.51	27.67	27.21	*	*	-	-
	NT2RP3000815	22.33	13.62	22.75	12.02	10.68	14.79	18.74	20.82	19.96	*	*	-	-
	NT2RP3000818	30.57	21.11	33.63	24.24	17.69	21.68	13.73	17.32	15.5	*	*	-	-
	NT2RP3000820	35.87	28.12	43.82	32.81	27.98	25.05	21.15	26.93	23.2	*	*	-	-
40	NT2RP3000821	3.51	4.2	7.15	6.21	2.3	3.01	3.82	2.8	1.62	*	*	-	-
	NT2RP3000825	16.22	23.18	33.6	11.67	17.67	13.25	9.13	8.99	16.22	*	*	-	-
	NT2RP3000826	57.22	56.7	80.61	55.4	48.67	48.17	57.78	64.97	54.17	*	*	-	-
	NT2RP3000836	3.1	3.53	3.85	7.53	2.33	2.42	3.69	4.81	2.68	*	*	-	-
	NT2RP3000838	14.56	14.22	18.93	20.92	12.46	10.78	11.08	17.41	54.13	*	*	-	-
	NT2RP3000839	45.25	36.9	44.36	35.78	27.32	20.79	19.28	33.14	25.15	*	*	-	-
45	NT2RP3000841	12.21	10.37	21.1	12.42	10.04	9.18	8.34	11.21	7.12	*	*	-	-
	NT2RP3000845	8.59	31.26	15.5	9.69	12.93	10.25	5.37	12.21	8.92	*	*	-	-
	NT2RP3000847	12.91	10.6	18.85	11.08	8.9	9.57	6.7	5.47	6.54	*	*	-	-
	NT2RP3000848	11.47	16.2	11.34	8.1	7	4.83	3.86	7.4	3.83	*	*	-	-
	NT2RP3000850	21.09	31.1	29.31	19.76	12.79	16.25	10.7	10.54	5.19	*	**	-	-
	NT2RP3000852	2.73	3.9	3.17	7.51	3.17	2.39	4.15	2.97	3.66	*	*	-	-
50	NT2RP3000859	32.3	21.43	36.02	18.9	21.77	13.31	16.61	18.23	32.52	**	*	-	-
	NT2RP3000861	15.56	12.49	16.59	9.02	5.36	4.49	4.53	5.88	27.25	*	*	-	-
	NT2RP3000862	12.15	10.89	17.99	10.36	6.14	6.17	5.59	8.92	5.21	*	*	-	-
	NT2RP3000865	9.02	6.17	10.68	7.46	4.29	4.01	2.73	4.35	3.2	*	*	-	-
	NT2RP3000866	43.46	38.1	57.47	39.52	40.18	44.87	37.48	37.57	27.56	*	*	-	-
	NT2RP3000868	10.55	23.22	17.15	7.33	6.65	4.58	6.64	9.1	10.81	*	*	-	-
55	NT2RP3000869	5.78	11.8	14.52	9.41	10.86	7.13	6.87	5.05	7.12	*	*	-	-
	NT2RP3000871	194.48	190.18	141.72	252.15	170.88	170.92	247.35	193.7	214.46	*	*	-	-
	NT2RP3000875	14.37	14.46	23.84	13.76	12.05	11.47	7.45	6.27	6.52	*	*	-	-

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Table 440

	NT2RP3000895	2.84	2.51	12.27	4.16	1.17	2.03	1.28	3.4	1.59			
	NT2RP3000900	10.4	8.3	14.31	18.92	3.45	5.38	4.15	13.51	4.93			
5	NT2RP3000901	14.3	18.5	22.78	13.03	13.47	11.77	11.97	9.53	14.53			
	NT2RP3000903	5.01	6.85	6.69	5.82	1.64	3.35	1.28	1.92	1.35	**	-	
	NT2RP3000904	108.6	100.47	129.83	118.07	108.3	100.81	97.74	77.69	108.28			
	NT2RP3000907	84.64	90.19	89.66	84.77	80.01	92.59	125.26	82.21	80.83			
	NT2RP3000913	19.19	19.49	20.62	24.35	9.57	18.44	17.39	14.75	19.21			
	NT2RP3000917	16.28	18.3	30.01	16.96	15.22	12.11	11.68	16.63	14.88			
10	NT2RP3000919	9.33	7.65	14.92	9.52	7.41	6.8	4.46	8.2	5.92			
	NT2RP3000921	112.89	136.59	133.65	119.03	103.41	74.11	25.71	35.79	29.01	**	-	
	NT2RP3000942	67.7	68.21	86.84	75.24	51.25	30.13	38.31	52.76	48.83	*	-	
	NT2RP3000968	50.83	31.86	37.11	29.89	24.92	14.66	9.86	11.81	12.71	**	-	
	NT2RP3000974	8.96	8.74	9.35	9.04	12.66	5.51	4.39	4.92	2.99	**	-	
15	NT2RP3000980	52.51	65.55	64.13	24.76	40.04	30.49	19.39	8.08	16.43	**	**	-
	NT2RP3000984	21.27	24.19	17.57	32.72	12.14	21.58	18.47	14.77	17.87			
	NT2RP3000984	13.76	10.35	18.12	10.02	5.77	7.25	4.5	8.07	7.2	*	-	
	NT2RP3001001	26.43	28.79	25.4	17.26	14.54	13.11	11.19	38.41	33.45	**	-	
	NT2RP3001004	4.86	4.98	10.62	7.73	3.07	4.03	3.13	4.4	2.41			
	NT2RP3001007	7.65	8.96	16.59	12.13	9.28	3.44	5.05	6.53	5.77			
20	NT2RP3001012	29.74	22.53	33.06	15.24	16.46	13.42	12.28	11.59	13.53	*	**	-
	NT2RP3001042	8.82	8.59	12.15	8.9	5.69	3.5	3.15	4.09	3.65	**	-	
	NT2RP3001044	9.07	11.65	10.99	8.25	9.28	5.59	7.83	7.51	5.88	*	-	
	NT2RP3001048	6.16	7.8	4.48	10.05	2.76	3.93	4.91	5.32	6.21			
	NT2RP3001050	13.37	10.61	15.08	10.7	4.83	9.6	6.34	11.26	9.4			
	NT2RP3001055	13.05	10.48	21.89	13.3	7.76	7.17	10.39	12.83	10.26			
25	NT2RP3001057	402.89	324.38	250.29	272.31	285.99	209.38	216.17	328.86	144.63			
	NT2RP3001061	7.38	5.55	10.57	7.56	3.5	2.09	3.67	3.84	2.18	*	-	
	NT2RP3001069	5.39	4.71	9.6	4.84	1.4	2.62	2.39	2.57	3.49			
	NT2RP3001074	12.1	8.82	12.25	8.98	3.61	6.95	9.25	6.39	6.94			
	NT2RP3001078	13.01	11.28	14.67	14.05	9.24	8.9	10.46	7.65	9.46	*	-	
	NT2RP3001081	8.54	6.06	5.96	10.22	3.89	7.03	6.21	3.36	4.4			
30	NT2RP3001084	37.48	37.33	40.93	15.51	10.29	21.45	23.22	30.25	29.17	**	*	-
	NT2RP3001095	7.76	24.69	13.38	9.04	3.7	5.9	3.38	7.52	4.23			
	NT2RP3001096	10.65	10.08	12.53	7.44	5.06	4.16	3.27	5.66	3.18	*	**	-
	NT2RP3001097	16.83	38.99	30.48	15.02	9.07	10.26	12.7	8.94	6.97	*	-	
	NT2RP3001107	28.61	24.48	44.48	22.05	25.16	18.26	10.04	8.83	11.02	*	-	
	NT2RP3001109	17.96	17.48	18.06	10.7	9.3	6.66	7.73	5.5	3.91	**	*	-
35	NT2RP3001111	10.67	15.58	14.57	9.33	6.41	6.38	8.41	3.97	4.53	*	*	-
	NT2RP3001112	31.69	26.22	26.11	22.8	9.31	16.42	16.88	9.36	14.31	**	-	
	NT2RP3001113	14.44	9.43	17.91	10.99	5.21	10.46	6.16	6.79	9.04			
	NT2RP3001115	254.68	276.58	258.3	135.39	153.31	123.7	118.47	299.67	339.02	**	-	
	NT2RP3001116	5.38	8	8.83	6.23	4.02	2.69	4.29	3.33	3.99	*	-	
40	NT2RP3001119	18.64	22.98	19.35	7.26	6.2	5.92	8.84	7.37	9.08	**	*	-
	NT2RP3001120	6.46	9.54	10.55	5.21	2.06	2.39	3.48	2.35	2.85	*	**	-
	NT2RP3001126	20.13	19.18	15.24	6.77	6.2	4.55	4.46	2.87	5.52	**	**	-
	NT2RP3001127	348.14	574.68	264.45	161.21	220.83	168.52	563.89	269.72	342.5			
	NT2RP3001133	93.42	110.08	112.43	155.23	89.96	129.37	108.06	86.85	85.22			
	NT2RP3001140	96.94	96.61	111.2	55.83	46.1	51.01	55.61	103.28	84.66	**	-	
45	NT2RP3001147	4.72	7.64	8.71	6.37	2.09	3.65	2.74	3.66	2.93	*	-	
	NT2RP3001150	11.47	12.3	12.64	9.98	10.24	3.21	4.96	7.94	6.36	**	-	
	NT2RP3001152	36.54	72.08	61.62	66.57	55.9	58.11	48.19	41.6	53.56			
	NT2RP3001155	19.7	23.76	17.71	11.79	7.15	8.62	14.02	11.36	10.16	**	*	-
	NT2RP3001156	19.46	20.53	21.5	20.77	20.49	12.08	20.09	17.5	18.2			
	NT2RP3001159	18.55	19.29	22.76	15.71	9.43	11.61	19.86	20.4	20.19	*	-	
50	NT2RP3001170	16.8	14.86	12.69	11.85	4.5	6.68	9.82	3.85	4.53	*	*	-
	NT2RP3001176	17.96	17.32	14.24	8.81	7.86	12.88	9.17	14.49	11.22	*	-	
	NT2RP3001195	197.73	229.27	190.42	299.15	260.22	386.11	194.62	191.1	184.16	*	+	
	NT2RP3001209	74.83	67.88	81.64	88.53	60.41	90.53	81.32	84.97	83.11			
	NT2RP3001214	17.39	13.69	27.12	17.15	13.89	13.51	7.67	14.21	13.2			
	NT2RP3001216	18.74	16.38	19.13	19.54	12.84	10.16	26.01	26.17	21.52	*	+	
55	NT2RP3001221	6.31	7.39	8.65	9.62	5.18	6.37	8.56	6.05	7.92			
	NT2RP3001226	22.75	26.78	31.16	8.49	9.07	6.76	11.49	9.21	9.9	**	**	-
	NT2RP3001230	6.51	6.56	3.99	9.46	3.93	5.31	7.3	6.36	5.9			
	NT2RP3001232	6.36	3.81	12.04	7.09	3.34	3.56	1.97	4.41	3			

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	NT2RP3001236	30.11	19.17	30.67	17.48	11.33	17.06	7.98	12.61	12.49	*	-
	NT2RP3001239	12.58	7.93	16.69	7.8	5.43	5.92	7.31	5.36	3.8		
5	NT2RP3001240	16.64	15.42	32.69	20.34	13.57	11.75	7.09	11.44	8.12		
	NT2RP3001245	8.04	12.54	22.57	10.74	8.24	10.53	7.27	7.75	6.31		
	NT2RP3001253	5.41	9.93	13.75	5.39	2.74	1.6	4.68	3.73	2.31		
	NT2RP3001259	278.9	310.98	327.25	256.7	262.84	274.28	334.89	289.89	242.91		
	NT2RP3001260	18.94	14.44	22.33	34.17	17.19	23.22	21.96	25.77	20.83		
	NT2RP3001264	67.04	56.89	77.24	82.42	71.22	82.52	43.6	44.18	61.74		
10	NT2RP3001268	54.13	43.25	63.3	45.53	25.93	35.18	39.08	48.29	54.07		
	NT2RP3001271	7.61	5.79	12.88	6.16	2.76	3.69	3.87	7.7	5.38		
	NT2RP3001272	23.18	22.6	31.48	18.93	15.25	15.77	18.56	19.39	20.08	*	-
	NT2RP3001274	143.91	121	164.35	135.41	115.24	154.69	133.08	136.37	139.51		
	NT2RP3001275	7.03	7.19	20.08	7.2	8.45	4.21	4.17	4.56	3.94		
	NT2RP3001280	14.64	18.72	19.46	9.93	11.17	5.67	7.5	8.91	6.46	*	**
15	NT2RP3001281	0.38	2.63	0.7	4.71	1.73	1.17	1.88	0.77	0.6		
	NT2RP3001288	43.86	21.34	42.34	25.62	18.43	26.29	27.01	32.19	37.1		
	NT2RP3001297	77.1	64.75	81.93	35.55	27.23	38.6	12.09	28.24	29.77	**	**
	NT2RP3001300	9.48	9.06	13.81	7.61	5.56	4.66	4.6	5.82	8.28		
	NT2RP3001301	5.4	3.52	7.37	3.86	1.62	1.26	1.66	3.26	1.26		
20	NT2RP3001307	13.22	10.36	15.55	10.66	10.08	6.04	5.09	8.17	7.35	*	-
	NT2RP3001310	9.88	12.87	16.58	11.85	7.95	6.71	4.27	4.42	3.89	*	-
	NT2RP3001318	7.4	8.54	9.21	7.25	6.79	6.73	5.34	5.32	3.43	*	-
	NT2RP3001322	11.09	11.38	14.04	15.94	12.19	11.47	14.66	6.17	7.73		
	NT2RP3001325	1201.7	1025	1099	286.93	377.86	405.84	75.06	206.06	219.63	**	**
	NT2RP3001338	162.73	132.54	198.96	171.74	181.83	241.04	134.27	161.16	143.19		
25	NT2RP3001339	16.04	11.7	17.8	11.35	7.84	6.88	2.83	5.64	4.58	*	**
	NT2RP3001340	35.84	31.42	47.79	30.03	31.99	45.26	31.64	27.19	27.6		
	NT2RP3001341	37.44	66.22	47.17	33.31	24.96	24.34	25.96	38.56	34.37		
	NT2RP3001354	42.85	32.23	43.99	23.31	23.56	19.16	13.01	13.77	11.4	*	**
	NT2RP3001355	2.26	7.76	10.15	5.3	3.13	3.72	4.66	3.96	2.91		
	NT2RP3001356	43	54.12	51.32	62.98	37.84	46.81	81.45	50.61	59.12		
30	NT2RP3001359	34.72	29.05	42.17	41.55	33.32	37.07	21.86	23.34	24.66	*	-
	NT2RP3001364	19.26	26.46	29.33	17.86	11.52	13.89	13.78	18.18	15.95	*	*
	NT2RP3001373	16.79	12.24	26.6	10.58	10.1	9.34	9.17	17.19	12.49		
	NT2RP3001374	95.59	73.12	108.77	136.19	114.69	107.19	68.33	56.48	69.32		
	NT2RP3001383	12	19.08	15.5	12.1	5.75	6.51	13.27	9.62	6.82		
35	NT2RP3001384	22.91	17.21	30.7	33.57	22.7	20.56	19.13	14.74	15.12		
	NT2RP3001388	9.38	9.17	7.78	9.06	5.69	4.27	7.73	5.71	5.18	*	-
	NT2RP3001392	4.64	4.2	2.65	5.43	2.03	2.78	2.37	2.94	3.1		
	NT2RP3001396	47.27	37.6	60.04	23.62	14.23	34.71	12.93	30.54	38.42		
	NT2RP3001398	13.09	9.85	15.48	8.92	6.22	7.1	4.4	8.04	6.53	*	*
	NT2RP3001399	17.91	14.49	24.37	16.05	7.15	6.8	6.07	7.51	6.62	*	-
40	NT2RP3001402	30.22	31.51	33.24	60.13	23.85	9.5	15.21	24.77	23.82	*	-
	NT2RP3001407	72.56	60.86	88.74	96.01	74.06	85.12	43.61	63.39	61.28		
	NT2RP3001416	18.88	22.22	16.48	16.79	17.16	5.73	3.31	4.98	5	**	-
	NT2RP3001420	5.88	3.11	4.79	4.91	2.62	1.74	1.34	1.67	2.52	*	-
	NT2RP3001425	11.74	10.47	11.8	11.91	6.37	9.11	8.4	4.94	6.04	*	-
45	NT2RP3001426	12.17	11.79	16.88	9.1	9.64	6.43	5.51	9.62	7.81	*	-
	NT2RP3001427	10.81	11	21.59	12.3	6.43	8.87	17.63	22.78	19.89		
	NT2RP3001428	7.7	10.58	20.16	8.58	3.38	6.04	5.05	8.84	8.9		
	NT2RP3001429	4.55	6.04	12.09	5.05	1.79	1.93	2.26	1.46	1.89		
	NT2RP3001432	20.32	18.99	30.96	16.39	14.24	12.25	16.49	28.23	11.89		
	NT2RP3001439	31.43	37.32	28.95	26.93	25.44	19.21	14.96	11	10.21	**	-
	NT2RP3001441	34.77	41.28	46.38	53.64	42.72	50.36	30.69	23.25	24.74	*	-
50	NT2RP3001446	4.24	2.49	4.94	4.53	3.01	2.2	2.82	2.01	1.51		
	NT2RP3001447	22.35	21.24	25.11	13.3	8.65	15.94	13.67	37.08	14.99	*	-
	NT2RP3001449	139.79	126.76	203.02	199.4	166.47	178.45	131.32	106.74	139.38		
	NT2RP3001453	31.6	35.5	49.48	34.98	29.3	36.04	28.49	31.86	35.69		
	NT2RP3001457	13.38	17.23	17.13	11.75	10.12	6.15	5.98	6.75	6.92	*	**
55	NT2RP3001459	11.29	13.84	13.09	7	3.75	5.3	5.53	4.44	5.41	**	**
	NT2RP3001463	6.65	4.84	3.81	4.67	1.94	1.07	1.96	2.08	0.69	*	-
	NT2RP3001466	5.28	4.9	5.4	5.77	2.51	1.55	2.18	1.94	1.06	**	-
	NT2RP3001472	5.37	5.26	7.06	12.24	7.01	3.59	1.12	2.87	2.9	*	-
	NT2RP3001475	239.39	301.8	150.57	92.73	106.13	95.77	29.54	68.35	93.78	*	*

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	NT2RP3001479	6.51	3.77	10.27	6.45	4.18	2.21	2.6	4.56	5.3			
	NT2RP3001490	15.72	6.25	23.45	15.28	5.31	6.47	7.24	7.84	8.04			
	NT2RP3001492	14	14.91	21.99	13.76	7.53	9.81	14.28	13.21	12.48			
5	NT2RP3001495	18.56	21.11	19.03	12.08	9.76	9.93	15.89	18.33	21.35	**	-	-
	NT2RP3001497	36.57	27.99	40.31	47.7	28.75	36.07	23.59	21.43	24.3	*	*	-
	NT2RP3001501	16.76	28.67	29.3	12.62	8.54	7.31	11.78	2.93	8.97	*	*	-
	NT2RP3001527	5.54	5.56	5.02	7.34	2.65	3.31	4.71	3	2.59	*	*	-
	NT2RP3001529	21.9	27.01	22.29	20.64	12.59	16.78	7.77	18.39	18.96			
10	NT2RP3001538	80.06	67.26	76.24	89.51	76.4	114.47	59.99	77.08	72.65			
	NT2RP3001539	4.24	4.99	8.09	6.1	3.34	4.14	3.58	5.72	3.56			
	NT2RP3001542	17.53	25.89	26.44	14.74	14.15	8.68	14.26	12.41	17.97	*	-	-
	NT2RP3001549	6.14	6.2	5.77	5.79	1.73	1.92	2.67	2.05	1.89	**	**	-
	NT2RP3001554	28.4	40.66	43.76	10.47	10.16	7.96	15.92	6.96	13.22	**	**	-
	NT2RP3001560	79.18	91.03	86.96	84.47	48.32	76.97	115.31	93.32	84			
15	NT2RP3001561	3.47	3.93	2.29	6.28	2.06	3.29	2.23	2.16	2.49			
	NT2RP3001564	34.74	32.97	34.99	17.25	16.65	19.41	10.11	30.58	15.23	**	-	-
	NT2RP3001568	23.08	14.44	30.67	16.92	14.73	6.11	7.97	12.05	7.85			
	NT2RP3001575	34.43	18.91	39.8	19.69	12.66	21.53	16.47	22.21	25.65			
	NT2RP3001580	17.53	21.3	27.37	11.9	7.8	11.25	7.5	7.41	8.67	*	**	-
	NT2RP3001587	14.32	16.9	20.18	11.06	6.6	9.89	19.28	18.65	20.31	*	-	-
20	NT2RP3001589	6.31	5.44	5.39	5.29	2.4	2.48	2.34	4.87	3.41			
	NT2RP3001592	37.3	61.22	57.18	30.41	23.17	28.18	46.3	38.66	32.65	*	-	-
	NT2RP3001607	11.49	11.68	9.02	7.34	3.49	8.45	5.15	2.53	3.96	**	-	-
	NT2RP3001608	30.61	24.16	28.98	15.14	18	18.45	9.66	10.92	10.91	**	**	-
	NT2RP3001613	55.34	46.31	54.71	81.86	48.17	86.77	51.11	48.11	44.78			
25	NT2RP3001619	162.64	181.38	185.09	152.03	118.43	125.85	144.48	167.59	158.06	*	-	-
	NT2RP3001621	29.97	24.25	25.08	33.83	16.83	30.34	32.22	27.66	24.11			
	NT2RP3001629	28	13.33	26.21	16.28	12.69	19.85	19.79	23.48	12.56			
	NT2RP3001630	3.51	2.38	4.56	4.63	1.01	2.11	3.79	2.64	3.67			
	NT2RP3001631	64.16	51.12	67.22	112.91	65.5	60.67	59.38	50.82	71.84			
	NT2RP3001634	3.71	4.65	2.94	7.85	2.25	2.09	4.62	2.51	1.18			
30	NT2RP3001642	29.24	22.78	34.25	25.21	18.32	21.46	34.78	35.92	40.14			
	NT2RP3001646	18.72	13.31	23.84	17.34	7.46	8.49	11.13	12.12	12.05			
	NT2RP3001650	4.88	6.33	12.48	7.77	5.89	4.37	3.47	3.76	3.82			
	NT2RP3001667	17.36	19.67	39.76	21.84	7.89	10.07	11.81	14.81	13.16			
	NT2RP3001671	13.32	10.22	13.86	10.05	5.86	9.27	7.9	6.32	3.97	*	-	-
	NT2RP3001672	56.18	72.22	87.94	28.72	18.36	21.55	10.7	4.04	14.95	**	**	-
35	NT2RP3001676	11.94	10.66	12.76	8.88	5.99	6.36	7.09	3.31	6.98	*	*	-
	NT2RP3001678	368.4	207.45	268.13	268.3	249.2	237.9	189.86	337.31	274.16			
	NT2RP3001679	19.45	8.41	17.68	13.47	5.77	7.99	3.71	6.54	7.99			
	NT2RP3001682	115.37	82.43	118.94	71.89	66.26	91.02	56.88	114.15	137.5			
	NT2RP3001685	4.91	3.52	11.94	5.16	2.78	2.73	5	2.99	2.91			
	NT2RP3001688	4.75	1.41	4.66	3.33	0.27	0.64	0.99	2.07	0			
40	NT2RP3001690	8.33	10.1	11.83	11.07	4.69	5.02	5.74	5.13	6.32	*	-	-
	NT2RP3001693	2.22	6.17	10.5	5.55	2.56	2.65	2.84	2.33	2.39			
	NT2RP3001696	7.34	11.29	11.31	6.93	5.94	11.43	6.97	3.31	6.44			
	NT2RP3001698	780.45	572.31	725.4	616.13	658.96	0.94	533.83	1241.6	1289.4			
	NT2RP3001708	348.43	297.84	257.74	514.57	355.27	1.82	148.2	628.13	519.33			
45	NT2RP3001712	32.9	21.37	35.65	18.32	14.72	16.28	22.44	33.16	22.67	*	-	-
	NT2RP3001716	13.86	9.55	15.36	8.27	11.28	8.27	5.55	15.45	9.22			
	NT2RP3001724	28.26	21.7	18.91	32.47	31.93	25.73	16.65	23.86	18.15			
	NT2RP3001727	27.92	15.82	33.03	18.01	12.47	12.24	8.97	9.14	8.89	*	-	-
	NT2RP3001729	2.64	5.64	5.12	5.09	2.61	2.56	2.6	2.88	1.65			
	NT2RP3001730	421.81	524.98	490.91	328.42	274.16	316.08	179.32	117.74	101.94	**	**	-
50	NT2RP3001733	1.54	1.62	4.9	4.53	0	1.49	0.54	0.39	1.87			
	NT2RP3001737	7.85	25.52	17.42	10.76	4.14	4.59	3.35	7.04	17.36			
	NT2RP3001738	28.07	24.45	41.36	18.76	13.82	15.18	12.56	15.63	32.84	*	-	-
	NT2RP3001739	2.19	2.42	9.16	4.78	1.8	1.62	1.06	2.07	0.9			
	NT2RP3001742	11.1	11.43	14.41	9.77	5.51	6.65	7.73	6.52	8.12	*	*	-
	NT2RP3001751	1.19	3.87	3.32	5.53	0.3	1.67	1.29	0.92	0.82			
55	NT2RP3001752	2.48	4.8	2.87	3.47	0.21	1.52	1.75	2.38	0.9			
	NT2RP3001753	3.96	5.83	5.77	7.82	4.31	2.86	4.73	5.28	2.61			
	NT2RP3001754	3.14	1.28	9.55	3.89	0.47	2.48	0.99	1.82	0.86			
	NT2RP3001756	4.67	4.56	13.42	7.12	2.77	3.58	2.62	4.94	3.56			

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	NT2RP3001764	3.84	4.67	12.85	4.07	1.87	1.79	1.19	3.02	2.08			
	NT2RP3001771	10.53	6.71	15.52	12	8.69	4.55	2.42	4.06	4.07	*	-	
5	NT2RP3001777	40.65	47.79	33.95	47.7	28.57	21.63	29.91	18.82	40.09	*	*	-
	NT2RP3001782	18.47	18.59	14.66	13.14	8.87	10.49	5.89	13.23	9.56	*	*	-
	NT2RP3001792	51.98	43.73	63.18	42.18	33.54	33.35	80.48	61.45	65.58	*	*	-
	NT2RP3001799	7.5	9.23	9.91	6.52	4.07	3.35	7.42	5.61	3.54	*	-	
	NT2RP3001819	9.21	8.05	11.94	7.62	3.17	5.23	2.57	7.27	6.12			
	NT2RP3001829	0.79	0.98	6.7	3.6	0.17	1.25	3.26	1.13	0.11			
10	NT2RP3001836	16.84	18.26	30.32	14.13	7.32	15.63	6.9	7.75	7.46	*	-	
	NT2RP3001839	6.81	9.19	13.79	8.6	4.4	4.34	2.3	5.79	3.54			
	NT2RP3001844	5.94	4.03	11.89	5.39	1.37	2.09	2.04	1.24	1.53			
	NT2RP3001848	53.13	36.02	38.27	40.15	39.26	28.02	46.65	51.58	51.5			
	NT2RP3001854	53.05	46.79	83.54	47.02	38.11	28.76	72.37	61.23	74.82			
	NT2RP3001855	8.77	9.33	11.43	9.53	8.22	8.62	9.1	7.34	5.15			
15	NT2RP3001857	2.78	1.95	7.57	5.8	0.8	2.63	1.53	2.14	0.96			
	NT2RP3001858	1.48	1.77	7.55	6.01	1.18	1.83	0	1.41	1.37			
	NT2RP3001861	4.86	3.76	12.83	6.03	2.09	1.54	1.75	2.42	0.53			
	NT2RP3001866	4.29	4.19	8.56	7.38	2.36	3.86	2.27	2.97	2.71			
	NT2RP3001871	4.11	2.37	11.14	4.75	0.71	0.4	0.62	1.36	0.06			
20	NT2RP3001874	10.44	5.38	11.3	5.07	2.46	1.93	2.08	3.65	5.3	*	-	
	NT2RP3001878	6.84	8.82	7.25	6.09	2.26	2.81	4.01	2.14	3.46	*	**	-
	NT2RP3001885	6.75	5.91	9.28	7.33	5.82	5.26	4.29	3.86	3.96	*	*	-
	NT2RP3001896	15.8	9.61	18.78	10.19	5.77	12.23	2.88	7.21	8.15			
	NT2RP3001898	10.12	6.81	17.59	9.29	3.83	4.48	2.35	4.36	3.15			
	NT2RP3001899	4.46	3.48	9.66	6.74	4	4.77	3.33	4.48	3.02			
25	NT2RP3001901	2.97	2.49	8.51	4.89	2.11	2.05	1.6	0.22	0.74			
	NT2RP3001915	21.98	18.4	24.23	18.83	15.46	12.75	6.48	6.95	5.98	**	-	
	NT2RP3001926	42.5	70.22	59.74	46.58	37.18	35.96	45.08	32.42	25.88			
	NT2RP3001929	7.58	7.59	9	5.33	1.89	5.28	3.26	1.47	1.63	*	**	-
	NT2RP3001931	7.03	5.58	8.39	8.57	1.83	4.32	4.68	3.69	4.06	*	-	
	NT2RP3001938	0.69	0.54	7.42	4.87	0	1.52	0	1.16	0.26			
30	NT2RP3001943	188.81	183.6	152.87	80.5	86.76	128.25	85.31	121.73	115.26	*	*	-
	NT2RP3001944	17.12	20.99	26.58	14.69	15.73	4.63	10.12	15.18	9.75	*	-	
	NT2RP3001945	39.73	40.32	37.82	24.74	26.95	28.23	17.61	14.81	14.26	**	**	-
	NT2RP3001947	47.48	38.36	48.19	30.55	15.52	22.26	24.69	18.23	25.96	*	**	-
	NT2RP3001949	37.29	38.85	47.2	29.25	26.76	28.05	30.76	28.58	28.74	*	*	-
	NT2RP3001952	10.17	10.07	6.99	3.68	1.57	0.37	2.44	1.18	1.17	**	**	-
35	NT2RP3001954	9.56	18.54	17.64	8.37	4.32	7.01	11.86	5.36	4.75	*	-	
	NT2RP3001956	3.88	4.98	8.37	7.17	1.4	2.11	0.35	2.86	1.91			
	NT2RP3001967	7.48	3.68	9.02	8.89	3.53	3.86	3.05	4.36	2.97			
	NT2RP3001969	2.15	1.05	4.78	4.72	1.42	2.2	1.63	2.56	0.82			
	NT2RP3001976	1.89	2.22	5.25	5.93	1.38	2.82	1.33	1.09	1.87			
40	NT2RP3001986	3.89	3.3	6.39	4.22	1.46	2.65	3.43	6.44	2.42			
	NT2RP3001989	6.56	8.64	5.36	8.05	1.81	1.73	3.37	1.97	1.12	*	-	
	NT2RP3002002	7.76	11.38	8.57	5.38	2.01	2.22	6.25	3.04	6.16	*	-	
	NT2RP3002004	7.76	12.41	12.06	6.85	3.16	4.05	3.73	2.48	3.6	*	**	-
	NT2RP3002007	14.2	10.34	19.96	11.2	4.92	6.87	4.6	9.34	6.75			
	NT2RP3002014	2.11	1.84	5.64	7.64	3.81	2.33	1.74	3.76	3.1			
45	NT2RP3002015	10.24	10.71	16.79	11.66	11.36	10.59	8.67	8.67	11.36			
	NT2RP3002033	8	5.97	11.92	6.98	3.29	5.92	6.91	8.34	9.48			
	NT2RP3002045	7.45	16.7	16.88	5.97	3.53	4.5	4.78	3.11	3.05	*	*	-
	NT2RP3002054	292.36	495.82	456.61	206.09	224.87	171.68	441.79	291.3	543.12	*	-	
	NT2RP3002056	3.09	3.6	0.88	3.45	0.32	0.79	0.92	1.02	0.67			
	NT2RP3002057	10.26	15.21	13.61	7.78	1.9	3.69	9.33	6.11	3.21	*	*	-
50	NT2RP3002061	3.7	2.82	3.37	5.14	1.22	2.6	0	1.37	0.53	**	-	
	NT2RP3002062	14.95	11.22	12.96	12.28	11.33	13.44	7.88	11.32	11.12			
	NT2RP3002063	3.07	0.91	3.18	5.76	3.45	2.53	1.35	2.57	1.94			
	NT2RP3002064	4.75	4.07	6.06	8.44	3.11	3.26	2.69	6.61	3.66			
	NT2RP3002071	2.99	2.02	2.84	4.58	1.41	2.26	2.09	2.02	0.69			
	NT2RP3002073	4.16	1.73	3.01	5.39	0.35	0	3.4	1.98	3.29			
55	NT2RP3002074	3.97	4.7	9.59	5.64	1.52	1.74	2.26	2.79	1.06			
	NT2RP3002075	115.61	136.72	152.03	61.15	60.41	66.84	138.08	127.44	140.01	**	-	
	NT2RP3002077	1.88	1.37	7.12	4.73	0	2.99	1.52	0.95	1.4			
	NT2RP3002081	9.52	4.64	17.43	9.04	2.14	3.16	6.77	6.6	8.59			

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	NT2RP3002086	9.1	5.64	14.68	7.72	4.13	4.75	9.35	9.69	7.69				
	NT2RP3002094	3.34	2.83	6.44	4.61	2.06	2.3	2.41	5.92	1.29				
	NT2RP3002096	12.33	8.92	11.73	8.59	3.97	5.5	5.94	5.18	4.01	*	**	-	-
5	NT2RP3002097	23.91	20.85	34.1	19.75	11.2	19.57	12.95	19.73	14.4				
	NT2RP3002098	5.03	5.84	6.49	7.72	2.61	2.62	5.48	4.78	3.63				
	NT2RP3002102	13.2	5.06	15.39	11.41	5.66	7.42	3.96	4.11	3.36				
	NT2RP3002106	10.36	7.3	14.64	10.63	8.57	6.26	3.35	4.87	10.6				
	NT2RP3002108	4.96	2.64	12.49	5.65	1.44	2.35	2.54	2.99	5.43				
10	NT2RP3002109	40.98	15.02	38.55	15.39	16.89	11.31	8.11	16.82	8.14				
	NT2RP3002110	5.34	2.87	6.32	5.23	2.17	1.37	2.33	2.43	0.38				
	NT2RP3002113	9.48	7.75	15.49	10.55	5.09	3.01	6.14	4.67	6.08				
	NT2RP3002120	7.73	8.74	11.8	6.57	3.91	2.89	5.04	3.74	4.99	*	*	-	-
	NT2RP3002121	1.11	4.94	1.77	5.17	1.32	0.68	2.8	1.37	1.2				
	NT2RP3002126	64.09	54.26	55.37	40.43	28.8	44.09	33.92	65.97	39.23	*			
15	NT2RP3002128	8.94	4.6	9.8	7.18	4.51	3.23	4.1	5.32	11.38				
	NT2RP3002130	45.15	21.81	38.29	25.97	19.96	17.62	5.74	23.29	23.75				
	NT2RP3002133	713.78	729.07	666.05	842.53	766.78	697.72	544.62	1065.2	813.76				
	NT2RP3002136	99.29	50.26	79.88	69.55	58.35	39.45	17.4	37.71	52.59				
	NT2RP3002140	3.69	7.52	7.94	5.4	2.45	3.08	2.99	3.81	3.42				
20	NT2RP3002142	9.07	12.94	11.89	8.33	6.6	5.19	5.4	5.06	2.64	*	**	-	-
	NT2RP3002146	9.3	10.61	11.18	9.37	7.32	7.23	12.19	11.03	8.72				
	NT2RP3002147	11.07	11.26	19.71	10.63	7.44	5.02	4.38	6.88	4.67	*			
	NT2RP3002151	15	10.97	25.17	14.01	7.18	7.82	7.02	15.09	18.04				
	NT2RP3002155	53.25	66.04	47.55	73.17	43.36	52.61	36.35	94.67	86.47				
	NT2RP3002156	3.79	2.7	6.74	4.59	0.75	1.4	1.04	0.59	1.13	*			
25	NT2RP3002160	9.08	10.25	12.47	12.87	7.96	7.04	2.86	3.65	6.87	*			
	NT2RP3002163	13.64	21.03	16.3	10.69	7.06	4.19	9.73	11.32	12.78	*			
	NT2RP3002165	6.75	7.58	8.41	6.08	1.96	1.96	2.6	3.84	1.9	*	**	-	-
	NT2RP3002166	5.43	5.03	4.69	5.27	1.55	0.67	2.88	6.31	2.47				
	NT2RP3002173	517.9	446.69	509.69	297.97	240.6	253.29	44.66	135.22	128.7	**	**	-	-
	NT2RP3002174	130.22	107.95	156.75	150.48	138.99	121.68	76.48	86.96	88.77	*			
30	NT2RP3002181	5.97	4.69	12.81	5.8	2.39	3.23	1.84	5.23	1.34				
	NT2RP3002185	44.31	38.54	51.77	25.79	16.42	22.4	38.06	52.39	48.7	**			
	NT2RP3002193	7.33	7.63	13.87	8.26	3.71	3.99	4.19	5.78	8.23				
	NT2RP3002204	41.05	45.66	52.03	45.02	28.36	25.63	28.31	47.28	47.76				
	NT2RP3002244	12.8	20.63	18.31	13.33	15.24	10.05	9.17	7.08	5.13	*			
	NT2RP3002248	7.98	7.8	12.04	10.57	4.97	3.5	9.37	6.63	3.98				
35	NT2RP3002253	17.21	11.16	18.79	9.56	7.33	7.05	3.72	10.84	9.39	*			
	NT2RP3002255	3.26	2.63	8.57	4.41	1.65	2.02	1.36	3.59	1.93				
	NT2RP3002264	81.68	74.91	64.3	98.72	70.97	43.12	54.37	98.78	53.26				
	NT2RP3002267	2.25	3.31	8.07	3.82	0.82	1.41	0.79	1.35	0.88				
	NT2RP3002273	20.4	16.49	19.5	15.02	8.97	5.71	10.11	9.27	13.28	*	**	-	-
	NT2RP3002276	3.97	2.93	8.36	4.35	0.7	1.55	1.24	0.89	0.84				
40	NT2RP3002281	13.35	12.31	15.77	11.45	7.06	7.28	10.16	10.76	11.32	*	*	-	-
	NT2RP3002286	16.62	19.5	20.21	12.28	6.1	7.69	4.25	3.16	1.57	**	**	-	-
	NT2RP3002297	94.9	98.81	132.4	64.72	33.84	39.88	11.41	37.45	29.98	*	**	-	-
	NT2RP3002301	11.34	12.34	18.57	7.11	3.98	4.21	2.56	4.64	4.68	*	*	-	-
	NT2RP3002303	7.54	10.15	16.1	7.32	5.62	4.17	5.05	6.82	7.85				
	NT2RP3002304	91.67	49.25	50.79	81	77.65	34.95	31.29	39.07	25.04				
45	NT2RP3002308	4.32	3.35	10.38	4.01	1.44	1.07	2.59	1.36	0.22				
	NT2RP3002311	9.65	9.45	12.73	9.08	6.57	4.41	3.9	4.09	5.31	**			
	NT2RP3002315	16.31	24.1	16.79	7.96	7.42	8.29	9.67	8.19	10.65	*	*	-	-
	NT2RP3002319	8.49	14.45	8.47	9.99	3.2	4.43	5.43	3.04	5.3	*	*	-	-
	NT2RP3002324	18.48	20.79	21.07	16.08	9.05	11.92	2.65	9.16	8.78	*	**	-	-
50	NT2RP3002330	14.44	26.39	29.36	13.92	12.3	11.42	5.88	11.72	10.72	*			
	NT2RP3002333	41.51	67.04	49.57	36.81	41.81	35.64	33.68	44.76	37.87				
	NT2RP3002337	4.44	8.96	11.93	5.8	1.82	3.91	2.32	2.11	2.55	*			
	NT2RP3002342	25.61	22.15	24.13	19.61	11.87	9.75	11.85	13.94	20.4	*	*	-	-
	NT2RP3002343	3.99	7.39	7.92	5.18	2.92	2.42	2.4	1.77	3.64	*			
	NT2RP3002351	20.96	17.51	19.58	6.79	4.97	3.6	9.93	4.83	3.54	**	**	-	-
55	NT2RP3002352	29.92	68.54	51.75	25.45	36.1	22.42	47.8	10.88	7.27				
	NT2RP3002353	26.94	28.46	26.72	23.44	18.05	15.48	14.2	29.02	22.52	*			
	NT2RP3002362	18.42	12.38	24.27	11.02	6.28	7.66	12.53	15.38	16.92				
	NT2RP3002363	11.71	14.02	21.35	9.9	11.24	7.29	10.05	11.93	6.97				

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	NT2RP3002377	20.63	15.78	16.8	13.04	9.6	12.99	16.42	23.7	18.15	*	-	-
	NT2RP3002397	5.32	9.77	13.16	6.81	2.98	3.19	4.39	2.85	3.63			
	NT2RP3002404	6.54	8.21	7.65	4.33	1.3	1.29	2.68	0.69	1.15	* **	-	-
5	NT2RP3002410	7.62	4.7	8.02	3.73	3.33	1.2	3.81	3.45	2.67	* *	-	-
	NT2RP3002414	5.43	4.93	6.09	6.64	1.85	2.91	4.09	1.68	3.33	*	-	-
	NT2RP3002430	5.86	5.44	9.44	4.78	1.52	1.85	3.2	1.23	1.16	*	-	-
	NT2RP3002448	12.97	9.25	9.52	5.21	1.95	1.81	2.67	2	4.7	** **	-	-
	NT2RP3002454	12.06	19.92	16.37	13.74	7.64	12.02	13.75	9.17	8.67			
10	NT2RP3002455	4.76	3.53	5.11	6.77	1.51	4.71	3.7	5.48	5.26			
	NT2RP3002456	58.03	38.92	43.81	27.96	14.69	15.06	14.57	36.86	33.26	*	-	-
	NT2RP3002462	20.18	13.39	21.5	10.24	9.33	4.6	3.9	5.28	3.19	* **	-	-
	NT2RP3002469	3.83	1.84	6.7	6.03	3.37	1.62	2.45	1.7	0.82			
	NT2RP3002470	35.44	35.5	72.47	34.81	21.72	19.39	33.8	20.85	19.08			
	NT2RP3002484	3.62	2.13	4.4	4.15	1.03	1.2	2.28	1.6	1.75			
15	NT2RP3002491	13.97	21.34	15.21	12.05	5.93	4.04	5.95	7.05	7.23	* *	-	-
	NT2RP3002494	24.09	40.78	35.02	15.6	8.77	12.21	26.54	16.61	15.03	*	-	-
	NT2RP3002497	1.45	2.72	2.12	3.96	0.95	2.47	1.03	1.64	2.67			
	NT2RP3002500	16.58	14.89	20.26	24.82	15.49	27.1	14.57	11.42	19.8			
	NT2RP3002501	32.52	29.62	45.43	41.64	21.97	31.25	12.71	18.89	18.63	*	-	-
	NT2RP3002512	5.61	3.7	5.13	8.12	4.35	5.53	3.81	5.5	5.08			
20	NT2RP3002529	570.71	676.56	723.55	824.94	401.81	698.08	438.95	899.52	707.21			
	NT2RP3002533	33.09	38.94	36.28	44.79	15.69	31.1	9.54	21.79	17.75	**	-	-
	NT2RP3002539	6.02	8.36	9.74	6.07	3.74	0.01	2.47	0	0.12	**	-	-
	NT2RP3002540	4.32	7.97	5.52	9.08	2.78	5.47	9.44	4.32	6.18			
	NT2RP3002543	12.62	4.6	12.88	12.84	5.24	6.49	9.1	11.85	10.42			
25	NT2RP3002545	2.99	1.16	9.33	6.12	1.46	2.25	2.07	3.55	0.82			
	NT2RP3002549	6.99	4.28	13.6	7.32	1.84	2.44	4.48	4.56	2.91			
	NT2RP3002552	4.39	5.59	10.04	7.03	1.31	2.23	3.66	3.6	2.29			
	NT2RP3002558	34.53	21.49	27.53	25.41	11.35	21.08	37	39.71	40.69	*	+	
	NT2RP3002565	13.64	7.8	14.18	11.1	3.88	9.31	11.41	13.37	16.44			
	NT2RP3002566	7.8	8.76	13.33	16.41	6.98	8.51	6.63	7.76	8.89			
30	NT2RP3002571	8.13	11.03	10.93	9.57	4.89	4.39	4.63	2.67	3.9	**	-	-
	NT2RP3002572	74.15	45.74	56.76	41.43	36.41	30.38	19.06	45.1	46.35			
	NT2RP3002573	32.62	15.75	29.51	19.71	16.82	14.99	13.13	13.23	21.22			
	NT2RP3002577	47.28	29.36	41.83	19.87	14.5	21	17.59	15.85	17.3	* *	-	-
	NT2RP3002579	8.63	6.06	12.6	7.23	3.12	4.38	5.33	4.66	5.1			
	NT2RP3002582	6.19	3.82	10.45	7.84	3.56	3.38	4.87	4.78	3.74			
35	NT2RP3002587	10.07	10.45	15.76	10.84	6.77	7.46	4.8	4.74	3.88	*	-	-
	NT2RP3002590	544.94	699.14	857.26	489.72	627.82	453.24	363.97	273.66	582.87			
	NT2RP3002602	7.18	7.63	10.58	10.16	7.38	6.68	4.87	4.34	6.16	*	-	-
	NT2RP3002603	14.44	13.52	18.75	16.38	10.66	15.03	8.16	15.4	88.12			
	NT2RP3002621	6.81	5.15	9.83	8.56	3.04	3.97	3.12	5.17	6.09			
40	NT2RP3002622	6.75	5.01	13.82	8.8	3.27	3.73	2.74	4.44	11.45			
	NT2RP3002624	26.96	16.99	21.5	17.24	10.36	13.21	17.97	25.27	18.08			
	NT2RP3002628	6.59	5.38	9.7	6.43	2.65	4.46	4.24	5.21	2.97			
	NT2RP3002629	5.76	11.73	14.59	10	6.43	5.93	6.71	4.48	3.96			
	NT2RP3002631	48.35	45.23	46.18	26.1	22.1	27.75	26.27	23.38	21.25	** **	-	-
	NT2RP3002647	12	15.89	13.32	16.2	15.29	15.81	10.24	7.5	7.23	*	-	-
45	NT2RP3002649	9.3	7.92	12.59	9.96	4.23	5.01	3.45	5.1	5.57	*	-	-
	NT2RP3002650	26.86	18.53	27.47	18.25	9.68	13.45	17.35	20.46	18.82			
	NT2RP3002652	5.52	5.57	14.03	5.61	3.76	3.01	2.75	4.84	3.27			
	NT2RP3002654	20.14	13.49	14.7	11.91	10.11	6.69	5.42	7.8	5.1	*	-	-
	NT2RP3002657	16.5	15.29	20.85	14.05	6.31	13.07	15.2	14.6	14.98			
	NT2RP3002659	15.92	19.34	18.66	13.66	10.7	8.74	4.85	10.09	6.73	* **	-	-
50	NT2RP3002660	5.66	10.19	9.81	8.43	3.68	4.95	6.72	4.39	3.92			
	NT2RP3002663	10.53	17.57	11.68	14.14	15.43	9.63	19.1	11.04	8.75			
	NT2RP3002664	28.81	23.63	39.16	18.72	11.43	13.27	7.92	17.21	15.51	* *	-	-
	NT2RP3002667	32.83	27.15	33.62	23.94	18.84	19.81	15.18	21.3	26.19	*	-	-
	NT2RP3002671	38.88	30.21	40.39	24.11	16.4	14.74	30.8	35.93	33.74	*	-	-
	NT2RP3002682	8.45	6.51	13.68	7.64	3.93	4.02	2.41	3.04	2.62	*	-	-
55	NT2RP3002684	20.03	14.16	18.81	8.9	9.81	5.51	4.13	6.96	4.79	* **	-	-
	NT2RP3002687	9.25	11.21	13.71	14.12	8.33	10.78	7.86	7.74	7.01	*	-	-
	NT2RP3002688	168.35	106.47	188.15	190.36	164.88	199.08	153.97	87.55	117.43			
	NT2RP3002698	8.07	8.3	9.14	8.34	5.8	6.56	5.59	5.87	4.73	**	-	-

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Table 446

	NT2RP3002701	11.4	8.8	15.19	9.64	4.21	7.04	4.79	10.11	7.18			
	NT2RP3002705	30.23	29.89	43.68	30.05	23.71	23.42	20.15	25.03	27.52			
5	NT2RP3002708	25.52	23.92	35.27	19.02	13.81	19.8	19.34	22.92	17.32			
	NT2RP3002711	87.34	128.24	131.86	149.35	126.88	84.65	16.56	37.78	36.54	**	-	
	NT2RP3002712	11.51	9.81	14.14	7.18	5.15	2.41	5.29	7.06	4.76	*	*	-
	NT2RP3002713	17.13	13.75	17.42	8.41	9.55	4.36	13.41	9.28	8.38	*	*	-
	NT2RP3002721	70.06	117.72	122.3	101.88	70.22	94.12	113.7	122.46	107.46			
	NT2RP3002722	20.45	20.54	15.56	16.97	11.11	10.65	14.55	10.8	10.74	*	-	
10	NT2RP3002723	12.21	14.76	21.14	7.75	4.55	7.76	4.96	7.72	6.61	*	*	-
	NT2RP3002737	4.67	4.9	12.9	7.24	2.22	4.66	2.62	1.49	3.15			
	NT2RP3002738	122.73	88.31	164.33	156.37	134.11	152.93	81.07	85.63	82.42			
	NT2RP3002742	4.62	5.31	8.06	6.59	2.59	2.11	2.29	3.26	2.78	*	-	
	NT2RP3002744	11.76	7.9	17.24	10.03	4.45	6.38	6.88	8.18	6.87			
	NT2RP3002756	8.91	6.64	6.82	7.81	5.13	2.63	2.84	1.31	1.38	**	-	
15	NT2RP3002757	18.22	14.86	15.65	13.62	6.41	8.83	10.99	9.29	10.38	*	**	-
	NT2RP3002758	16.5	15.69	16.85	13.98	8.17	9.33	15.83	11.78	10.47	*	-	
	NT2RP3002762	6.55	8.17	14.93	9.33	2.38	7.36	4.56	5.11	6			
	NT2RP3002763	6.01	4.94	14.86	7.96	3.26	4.46	4.15	2.77	3.35			
	NT2RP3002770	13.79	15.86	20.19	13.26	7.67	4.65	6.38	6.79	5.16	**	-	
20	NT2RP3002771	6.48	3.94	12.36	8.16	4.01	1.77	3.51	4.07	2.45			
	NT2RP3002785	7.93	7.61	12.09	7.52	4.23	4.31	4.14	3.39	4.41	*	-	
	NT2RP3002790	12.74	8.68	16.54	10.03	4.49	9.67	11.67	8.3	11.43			
	NT2RP3002799	44.32	36.15	61.61	71.32	40.17	61.97	38.77	29.46	32.11			
	NT2RP3002801	9.13	7.96	8.02	8.82	3.17	7.55	6.99	2.43	2.63	*	-	
	NT2RP3002802	6.6	5.16	13.06	9.48	2.83	4.69	3.71	3.1	3.55			
25	NT2RP3002810	21.61	13.43	30.89	15.94	9.02	13.72	15.57	16.49	23.18			
	NT2RP3002818	12.26	21.33	22.29	12.03	10.84	9.9	12.06	10.85	7.02			
	NT2RP3002821	3.08	2.76	7.5	5.13	0.98	2.74	3.88	1.7	1.96			
	NT2RP3002823	5.94	5.9	9.87	7.27	1.84	2.08	2.79	3.12	3.09	*	-	
	NT2RP3002825	46.16	68.1	69.32	16.84	16.8	11.22	9.52	7.53	4.62	**	**	-
	NT2RP3002829	36.39	46.01	39.22	22.92	16.02	11.21	24.02	7.98	9.64	**	*	-
30	NT2RP3002831	9.11	9.95	10.41	14.39	9.89	8.12	9.96	4.98	9.9			
	NT2RP3002836	16.68	11.51	17.27	10.91	4.09	9.65	4.06	4.72	7.36	**	-	
	NT2RP3002845	38.76	32.47	30.9	12.04	7.1	5.17	5.18	12.27	9.29	**	**	-
	NT2RP3002852	27.07	21.18	24.92	24.24	10.22	18.18	20.47	22.49	18.97			
	NT2RP3002861	6.45	10.44	9.71	7.81	2.41	4.65	6.77	4.65	5.14			
	NT2RP3002869	6.19	9.1	10.7	6.8	3.23	3.7	4.89	3.27	3.99	*	-	
35	NT2RP3002874	12.63	13.11	17.2	9.07	5.37	6.1	8.08	3.93	8.06	*	*	-
	NT2RP3002876	143.63	148.27	181.51	254.93	163.87	216.77	137.83	99.6	141.63			
	NT2RP3002877	16.65	19.83	22.97	18.33	13.19	15.19	13.02	8.47	12.29	*	-	
	NT2RP3002887	11.91	8.65	14.58	12.86	6.78	9.6	8.16	11.65	6.83			
	NT2RP3002900	24.9	40	47.49	50.72	36.64	57.77	42.16	46.86	41.82			
40	NT2RP3002902	50.68	50.65	63.54	17.78	28.94	15.05	19.17	20.83	23.73	**	**	-
	NT2RP3002909	5.43	3.6	6.73	6.91	1.07	4.91	4.39	3.43	4.07			
	NT2RP3002911	32.27	38.37	39.37	37.75	22.31	32.66	41.96	41.35	47.38			
	NT2RP3002948	97.24	122.54	134.73	183.88	103.17	110.98	109.55	85.09	95.2			
	NT2RP3002953	130.69	155.36	174.07	145.08	99.42	98.1	201.22	181.14	165.58			
	NT2RP3002955	11	13.27	12.07	9.74	5.71	6.63	7.47	5.75	5.17	*	**	-
45	NT2RP3002958	11.7	7.18	10.81	11.8	6.8	11.76	8.8	13.15	14.41			
	NT2RP3002969	10.47	5.67	11.5	11.46	3.57	3.82	2.62	3.28	4.09	*	-	
	NT2RP3002972	9.18	3.34	9.31	7.48	3.85	0.87	5.21	5.53	7.19			
	NT2RP3002978	17.8	13.14	17.07	16.61	7.47	16.55	15.56	17.59	21.66			
	NT2RP3002983	14.39	16.02	14.98	15.99	6.52	11.68	18.52	16.38	19.45	*	+	
	NT2RP3002985	4.55	5.27	7.26	6.46	1.04	3.38	4.84	3.07	3.43			
50	NT2RP3002988	8.52	6.19	9.46	9	4.1	8.27	7.55	8.24	9.04			
	NT2RP3003000	3.67	3.71	3.5	6.2	1.26	2.48	2.37	2.4	2.73	**	-	
	NT2RP3003008	10.96	2.67	10.84	10.43	9.08	7.16	5.31	8.35	5.42			
	NT2RP3003012	2.33	3.47	10.69	4.62	0.4	1.73	0.84	1.69	1.54			
	NT2RP3003015	94.04	42.5	71.87	52.22	37.75	51.79	66.36	44.43	66.31			
55	NT2RP3003018	4.14	3.97	9.63	5.98	1.6	1.48	2.56	2.43	2.26			
	NT2RP3003028	3.8	4.39	9.49	7.13	4.25	1.98	3.07	2.68	1.64			
	NT2RP3003029	10.59	12.64	16.85	9.46	5.29	7.18	11.38	8.45	12.28			
	NT2RP3003032	18.44	16.02	27.77	16.77	11.22	12.42	15.36	17.44	10.46			
	NT2RP3003041	9.55	8.82	9.95	12.39	5.66	4.67	6.47	4.02	3.62	**	-	

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Table 447

	NT2RP3003044	20.51	12.05	18.28	17.95	10.92	17.93	12.47	17.92	24.95			
	NT2RP3003047	318.58	233.21	307.78	283.91	158.8	215.31	289.99	339.63	305.02			
5	NT2RP3003050	6.01	3.67	13.67	6.04	1.27	2.97	2.45	4.04	3.78			
	NT2RP3003053	4.73	4.39	9.42	5.4	1.52	3.2	1.65	2.69	4.02			
	NT2RP3003059	3.4	2.18	5.45	4.75	1.77	1.03	2.8	1.96	1.97			
	NT2RP3003061	3.92	4.63	10.62	7.14	5.71	3.17	3.68	3.67	3.35			
	NT2RP3003068	13.64	16.72	19.09	13.94	11.08	9.11	15.51	9.65	9.79			
	NT2RP3003071	501.47	582.68	529.35	407.82	335.95	447.01	379.51	122.11	170.7	*	*	-
10	NT2RP3003076	11.52	4.82	12.85	9.77	5.93	5.76	7.19	9.4	27.45			
	NT2RP3003078	14.69	14.12	17.86	9.88	7.71	7.1	3.81	7.38	11.24	**	*	-
	NT2RP3003081	14.34	14.21	20.22	13.69	9.02	9.23	12.85	17.91	10.55			
	NT2RP3003090	4.38	6.96	9.84	6.19	3.29	2.43	4.26	4.05	2.94			
	NT2RP3003097	14.02	15.06	14.8	11.66	5.57	6.77	8.05	9.19	6.11	*	**	-
	NT2RP3003098	6.1	7.46	9.23	6.48	4.67	4.01	3.99	4.01	3.93	*		-
15	NT2RP3003101	11.04	12.95	14.52	11.99	6.27	8.65	11.09	9.21	8.98			
	NT2RP3003109	27.77	29.32	24.18	32.49	26.06	31.9	22.67	12.21	14.33	*		-
	NT2RP3003121	14.74	6.75	15.15	12.65	4.66	5.96	4.11	5.09	12.75			
	NT2RP3003133	8.34	7.45	12.11	8.93	5.28	6.18	2.52	4.07	7.32			
	NT2RP3003137	4.53	5.11	11.1	4.41	2.55	1.77	1.57	3.58	2.61			
20	NT2RP3003138	14.49	14.02	31.57	15.47	8.83	7.42	8.07	6.92	9.16			
	NT2RP3003139	17.72	13.28	16.88	11.32	8.97	7.87	7.6	10.95	5.4	*	*	-
	NT2RP3003145	29.81	27.36	41.27	37.92	28.86	28.23	19.57	16.3	17.5	*		-
	NT2RP3003150	3.07	5.2	3.99	5.23	1.85	1.66	3.17	2.46	1.85			
	NT2RP3003157	36.91	28.34	31.25	37.59	20.43	24.91	16.55	12.31	12.99	**		-
	NT2RP3003185	12.88	12.16	22.32	13.29	10.08	11.04	7.56	13.67	13.84			
25	NT2RP3003193	56.79	51.34	61.74	61.27	47.04	47.44	61.96	79.57	80.02			
	NT2RP3003197	14.34	9.96	23.45	8.85	5.2	5.54	6.63	9.8	4.5			
	NT2RP3003203	13.42	14.29	19.75	14.19	7.85	8.04	8.52	12.56	10.13			
	NT2RP3003204	19.08	17.04	30.4	16.33	10.47	7.75	7.19	12.58	11.16			
	NT2RP3003210	6.33	8.19	12.29	9.16	9.84	6.28	6.27	7.36	5.46			
	NT2RP3003212	8.37	8.5	11.56	8.16	5.18	3.57	6.2	5.26	6.14	*		-
30	NT2RP3003213	5.67	4.05	5.85	6.17	2.96	2.21	4.78	3.56	3.34			
	NT2RP3003224	55.68	53.67	56.74	16.3	18.72	16.37	11.98	29.14	26.24	**	**	-
	NT2RP3003226	4.57	3.58	10.67	6.47	2.35	3.36	2.91	2.15	2.81			
	NT2RP3003230	7.29	5.28	14.91	8.17	2.63	3.43	3.72	2.45	3.81			
	NT2RP3003235	79.63	66.15	103.5	95.3	92.56	60.75	55.64	70.39	55.23			
35	NT2RP3003242	73.44	66.48	77.54	45.7	33.8	25.86	41.52	43.2	38.85	**	**	-
	NT2RP3003251	104.1	73.55	126.64	135.43	95.34	99.58	79.05	81.02	71.32			
	NT2RP3003252	10.37	11.27	12.13	9.17	5.92	6.54	5.47	5.61	2.73	*	**	-
	NT2RP3003258	15.2	11.75	13.65	15.47	7.62	6.38	7.6	4.08	5.36	**		-
	NT2RP3003260	20.33	21.23	23.55	13.01	8.75	11.13	14.98	15.72	16.47	**	**	-
	NT2RP3003264	39.02	33.18	49.85	37.17	29.58	23.32	18.19	26.52	25.18	*		-
40	NT2RP3003273	4.51	4.91	15.07	7.81	4.36	2.59	2.42	2.45	2.99			
	NT2RP3003278	10.07	13.81	15.32	10.69	5.74	4.93	4.88	5.26	3.08	**		-
	NT2RP3003280	8.01	8.36	9.74	5.35	2.41	1.56	1.8	2.02	2.23	*	**	-
	NT2RP3003282	6.34	4.14	6.3	6.51	1.72	3.27	3.2	1.42	0.91	*		-
	NT2RP3003290	5.35	4.64	5.82	6.64	2.67	3.3	2.13	0.74	2.31	**		-
	NT2RP3003301	10.24	13.13	10.58	8.04	5.22	4.9	4.68	1.19	1.93	*	**	-
45	NT2RP3003302	44.6	31.52	44.49	25.69	16.4	28.65	36.54	47.16	60.3	*		-
	NT2RP3003311	4.75	4.55	11.5	8.43	3.14	4.46	2.2	3.71	1.64			
	NT2RP3003312	24.36	35.16	29.14	9.01	9.9	12.13	5.11	5.46	5.49	**	**	-
	NT2RP3003313	11.85	10.76	12.83	7.95	5.85	3.91	3.77	4.31	3.7	*	**	-
	NT2RP3003327	9.48	7.49	11.81	7.32	3.83	2.89	4.61	4.57	4.3	*		-
	NT2RP3003330	28.77	45.14	40.86	24.02	22.59	18.95	15.05	12.99	8.77	*	**	-
50	NT2RP3003344	7.42	9.51	10.17	9.56	3.26	4.53	3.31	3.26	4.42	**		-
	NT2RP3003346	7.58	7.33	10.55	7.96	3.11	4.95	5.04	6.17	6.71			
	NT2RP3003349	77.06	82.34	60.61	59.72	39.01	41.31	20.2	47.64	67.66	*		-
	NT2RP3003353	5.79	9.35	12.49	5.84	3.66	3.54	2.78	3.58	3.64	*		-
	NT2RP3003354	50.09	93.38	122.44	53.2	56.67	30.98	100.88	61.77	52.32			
	NT2RP3003368	10.01	14.26	18.12	8.66	5.26	5.87	4.9	3.64	2.35	*	*	-
55	NT2RP3003375	13.81	11.33	19.09	11.92	5.85	11.47	12.29	9.6	11.66			
	NT2RP3003377	8.13	11.7	14	6.42	2.73	1.97	7.35	4.71	8.09	*		-
	NT2RP3003384	15.97	18.59	24.94	10.9	5.8	5.57	11.93	4.66	4.64	*	*	-
	NT2RP3003385	10.44	16.16	15.37	14.39	15.35	10.89	10.54	6.35	9.2			

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Table 448

	NT2RP3003396	16.4	12.74	16.94	16.32	6.79	16.93	14.73	19.34	18.49				
	NT2RP3003403	3.1	2.78	7.09	5.18	1.78	3.29	1.96	3.43	3.41				
5	NT2RP3003409	7.35	11.81	12.63	9.44	12.96	4.77	6.95	7.18	6.37				
	NT2RP3003411	11.06	12.25	14.86	7.42	4.83	5.8	7.12	7.74	6.44	**	**	-	-
	NT2RP3003420	19.06	32.9	36.55	21.71	11.78	14.57	23.43	20.87	21.3				
	NT2RP3003425	6.27	5.68	8.42	5.84	2.62	3.03	4.29	2.39	4.38		*	-	
	NT2RP3003426	7.48	8.53	6.3	7.22	3.59	4.34	6.93	6.05	8.2				
	NT2RP3003427	28.71	32.12	28.4	30.38	20.54	27.6	31.57	21.98	21.07				
10	NT2RP3003433	4.33	3.61	3.8	5.72	1.58	3.56	2.47	5.63	2.76				
	NT2RP3003437	3.79	2.73	8.27	7.3	2.16	3.14	2.83	3.31	4.36				
	NT2RP3003448	50.3	43.28	42.61	71.29	41.3	73.4	51.67	39.73	51.96				
	NT2RP3003455	10.05	10.38	13.46	9.15	4.03	7.96	7.2	5.64	6.56		*	-	
	NT2RP3003462	10.37	9.93	17.25	9.92	5.42	4.43	5.52	5.56	5.82		*	-	
	NT2RP3003464	14.66	13.89	13.26	12.87	7.49	6.91	18.26	16.54	18.68	**	+	+	
15	NT2RP3003469	17.22	14.94	13.68	14.5	4.68	9.94	19.05	18.28	19.4		*	+	
	NT2RP3003473	10.99	11.83	10.53	13.09	12.46	13.39	10.9	7.59	8.71	*			
	NT2RP3003474	3.37	3.95	4.83	6.73	2.05	5.69	2.42	1.56	2.61	*			
	NT2RP3003475	25.58	23.74	27.15	19.96	21.31	0.35	11.64	10.85	19.52	*			
	NT2RP3003490	6.09	2.59	4.63	5.62	1.54	3.26	2.21	16.1	3.36				
20	NT2RP3003491	18.8	17.56	17.3	22.58	14.42	27.63	10.64	13.18	15.87	*			
	NT2RP3003493	4.17	0.67	1.27	6.14	0.62	2.97	3.62	2.46	1.88				
	NT2RP3003500	5.9	4.89	5.02	7.76	1.8	6.18	6.6	5.32	6.99				
	NT2RP3003527	7.67	4.85	6.47	6.19	2.35	4.17	6.12	6.18	4.88				
	NT2RP3003532	10.61	16.22	14.72	12.47	4.81	8.89	14.42	12.45	12.16				
	NT2RP3003535	38.7	29.85	32.07	25.66	21.86	25.49	14.16	14.9	18.19	*	**	-	-
25	NT2RP3003536	5.83	2.22	11.18	6.74	1.99	4.05	4.59	4.1	3.31				
	NT2RP3003543	83.01	76.4	71.54	99.52	61.99	69.1	35.13	38.35	47.54	**			
	NT2RP3003549	5.05	3.61	9.39	4.68	1.49	3.34	2.95	6.92	3.73				
	NT2RP3003552	5.72	3.03	6.03	6.81	1.98	1.74	4.06	3.11	1.34				
	NT2RP3003555	7.3	5.08	11.06	9.46	2.64	6.2	9.1	6.02	7.32	*	**	-	-
	NT2RP3003559	16.08	18.05	20.35	13.82	7.72	7.64	10.69	7.28	10				
30	NT2RP3003564	21.9	11.18	19.14	32.64	13.35	24.42	5.9	11.04	13.84				
	NT2RP3003572	4.45	3.71	12.53	6.23	1.91	3.3	2.99	5.76	5.28				
	NT2RP3003576	10.13	4.39	10.89	7.2	4.48	6.35	2.89	3.48	6.99				
	NT2RP3003587	4.99	3.94	10.87	4.59	3.45	2.48	4.61	2.31	2.5				
	NT2RP3003589	8.81	6.29	8.93	5.98	6.78	3.45	8.93	5.16	5.31				
	NT2RP3003592	16.97	13.2	13.23	12.11	9.09	12.9	9.83	6.59	9.69	*			
35	NT2RP3003593	8.95	15.57	14.21	12.38	7.8	13.05	6.6	6.07	15.06				
	NT2RP3003614	16.19	15.38	25.69	16.13	12.3	18.94	17.5	16.33	15.44				
	NT2RP3003621	23.31	9.78	21.55	19.16	8.76	10.65	10.2	15.44	18.25				
	NT2RP3003625	30.15	13.92	27.9	27.09	17.35	16.31	10.08	25.7	26.09				
	NT2RP3003627	13.85	10.22	17.05	10.88	8	10.73	7.14	16.59	27.58				
	NT2RP3003636	43.56	19.06	24.94	24.57	26.12	25.77	9.71	16.11	10.76				
40	NT2RP3003642	9.55	5.41	10.21	6.42	5.7	4.71	4.31	4.84	5.36				
	NT2RP3003645	11.93	7.13	13.91	10.67	5.31	7.85	4.02	4.25	4.25	*			
	NT2RP3003648	6.56	6.34	9.24	8.44	4.41	4.52	4.4	2.95	3.73	*			
	NT2RP3003649	26.09	26.77	29.81	22.55	18.26	23.64	34.18	24.81	32.1	*			
	NT2RP3003650	12.61	11.46	21.64	12.68	6.46	10.24	6.28	12.27	13.31				
	NT2RP3003656	6.54	4.65	10.33	8.68	1.7	4.51	3.42	4.72	11.15				
45	NT2RP3003659	9.46	5.9	15.28	7.57	5.1	6.1	4.35	6.43	5.32				
	NT2RP3003662	8.5	8.39	10.9	5.37	1.92	5.94	1.35	3.6	1.87	*	**	-	-
	NT2RP3003664	4.6	5.97	8.27	6.79	3.03	4.25	2.14	1.93	3.82	*			
	NT2RP3003665	11.75	13.45	13.25	12.32	5.11	5.74	4.75	7.06	5.47	**			
	NT2RP3003671	70.45	72.23	46.58	69.47	88.76	53.27	45.85	13.94	22.44	*			
50	NT2RP3003672	12.42	9.87	13.46	13.04	14.86	11.85	11.18	14.12	13.48				
	NT2RP3003673	8.49	4.06	14.72	9.56	3.98	4.91	4.97	6.88	5.68				
	NT2RP3003679	10.33	6.46	20.68	8.71	5.36	8.11	4.9	8.58	8.08				
	NT2RP3003680	13.23	15.82	26.63	9.67	11.59	10.92	6.46	10.89	9.67				
	NT2RP3003686	3.02	3.35	12.97	5.63	1.59	1.88	2.06	1.47	1.07				
	NT2RP3003689	9.23	7.33	11.82	8.17	6.77	3.83	2.32	5.97	3.24	*			
55	NT2RP3003697	6.83	7.26	6.91	7.08	5.61	6.06	2.11	3.71	4.84	*			
	NT2RP3003701	9.67	9.01	11.76	7.31	4.84	5.18	3.31	2.62	4.46	*	**	-	-
	NT2RP3003704	10.73	9.76	12.38	10.7	7.93	10.02	15.67	9.66	12.47				
	NT2RP3003714	6.87	2.51	9.56	7.86	2.41	3.23	1.8	2.83	0.8				

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	NT2RP3003716	7.01	8.27	14.18	5.47	2.75	3.52	6.58	5.29	3.63			
	NT2RP3003721	13.04	10.15	23.8	10.64	5.81	9.58	11.26	11.19	10.89			
	NT2RP3003722	3.89	8.42	15.57	8.33	6.34	5.67	3.09	6.47	3.17			
5	NT2RP3003726	9.91	10.2	12.37	9.7	5.8	5.18	6.04	11.22	5.51			
	NT2RP3003729	15.24	10.41	15.84	9.27	8.89	4.46	6.77	7.5	6.93			
	NT2RP3003731	21.75	24.76	24.08	12.03	11.65	6.88	4.57	8.08	5.08	**	**	-
	NT2RP3003740	6.25	8.21	13.85	9.2	5.84	6.01	5.86	5.22	4.61			
	NT2RP3003746	8.07	4.76	18.45	7.1	1.15	4.58	3.94	4.56	4.9			
10	NT2RP3003749	12.41	10.83	19.25	6.47	8	6.02	6.17	7.75	8.42			
	NT2RP3003754	6.51	6.89	16.88	6.39	6.73	2.6	13.69	10.54	7.77			
	NT2RP3003759	5.04	4.82	10.4	5.36	1.64	1.95	2.96	2.71	1.17			
	NT2RP3003764	37.79	25.83	53.35	42.39	40.22	42.13	25.68	27.55	28.87			
	NT2RP3003765	53.84	52.07	31.23	39.67	26.34	21.22	14.6	22.88	28.5	*		-
	NT2RP3003767	8.01	8.08	7.88	8.43	4.34	4.24	4.39	2.88	4.34	**		-
15	NT2RP3003778	24.16	27.96	20.47	21.14	16.84	15.25	32.15	22.31	26.7			
	NT2RP3003779	12.68	5.29	15.64	10.68	4.35	10.53	3.1	5.95	4.41			
	NT2RP3003783	21.6	12.18	19.59	7.99	4.9	7.06	6.28	6.7	5.9	*	*	-
	NT2RP3003787	6.7	5.75	13.41	6.04	3.64	1.85	4.2	4.99	1.46			
	NT2RP3003789	8.11	11.36	13.5	7.92	6.55	6.67	5.52	5.69	3.28	*		-
20	NT2RP3003795	28.23	17.85	14.78	13.94	17.1	12.18	13.09	11.24	13.99			
	NT2RP3003799	7.73	3.87	9.64	5.67	2.6	3.17	2.83	1.93	2.55			
	NT2RP3003800	80.77	76.75	98.8	62.18	49.64	73.93	101.61	58.63	58.22			
	NT2RP3003805	19.72	20.08	15.07	17.29	8.51	14.67	17.48	12.39	11.94			
	NT2RP3003809	8.63	14.84	28.37	7.81	4.06	5.86	6.78	7.04	6.7			
	NT2RP3003819	19.91	12.71	21.8	8.29	12.89	15.12	8.35	11.58	14.32			
25	NT2RP3003824	4.44	5.34	16.42	6	3.26	2.18	5.16	4	3.14			
	NT2RP3003825	15.83	8.99	17.57	10.52	9.35	8.99	8.88	7.14	8.67			
	NT2RP3003828	7.18	6.66	13.27	7.4	5.95	4.81	5.75	3.03	3.24			
	NT2RP3003831	49.77	38.05	46.92	12.19	13.59	13	11.7	8.2	8.68	**	**	-
	NT2RP3003833	7	12.76	5.52	6.51	1.52	3.02	3.01	1.46	3.08			
	NT2RP3003836	22.92	45.16	37.16	16	14.78	18.49	26.73	7.91	11.58	*		-
30	NT2RP3003842	3.09	1.45	4.55	4.66	0.91	2.25	1.5	2.49	0.97			
	NT2RP3003843	23.17	13.66	18.94	21.62	11.25	18.44	16.81	22.17	19.21			
	NT2RP3003844	11.64	8.51	12	9.56	4.9	7.1	7.94	10.02	13.51			
	NT2RP3003846	11.56	8.88	8.25	8.42	3.89	7.04	8.15	6.21	10.88			
	NT2RP3003849	5.16	5.61	9.2	5.16	1.5	2.43	2.36	2.09	1.97	*		-
	NT2RP3003862	8.43	6.43	11.03	6.94	2.53	2.38	2.84	2.47	3.72	*		-
35	NT2RP3003870	9.39	14.91	15.6	7.42	3.58	2.61	4.29	2.22	5.4	*	*	-
	NT2RP3003874	8.27	8.06	7.54	6.09	3.19	3.65	2.59	2.64	5.21	*	**	-
	NT2RP3003876	6.84	5.28	7.66	10.08	2.52	6.72	2.11	6.22	4.3			
	NT2RP3003880	11.2	8.02	13.91	8.47	2.77	7.12	3.7	8.83	6.95			
	NT2RP3003889	6.9	11.63	11.35	8.75	7.41	9.51	7.37	8.06	5.22			
40	NT2RP3003891	13.51	11.29	17.94	8.42	7.04	7.49	10.43	12.21	12.8	*		-
	NT2RP3003914	2.72	1.62	6.58	5.33	2.56	2.54	2.7	1.4	2.69			
	NT2RP3003915	13.41	9.87	16.94	9.16	3.98	5.29	7.39	4.87	7.36	*	*	-
	NT2RP3003918	7.35	6.41	5.09	8.06	2.84	2.93	4.26	2.94	4.43	*		-
	NT2RP3003920	10.75	6.92	10.79	7.41	1.85	6.22	6.71	4.36	3.03	*		-
45	NT2RP3003924	33.52	17.52	18.55	12.63	9.6	13.46	9.41	16.64	13.76			
	NT2RP3003932	13.16	5.83	7.58	6.21	2.22	4.38	1.9	2.22	2.59	*		-
	NT2RP3003939	11.85	14.76	15.54	9.97	7.98	8.34	3.34	3.94	3.84	*	**	-
	NT2RP3003940	12.22	9.19	12.29	11.49	8.56	4.42	7.78	12.51	10.79			
	NT2RP3003943	7.2	4.68	6.57	7.12	5.58	5.18	4.42	3.92	6.05			
	NT2RP3003959	7.72	13.55	11.27	9.14	1.71	5.64	6.69	7.88	9.75			
50	NT2RP3003963	75.69	75.77	72.03	129.26	82.85	106.1	81.78	51.98	65.78			
	NT2RP3003965	18.74	14.24	13.95	14.48	9.03	12.62	20.67	19.68	26.47			
	NT2RP3003972	4.57	5.37	14.74	8.17	2.14	5.46	5	3.91	5.17			
	NT2RP3003973	6.48	6.48	12.61	7.2	3.25	3.55	3.26	4.26	5.78			
	NT2RP3003979	4.45	3.72	9.63	4.82	2.41	2.62	1.15	1.72	1.66			
	NT2RP3003980	146.06	117.79	158.74	103.46	88.31	102.32	155.94	132.47	147.6	*		-
55	NT2RP3003982	7.33	5.76	16.01	6.18	2.48	3	4.61	2.79	5.02			
	NT2RP3003989	10.71	10.02	27.87	8.13	4.12	8.61	5.84	9.52	13.56			
	NT2RP3003992	46.04	43.58	55.68	31.62	22.83	36.4	32.87	30.71	18.85	*	*	-
	NT2RP3004000	75.38	38.37	57.12	93.25	54.67	51.6	36.78	36.39	33.4			
	NT2RP3004001	14.94	10.16	22.03	15.95	8.73	15.13	13.16	15.23	21.06			

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	NT2RP3004005	23.75	15.81	26.46	14	10.64	14.12	16.28	18.58	18.43				
	NT2RP3004013	22.54	11.33	21.98	6.11	3.13	3.73	3.05	4.94	3.43	*	*	-	-
	NT2RP3004016	7.39	7.18	13.3	10.92	9.82	5.35	6.27	5.44	4.76				
5	NT2RP3004025	22.82	15.93	25.25	22.37	10.03	12.12	21.2	17.91	21.7				
	NT2RP3004030	4.66	4.65	8.61	4.83	3.44	3.8	4.36	2.41	1.96				
	NT2RP3004041	4.1	2.26	3.06	5.03	2.28	1.57	2.62	0.7	0.71				
	NT2RP3004042	2602.1	1724.7	1778.2	2098.3	1690	1795.1	1947.3	2828.9	2085.3				
	NT2RP3004044	32.34	21.11	30.01	12.91	11.29	11.35	7.18	15.29	26.2	**		-	-
10	NT2RP3004051	19.22	22.27	34.06	33.29	21.4	25.83	12.31	39.18	27.89				
	NT2RP3004052	20.9	17.89	21.89	18.39	15.57	16.97	13.27	17.39	19.16				
	NT2RP3004053	19.14	11.65	20.87	15.13	10.18	12.84	3.1	7.99	5.77	*		-	-
	NT2RP3004055	5.06	6.81	8.6	5.35	3.54	2.7	2.8	3.03	2.13	*		-	-
	NT2RP3004059	26.03	28.01	36.98	19.3	19.54	21.1	20.16	18	15.03	*	*	-	-
	NT2RP3004063	29.14	22.42	34.14	23.83	23.28	19.51	31.01	26.64	12.72				
15	NT2RP3004067	7.95	8.62	20.76	10	4.39	4.65	3.75	4.12	8.39				
	NT2RP3004070	905.61	934.59	965.28	291.19	622.85	595.78	278.31	1360.6	1279.5	*		-	-
	NT2RP3004075	11.59	15.27	23.01	8.7	5.82	8.89	3.95	5.77	5.73	*		-	-
	NT2RP3004078	13.83	11.53	17.13	13.53	5.08	9.69	12.68	11.48	12.45				
	NT2RP3004083	33.39	27.25	43.84	12.1	13.49	7.53	6.38	6.07	6.79	*	**	-	-
20	NT2RP3004084	25.34	24.44	39.2	27	15.25	16.2	38.67	47.1	47.33				
	NT2RP3004087	13.47	17.06	17.12	15.44	8.85	8.53	10.22	10.37	8.13	*		-	-
	NT2RP3004090	72.24	81.09	78.4	57.09	57.97	55.36	77.78	70.88	90.98	**		-	-
	NT2RP3004093	28.49	18.68	45.95	14.41	12.09	18.33	8.92	23.19	25.5				
	NT2RP3004095	33.26	26.66	48.11	23.16	21.66	33.49	19.24	23.44	21.47				
	NT2RP3004102	34.73	35.32	40.77	25.98	17.76	24.22	15.74	23.36	12.18	*	**	-	-
25	NT2RP3004110	7.05	4.57	10.07	7.67	1.49	3.89	2.25	3.65	1.62	*		-	-
	NT2RP3004119	11.05	7.96	13.76	6.77	3.42	4.11	3.84	3.73	1.51	*	*	-	-
	NT2RP3004125	3.06	3.32	9.52	6.05	1.93	1.78	1.81	1.49	1				
	NT2RP3004129	11.05	13	16.54	13.66	11.08	8.18	7.67	3.97	5.87	*		-	-
	NT2RP3004130	6.85	5.7	8.22	6.11	4.3	3.04	1.91	3.1	2.41	**		-	-
30	NT2RP3004133	8.31	5.24	20.22	8.3	3.21	4.09	3.33	4.08	3.29				
	NT2RP3004145	5.99	4.29	13.16	5.33	2.78	2.69	2.63	4.11	3.14				
	NT2RP3004148	53	37.5	49.88	32.7	23.92	15.17	30.82	36.4	44.13	*		-	-
	NT2RP3004155	8.18	8.86	12.7	12.14	3.98	4.25	2.59	2.94	3.13	**		-	-
	NT2RP3004165	77.97	53.41	68.62	51.37	46.12	31.89	49.51	25.55	55.19				
	NT2RP3004179	9.55	6.18	11.2	6.95	2.94	2.88	4.01	3	3.7	*		-	-
	NT2RP3004185	6.31	5.21	6.12	9.04	2.95	2.38	1.55	0.61	2.3	**		-	-
35	NT2RP3004188	6.31	7.01	6.86	7.94	4.08	2.67	3.74	2.3	1.82	**		-	-
	NT2RP3004189	15.63	7.3	21.16	9.58	5.21	8.89	4.83	8.4	6.14				
	NT2RP3004190	64.52	34.39	57.67	48.45	40.38	53.55	47.37	42.21	45.49				
	NT2RP3004191	122.58	123.5	136.79	74.78	46.86	44.19	48.51	70.16	47.4	**	**	-	-
	NT2RP3004202	18.55	13.31	21.41	14.01	15.47	6.42	10.97	12.13	10.67				
40	NT2RP3004205	10.59	7.33	14.79	6.1	4.73	2.92	2.52	2.35	2.6	*		-	-
	NT2RP3004206	15.55	12.16	17.94	7.47	8.64	7.63	5.69	7.13	12.18	*		-	-
	NT2RP3004207	8.65	8.42	9.24	5.53	2.88	3.67	2.31	1.22	2.02	**	**	-	-
	NT2RP3004209	27.4	23.65	14.82	17	13.67	16.8	19.95	17.39	12.49				
	NT2RP3004215	22.45	23.53	27.86	11	7.75	10.82	4.22	8.07	7.54	**	**	-	-
	NT2RP3004219	5.58	5.12	13.51	6.61	2.08	4.81	3.19	3.17	3.09				
45	NT2RP3004242	4.18	6.26	13.02	6.15	3.05	4.41	4.72	3.98	3.45				
	NT2RP3004246	3.85	4.1	9.37	4.89	2.24	1.94	1.48	3.04	2.11				
	NT2RP3004253	7.46	3.55	9.07	5.38	2.69	1.44	2.57	2.47	3.21				
	NT2RP3004258	8.43	4.33	9.6	7.18	4.84	3.38	6.14	4.76	3.41				
	NT2RP3004262	5.75	6.49	6.12	6.38	2.36	2.74	4.69	0.6	2.65	*		-	-
	NT2RP3004275	5.37	6.56	6.47	6.33	1.33	2.3	2.5	1.89	3.75	**		-	-
50	NT2RP3004282	4.86	27.86	18.63	6.39	3.74	5.05	2.71	3.54	3.27				
	NT2RP3004289	6.43	5.13	10.92	5.92	2.79	3.35	2.25	2.59	3.21				
	NT2RP3004294	4.71	4.44	6.56	4.95	2.62	3.32	2.88	6.45	3.88				
	NT2RP3004298	64.72	55.93	73.74	63.66	58.3	70.43	70.1	51.46	68.44				
	NT2RP3004309	10	7.69	11.97	7.21	2.5	3.75	5.84	3.48	5.36	*	*	-	-
	NT2RP3004321	23.29	38.14	42.57	12.44	16.53	8.76	14.14	5.43	9.71	*	*	-	-
55	NT2RP3004322	4.19	4.29	4.98	4.8	1.3	0.91	2.93	1.84	2.18	**		-	-
	NT2RP3004332	9.53	11.83	11.13	7.92	3.85	4.05	4.3	2.24	2.92	*	**	-	-
	NT2RP3004334	14.9	13.13	17.93	15.28	11.06	7.25	6.62	11.71	9.43	*		-	-
	NT2RP3004336	9.94	8.5	13.66	9.26	7.37	6.68	4.73	8.17	4.32				

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Table 451

	NT2RP3004338	20.15	16.11	15.61	11.35	11.45	16.93	14.61	18.8	16.46			
	NT2RP3004341	45.52	46.06	66.9	30.5	32.86	24.48	35.75	44.1	42.23	*	-	
5	NT2RP3004345	5.41	7.27	12.03	7.28	2.26	2.19	5.01	3.58	4.59			
	NT2RP3004348	8.2	11.9	19.15	6.37	5.32	6.29	9.92	4.97	6.08			
	NT2RP3004349	46.27	44.89	52.77	25.21	14.4	28.82	51.32	39.58	50.42	**	-	
	NT2RP3004355	13.69	17.95	13.45	12.62	8.18	11.72	10.41	5.58	7.23	*	-	
	NT2RP3004356	6.56	4.92	9.79	7.46	3.18	5.93	2.87	5.09	3.61			
	NT2RP3004360	11.41	7.43	12.2	11.26	4.38	7.34	4.62	4.39	7.23	*	-	
10	NT2RP3004361	22.43	16.96	27.29	12.91	14.7	16.73	18.55	21.02	26.27			
	NT2RP3004374	6.08	4.11	5.92	5.52	2.91	4.87	2.31	2.56	2.6	*	-	
	NT2RP3004378	50.03	39.45	48.92	39.78	39.18	55.24	61.97	46.46	63.83			
	NT2RP3004399	25.24	30.84	27.39	23.98	13.72	17.1	23.05	19.32	24.46	*	-	
	NT2RP3004405	5.46	2.89	3.95	6.86	3.8	2.54	2.58	3.57	3.49			
	NT2RP3004406	48.02	80.1	76.06	27.26	18.49	29.22	40.17	40.49	25.13	*	*	-
15	NT2RP3004411	21.84	13.45	15.39	11.3	8.55	12.78	6.83	10.8	17.8			
	NT2RP3004424	12.83	9.11	14	10.53	6.29	12.31	8.49	6.86	11.07			
	NT2RP3004428	9.06	4.59	7.61	7.92	3	6.19	2.13	2.45	2.73	*	-	
	NT2RP3004432	41.77	40.01	43.16	46.87	29.7	37.75	43.11	55.91	45.48			
	NT2RP3004434	6.59	6.36	9.2	19.42	10.09	11.41	8.35	8.97	10.87			
20	NT2RP3004446	5.55	1.31	2.23	5.8	1.27	2.52	2.84	1.81	2.66			
	NT2RP3004451	28.05	27.38	35.9	43.9	34.57	29.99	27.84	20.66	27.06			
	NT2RP3004454	3.04	4.95	3.07	5.17	2.65	2.97	3.32	1.95	4.76			
	NT2RP3004466	17.88	12.48	17.63	17.19	13.76	19.32	8.38	10.38	11.73	*	-	
	NT2RP3004470	6.58	4.48	12.1	9.37	2.81	3.83	6.66	6.76	5.57			
	NT2RP3004472	4.96	8.32	13.71	7.25	5.54	4.58	2.83	3.65	3.08			
25	NT2RP3004475	9.27	6	11.18	8.66	2.73	3.48	3.79	5.2	3.34	*	-	
	NT2RP3004480	22.33	15.69	32.46	17.18	10.83	15.46	12.05	10.67	10.95			
	NT2RP3004481	7.51	6.36	10.91	7.96	3.04	6.85	8.17	5.21	5.83			
	NT2RP3004490	1.96	3.67	4.31	5.07	2.67	3.48	2.86	2.05	1.78			
	NT2RP3004496	29.05	43.68	52.3	32.37	24.7	28.45	17.59	12.79	20.95	*	-	
	NT2RP3004498	6.1	6.29	10.2	8.29	5.15	5.43	3.36	4.35	5.77			
30	NT2RP3004503	13.34	8.17	15.98	13.28	6.98	13.95	9.69	13.04	16.21			
	NT2RP3004504	26.86	13.87	24.17	16.13	11.34	13.03	8.55	9.71	9.3	*	-	
	NT2RP3004505	60.88	42.22	65.16	60.93	61.18	59.93	38.93	40.66	35.92			
	NT2RP3004507	6.96	5.95	8.15	5.81	3.02	3.27	2.74	2.78	2.24	**	-	
	NT2RP3004519	3.09	3.32	8.34	4.29	1.92	0.77	1.76	0.64	1.58			
	NT2RP3004524	22.27	16.91	24.46	12.8	14.38	10.78	10.59	7.77	17.02	*	-	
35	NT2RP3004527	31.26	36.6	41.52	32.19	22.11	22.1	23.08	21.05	18.57	**	-	
	NT2RP3004534	1954.5	1225.4	1438.4	1526.7	1505.7	1779.6	777.34	2507.5	2418.6			
	NT2RP3004539	4.71	4.69	10.04	5.61	3.18	4.71	4.15	5.52	6.25			
	NT2RP3004541	14.72	10.14	22.05	12.49	7.26	9.05	8.78	11	10.96			
	NT2RP3004544	17.32	13.37	16.21	16.43	8.76	13.79	6.55	10.61	10.66	*	-	
40	NT2RP3004551	12.43	7.15	13.73	9.94	5.53	6.65	10.18	9.42	7.62			
	NT2RP3004552	19.37	11.98	21.3	18.2	12.57	16.98	18.98	16.22	18.63			
	NT2RP3004557	11.18	12.99	15.15	12.15	8.14	12.54	12.08	12.56	14.07			
	NT2RP3004561	2.52	4.37	4.66	6.9	2.44	3.94	3.97	3.31	3.2			
	NT2RP3004566	16.46	13.14	29	10.83	7.99	8.15	3.35	6.43	21.27			
	NT2RP3004569	20.41	16.28	28.7	14.13	11.71	13.43	13.97	16.78	16.76			
45	NT2RP3004572	12.48	13.38	19.74	11.19	9.39	9.67	3.98	9.35	8.35	*	-	
	NT2RP3004578	6.49	6.06	8.06	7.21	4.59	4.3	5.13	4.76	4.1	*	-	
	NT2RP3004584	8.34	6.1	9.57	5.07	2.29	4.9	3.85	3.5	2.08	*	*	-
	NT2RP3004588	4.64	4.62	7.46	7.78	2.88	3.22	3.01	5.54	3.28			
	NT2RP3004594	18.77	25.61	21.44	21.59	19.15	22.94	29.86	27.19	18.84			
	NT2RP3004603	4.79	6.26	5.77	8.8	3.9	4.9	5.46	7.72	5.82			
50	NT2RP3004612	6.46	6.92	12.58	12.71	4.69	5.32	2.31	10.42	14.75			
	NT2RP3004617	8.05	8.14	15.39	8.87	3.8	5.79	3.78	6.88	7.16			
	NT2RP3004618	36.56	23.11	37.29	24.87	25.7	22.47	22.39	33.72	29.91			
	NT2RP3004625	19.69	16.42	18.21	11.76	10.91	14.71	6.25	8.76	11.12	*	**	-
	NT2RP3004635	11.6	9.72	13.73	7.06	5.4	4.21	3.68	2.39	2.94	*	**	-
	NT2RP3004640	4.25	10.31	12.87	7.49	7.74	5.34	4.28	3.2	9.33			
55	NT2RP3004642	15.02	23.4	27.93	15.96	15.92	16.39	17.49	17.88	14.1			
	NT2RP3004647	10.52	11.7	14.69	13.69	6.27	6.34	18.22	14.86	18.18	*	*	-
	NT2RP3004652	28.1	24.38	41.76	13.95	14.47	12.02	4.02	12.27	12.65	*	*	-
	NT2RP3004669	7.74	7.41	20.24	7.31	6.69	6.49	4.02	6.68	4.21			

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Table 452

	NT2RP3004670	5.78	5.9	15.55	5.95	8.77	4.78	1.73	4.19	3.14				
	NT2RP4000008	4.28	3.76	9.74	7.01	3.13	2.8	0.87	1.61	1.16				
5	NT2RP4000018	777.26	720.79	779.71	458.85	552.02	180.81	608.14	341.39	573.73	*	*	-	-
	NT2RP4000023	12.08	13.49	11.95	6.59	4.27	3.03	5.43	2.46	2.58	**	**	-	-
	NT2RP4000025	10.92	10.01	10.19	8.87	3.46	6.52	5.55	3.38	7.2	*		-	-
	NT2RP4000035	13.64	12.06	18.1	13.28	10.2	10.62	12.01	14.28	15.16				
	NT2RP4000041	7.95	4.85	12.17	6.47	2.4	5.6	2.83	2.55	3.55				
	NT2RP4000049	5.5	8.69	14.31	6.89	4.49	2.04	3	3.25	4.73				
10	NT2RP4000050	7.92	6.2	13.4	9.91	4.4	3.61	2.52	5.2	2.39				
	NT2RP4000051	11.64	12.9	17.08	9.37	6.75	7.7	7.83	11.79	8.18	*		-	-
	NT2RP4000063	9.36	7.43	9.4	6.21	2.66	4.7	2.12	2.88	2.29	*	**	-	-
	NT2RP4000065	8.57	5.45	7.62	5.43	1.38	3.74	3.79	2.44	1.14	*		-	-
	NT2RP4000070	8.9	10.6	11.32	10.92	5.17	4.74	3.9	3	5.41	**		-	-
	NT2RP4000074	7.09	6.56	7.33	6.07	3.64	2.14	2.7	1.95	3.11	**		-	-
15	NT2RP4000078	10.64	7.98	15.22	9.04	4.02	9.72	4.12	7.85	6.44				
	NT2RP4000080	39.53	29.48	35.07	14.73	7.78	7.51	7.13	12.84	8.56	**	**	-	-
	NT2RP4000099	17.27	15.29	21.59	9.54	12.81	6.62	5.87	6.72	3.64	*	**	-	-
	NT2RP4000102	8.52	8.93	15.05	7.45	6.98	5.31	5.6	5.59	5.12				
	NT2RP4000103	20.66	29.01	31.17	15.7	16.08	13.47	20.04	13.58	12.68	*	*	-	-
20	NT2RP4000108	10.35	7.66	11.54	5.11	5.39	5.22	4.96	2.69	3.44	*	**	-	-
	NT2RP4000109	9.73	11.84	8.78	8.41	4.9	6.21	6.7	3.67	4.98	*		-	-
	NT2RP4000111	9.68	7.22	7.83	10.68	5.18	7.24	9.51	4.5	2.88				
	NT2RP4000112	16.91	11.4	24.28	20.79	19.36	22.3	16.09	13.49	17.44				
	NT2RP4000115	7.34	4.25	10.98	5.53	2.81	4.32	2.76	2.51	2.27				
	NT2RP4000129	24.84	25.48	33.51	13.19	12.49	13.21	12.38	15.5	12.9	**	**	-	-
25	NT2RP4000137	20.7	16.54	14.08	10.11	6.13	6.89	9.81	6.38	10.47	*	*	-	-
	NT2RP4000138	7.91	6.25	8.72	5.36	2.95	3.73	3.09	3.11	5.54	*	*	-	-
	NT2RP4000141	11.63	7.1	7.39	5.05	2.2	2.55	3.83	2.34	1.67	*	*	-	-
	NT2RP4000147	7.8	8.75	6.46	5.67	2.45	1.71	3.71	1.66	2.95	*	**	-	-
	NT2RP4000150	22.83	40.43	32.64	26.18	18.45	18.86	24.1	13.63	20.82				
	NT2RP4000151	5.35	2.77	7.92	5.7	2.57	4.58	2.81	1.73	3.64				
30	NT2RP4000157	5.03	3.17	7.55	5.12	2.41	3.03	2.61	4.59	2.88				
	NT2RP4000159	7.7	6.21	14	7.81	5.43	9.16	5.02	7.93	7.16				
	NT2RP4000163	11.36	16.35	22.24	7.82	6.7	5.1	11.58	8.66	14.17	*		-	-
	NT2RP4000167	5.72	10.76	11.28	6.86	1.93	2.94	6.09	1.64	2.98				
	NT2RP4000171	17.67	20.8	16.76	13.24	7.81	11.48	17.22	11.6	13.85	*		-	-
35	NT2RP4000175	7.68	11.5	9.21	7.19	5.94	7.44	5.84	4.86	6.71	*		-	-
	NT2RP4000180	8.25	9.87	9.45	8.5	4.86	7.21	9.47	6.55	7.72				
	NT2RP4000185	3.44	9.69	9.07	5.25	3.82	5.08	3.89	5.51	9.51				
	NT2RP4000192	3.66	2.3	7.85	7.16	4.58	3.22	2.99	2.89	2.84				
	NT2RP4000194	4.94	3.92	6.27	5.67	6.92	4.33	4.73	3.32	6.3				
	NT2RP4000196	4.44	3.86	8.22	4.42	2.19	1.89	2.14	2.44	1.01				
40	NT2RP4000210	4.32	3.9	5.46	5.03	2.17	1.97	3.58	2.52	3.91				
	NT2RP4000212	10.41	10.12	9.74	6.43	6.54	3.07	4.86	4.69	2.44	*	**	-	-
	NT2RP4000214	21.41	28.56	31.47	14.93	12.43	12.75	14.71	10.53	11	*	**	-	-
	NT2RP4000216	18.56	17.54	17.8	9.05	3.32	6.3	7.12	4.66	4.69	**	**	-	-
	NT2RP4000218	20.76	13.22	21.73	16.85	12.17	21.91	12.16	18.58	23.33				
	NT2RP4000223	11.85	6.5	8.31	9.5	4.18	9.75	8.04	7.05	11.94				
45	NT2RP4000243	10.56	9.93	12.96	11.2	9.86	11.7	8.64	9.69	10.23				
	NT2RP4000246	7.12	5.86	5.64	5.65	4.43	4.42	2.37	2.31	3.27	**		-	-
	NT2RP4000250	11.29	8.98	12.39	10.04	3.49	5.45	5.46	5.81	5.67	**		-	-
	NT2RP4000256	3.26	5.13	6.67	4.51	2.18	2.56	3.11	2.41	2.48				
	NT2RP4000257	23.54	23.13	30.8	34.24	27.3	37.51	26.44	19.58	27.22				
	NT2RP4000259	5.19	5.55	3.54	8.67	2.13	4.17	4.34	3.84	5.01				
50	NT2RP4000261	4.72	2.05	7.37	6.8	1.48	3.76	2.37	3.23	3.88				
	NT2RP4000262	2.93	2.46	11.12	5.21	1.63	2.61	2.49	2.62	2.71				
	NT2RP4000263	8.03	5.82	13.8	7.33	4.75	4.76	8.35	4.63	5.93				
	NT2RP4000280	36.69	25.69	34.43	21.81	13.93	11.89	23.3	25.5	21.75	*		-	-
	NT2RP4000286	7.96	5.71	10.34	8.48	4.4	5.47	4.56	4.72	2.93				
55	NT2RP4000290	6.28	5.27	10.35	7.67	3.77	4.58	5.45	2.24	4.35				
	NT2RP4000291	23.37	31.04	45.88	29.65	20.44	28.9	16.58	13.08	6.43	*		-	-
	NT2RP4000301	9.06	21.31	16.13	18.84	21.42	12.52	13.04	8.64	8.86				
	NT2RP4000312	7.37	5.86	10.71	6.75	4.45	5.45	4.08	4.23	5.32				
	NT2RP4000321	14.11	6.64	13.51	10.77	5.65	7.11	6.38	8.75	12.76				

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Table 453

	NT2RP4000323	42.99	31.25	39.68	23.73	23.52	24.08	25.22	26.31	20.02	*	*	-	-
	NT2RP4000324	28.87	20.72	25.53	23.74	16.73	21.66	28.32	24.57	21.68		**	-	-
	NT2RP4000334	11.51	10.77	15.15	9.55	9.47	9.13	6.39	6.12	5.89			-	-
5	NT2RP4000343	20.88	12.62	32.18	18.49	14.22	8.72	14.98	17.89	14.7			-	-
	NT2RP4000348	12.35	14.21	17.96	11.42	8.77	9.63	12.1	7.85	8.02			-	-
	NT2RP4000349	8.77	16.24	12.89	11.44	12.7	9.21	11.37	7.34	11.23			-	-
	NT2RP4000355	253.25	117.6	189.34	264.37	149.78	254.47	257.02	316.08	192.79			-	-
	NT2RP4000356	61.98	36.7	79.91	60.03	57.95	82.79	39.95	40.28	37.12		*	-	-
	NT2RP4000360	38.52	30.1	36.81	28.77	30.27	34.86	22.5	29.04	23			-	-
10	NT2RP4000367	5.32	7.72	13.11	9.15	7.75	8.58	5.65	7.52	4.05			-	-
	NT2RP4000370	6.13	3.8	7.29	7.4	4.81	4.6	4.29	3.27	2.44			-	-
	NT2RP4000373	52.16	35.56	49.83	33.3	22.86	20.18	8.95	13.1	7.55	*	**	-	-
	NT2RP4000376	4.35	4.76	3.85	5.98	2.55	3.6	3.64	2.24	1.76	*		-	-
	NT2RP4000381	4.21	7.62	7.46	8.53	4.41	5.48	6.16	4.44	4.11			-	-
15	NT2RP4000388	15.3	8.64	28.13	9.56	6.37	8.78	3.98	7.28	10.59			-	-
	NT2RP4000390	9.32	12.91	21.1	9.57	7.3	6.9	4.45	8	7.73			-	-
	NT2RP4000393	4.73	6.04	14.2	5.91	3.76	3.4	2.49	4.28	1.61			-	-
	NT2RP4000398	15.1	12.32	17.4	15.43	7.99	12.09	10.09	7.98	7.95	*		-	-
	NT2RP4000406	6.93	7.1	10	7.22	4.81	7.48	4.73	7.43	4.16			-	-
20	NT2RP4000407	14.2	8.65	18.88	9.39	7.38	7.23	8.05	7.66	8.08			-	-
	NT2RP4000413	6.36	8.44	8.74	7.32	6.23	4.25	14.9	11.64	8.91			-	-
	NT2RP4000415	5.58	6.36	5.25	8.19	3.66	6.69	6.61	5.43	4.11			-	-
	NT2RP4000417	4.81	3.78	14.82	6.27	2.89	2.96	1.78	3.56	2.97			-	-
	NT2RP4000423	8.56	11.85	52.11	7.59	6.28	6.14	5.59	8.25	4.46			-	-
	NT2RP4000424	5.63	6.45	12.58	7.04	3.08	2.9	3.66	4.14	1.14			-	-
25	NT2RP4000447	7.22	11.02	14.44	6.8	2.54	3.42	2.02	2.94	1.68	*		-	-
	NT2RP4000448	10.44	4.78	12.49	7.44	5.19	4.9	2.34	3.11	4.18	**	*	-	-
	NT2RP4000449	14.23	13.95	15.79	8.35	8.81	8.15	9.09	11.62	7.03			-	-
	NT2RP4000453	9.01	6.07	14.02	7.74	5.15	4.89	6.56	4.27	8.08	**		-	-
	NT2RP4000455	9.03	10.34	8.68	7.99	5.45	3.17	4.44	4.36	4.13			-	-
	NT2RP4000456	7.04	6.17	17.02	5.76	3.52	4.72	1.66	2.58	3.46			-	-
30	NT2RP4000457	13.26	8.71	17.6	8.13	4.23	7.52	11.15	9.14	8.56	*	*	-	-
	NT2RP4000461	55.44	37.43	46.46	34.13	24.48	24.96	29.53	26.44	29.5			-	-
	NT2RP4000462	42.85	30.75	56.94	75.69	50.54	40.64	52.98	43.57	42.53			-	-
	NT2RP4000463	85.58	62.21	92.77	65.01	52.89	43.38	67.48	75.6	83.4			-	-
	NT2RP4000471	25.28	34.12	24.81	15.24	25.16	15.87	19.6	16.58	11.2	*		-	-
	NT2RP4000472	7.71	9.85	9.52	10.37	5.54	5.62	6.84	6.67	3.82	*	**	-	-
35	NT2RP4000476	14.81	18.77	16.55	11.79	4.98	3.82	5.79	4.35	2.67			-	-
	NT2RP4000480	12.42	10.39	22.37	9.71	8.11	7.69	2.98	6.14	7.56			-	-
	NT2RP4000481	7.17	5.4	16.93	6.71	1.97	4.16	2.54	3.59	3.12			-	-
	NT2RP4000483	21.87	12.5	29.34	14.63	7.41	9.82	17.08	21.67	14.93			-	-
	NT2RP4000487	11.87	8.84	15.81	9.26	6.43	6.73	8.06	10.31	7.08			-	-
	NT2RP4000486	16.33	41.67	19.05	11.91	7.25	5.15	7.41	10.6	17.63			-	-
40	NT2RP4000497	5.81	3.81	10.08	3.87	3.09	2.81	2.48	1.77	2.22			-	-
	NT2RP4000498	26.54	11.6	46.3	21.94	11.56	20.83	11.71	6.48	8.74			-	-
	NT2RP4000500	16.19	14.2	13.24	21.4	11.25	11.2	15.02	6.9	5.02			-	-
	NT2RP4000507	14.47	9.74	21.49	11.59	12.91	17.96	12.44	18.01	18.95	*		-	-
	NT2RP4000515	34.88	29.88	36.21	23.73	25.4	27.8	24.2	28.54	29.19			-	-
45	NT2RP4000516	8.8	4.78	15.95	7.22	3.73	6.26	5.56	4.23	5.23			-	-
	NT2RP4000517	6.93	4.39	11.92	5.6	2.28	2.95	2.26	2.51	3.47		*	-	-
	NT2RP4000518	5.66	5.23	9.62	6.13	3.29	2.14	2.66	2.57	2.25			-	-
	NT2RP4000519	11.25	13.8	9.43	7.22	5.12	6.11	9.96	4.77	2.74	*		-	-
	NT2RP4000524	3.66	2.61	3.66	4.66	0.22	1.66	1.44	0.06	0.23	*	*	-	-
	NT2RP4000528	9.85	11.61	11.68	7.98	5.49	4.94	7.65	1.72	3.24	*	*	-	-
50	NT2RP4000537	22.62	26.04	23.49	9.39	8.19	12.07	6.5	9.43	12.67	**	**	-	-
	NT2RP4000541	6.77	5.01	14.31	6.57	5.43	3.77	2.53	4.6	6.37			-	-
	NT2RP4000543	7.3	6.98	11.29	8.27	7.56	3.29	6.55	3.66	5.22			-	-
	NT2RP4000545	22.52	30.13	32.57	13.3	16.56	19.62	18.71	21.42	13.96	*	*	-	-
	NT2RP4000546	4.78	4.57	9.21	6.74	1.72	3.53	3.64	0.82	4.41			-	-
	NT2RP4000549	11.61	18.79	20.98	6.99	2.21	3.33	4.79	2.09	3.96	*	*	-	-
55	NT2RP4000556	15.54	16.2	17.27	7.73	3.7	5.61	5.6	2.76	4.84	**	**	-	-
	NT2RP4000557	11.07	12.42	10.89	8.61	4	8.57	12.02	7.59	12.85			-	-
	NT2RP4000558	14.08	10.84	18.04	10.75	6.08	12.87	11.5	16.9	20.52			-	-
	NT2RP4000560	6.31	4.01	7.32	5.77	2.76	5.36	5.37	6.37	4.62			-	-

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	NT2RP4000568	23.22	25.79	25.36	10.18	10.21	8.47	12.24	9.65	11.67	**	**	-	-
	NT2RP4000583	5.85	2.98	7.97	6.46	2.06	2.6	3.62	4.57	3			-	-
	NT2RP4000585	9.33	19	28.37	6.6	3.13	5.64	10.5	7.96	7.04			-	-
5	NT2RP4000588	7.43	10.21	10.68	6.68	2.44	1.85	5.44	2.87	5.6	*	*	-	-
	NT2RP4000590	6.55	7.08	8.76	6.12	1.79	2.53	5.82	2.45	2.62			-	-
	NT2RP4000599	40.85	42.1	36.12	25.51	13.35	23.08	24.88	16.83	13.91	*	**	-	-
	NT2RP4000603	16.26	11.07	12.79	9.86	5.09	7.92	5.61	11.76	8.02	*		-	-
	NT2RP4000607	18.04	30.52	24.32	19.53	17.65	25.01	23.84	28.13	28.14			-	-
	NT2RP4000614	10.28	8.25	15.91	8.83	8.89	11.93	10.16	9.95	16.38			-	-
10	NT2RP4000634	6.36	4.3	5.27	7.5	2.83	3.42	3.64	2.83	2.88	*	*	-	-
	NT2RP4000638	23.34	31.48	44.47	17.42	11.63	10.92	16.58	9.75	15.96	*	*	-	-
	NT2RP4000648	20.24	25.67	26.97	19.17	9.45	12.88	31.67	25.66	31.95	*	*	-	-
	NT2RP4000657	29.17	33.57	37.98	49.46	41.57	42.06	36.04	23.15	32.67	*	*	-	-
	NT2RP4000691	5.59	4.16	3.63	5.96	2.37	3.18	5.01	2.34	4.68			-	-
15	NT2RP4000697	6.38	8.16	10.53	9.34	4.77	12.75	6.26	6.22	8.11			-	-
	NT2RP4000704	1.95	1.59	2.11	5.91	1.47	3.12	1.95	2.78	2.48	*		-	-
	NT2RP4000710	20.97	14	15.55	13.68	8.51	18.99	7.53	9.31	11.22			-	-
	NT2RP4000713	4.84	3.26	2.49	5.57	2.13	4.31	3.32	1.62	2.08			-	-
	NT2RP4000724	3.62	3.53	2.74	6.31	1.65	2.66	3.33	4.03	5.81			-	-
	NT2RP4000725	3.89	2.42	3.21	6.35	1.7	3.24	4.75	1.9	3.76			-	-
20	NT2RP4000728	11.56	10.9	20.97	12.34	10.22	7.45	16.8	22.52	15.47			-	-
	NT2RP4000737	13.76	11.71	16.21	12.21	6.25	7.06	13.63	12.39	10.01			-	-
	NT2RP4000739	8.74	4.93	10.91	9.95	3.76	6.63	5.46	5.27	7.1			-	-
	NT2RP4000749	16.46	11.21	22.1	13.84	13.31	13.35	10.75	11.02	11.19			-	-
	NT2RP4000769	9.99	10.26	18.79	12.18	3.6	7.13	3.73	5.86	5.05			-	-
25	NT2RP4000774	9.26	8.05	14.72	7.64	2.48	6.01	4.16	4.89	5.59			-	-
	NT2RP4000781	4.81	3.97	6.84	6.54	2.43	3.37	3.39	2.48	3.03			-	-
	NT2RP4000783	17.33	30.73	35.46	25.7	13.51	13.28	15.68	13.86	21.97			-	-
	NT2RP4000788	24.76	10.56	23.27	26.79	17.17	17.48	11.21	13.65	10.18			-	-
	NT2RP4000792	5.04	4.94	10.96	8.67	1.86	4.24	2.65	4.16	5.52			-	-
	NT2RP4000809	342.08	122.2	157.03	126.01	165.45	173.36	118.64	164.8	122.66			-	-
30	NT2RP4000817	8.94	6.91	14.48	7.71	3.01	5.35	5.37	3.63	4.85			-	-
	NT2RP4000821	136.37	90.35	131.55	91.69	114.89	72.17	100.95	73.86	85.69			-	-
	NT2RP4000822	14.55	12.26	20.9	11.12	8.44	15.29	16.17	13.27	18.76			-	-
	NT2RP4000823	2939.8	2567.2	3305.2	1530.8	2690.7	2293.4	1706.4	1550.9	2562.9			-	-
	NT2RP4000831	78.61	54.25	90.69	72.05	94.12	99.31	70.64	58.37	82.02			-	-
	NT2RP4000833	27.77	14.49	23.94	22.19	7.07	21.11	19.12	24.88	29.44			-	-
35	NT2RP4000837	6.72	4.87	9.85	8.02	2.92	3.66	2.57	4.16	7.79			-	-
	NT2RP4000839	145.23	125.82	232.83	173.61	169.29	177.66	124.91	117.96	102.54			-	-
	NT2RP4000846	29.27	18.32	20.88	21.05	17.61	12.28	9.05	14.78	13	*		-	-
	NT2RP4000848	18.2	11.65	15.75	19.15	9.44	13.53	19	14.72	12.39			-	-
	NT2RP4000855	6.13	7.14	11.29	10.66	4.62	6.62	4.65	3.21	3.53			-	-
40	NT2RP4000863	6.72	6.6	6.48	8.17	4.81	5.97	4.42	5.29	3.77	**		-	-
	NT2RP4000865	45.32	26.52	38.54	39.71	38.1	49.51	43.48	35.35	41.09			-	-
	NT2RP4000873	144.06	68.9	135.34	139.48	79.72	155.93	87.22	97.84	116.06			-	-
	NT2RP4000874	10.17	6.06	16.44	7.29	2.79	4.52	3.81	5.9	8.53			-	-
	NT2RP4000875	14.13	12.82	21.34	8.26	7.3	7.14	8.99	11.91	13.22	*		-	-
	NT2RP4000878	36.06	33.12	27.77	33.84	31.46	17.83	20.58	24.01	24.14	**		-	-
	NT2RP4000879	8.38	6.53	9.14	6.87	3.51	3.32	2.85	3.36	3.88			-	-
45	NT2RP4000880	35.09	26.71	47.85	50.74	42.76	41.2	29.03	30.06	33.07			-	-
	NT2RP4000891	701.32	715.69	430.85	696.54	840.24	746.75	898.32	124.76	792.55			-	-
	NT2RP4000894	21.41	14.41	21.14	15.13	8.85	12.55	11.08	19.34	17.24			-	-
	NT2RP4000898	2.97	2.72	11.52	4.95	1.01	2.82	2.18	3.29	4.66			-	-
	NT2RP4000899	44.53	41.78	65.07	39.31	37.51	42.09	31.81	35.26	42.89			-	-
50	NT2RP4000907	4.19	4.02	10.25	6.24	3.94	2.33	1.69	3.11	0.94			-	-
	NT2RP4000908	14.45	17.63	18.1	10.04	7.21	5.31	4.66	6.8	4.87	**	**	-	-
	NT2RP4000910	216.22	171.01	317.29	253.37	286.44	240.15	188.21	180.84	183.37			-	-
	NT2RP4000918	3.56	6.94	4.06	7.07	6.01	6.69	5.32	2.08	2.17			-	-
	NT2RP4000925	5.57	5.14	8.28	6.79	4.75	4.89	3.2	5.18	4.02			-	-
	NT2RP4000927	3.1	2.26	4.02	4.89	1.52	0.68	2.5	1.38	1.2			-	-
55	NT2RP4000928	9.4	7.34	14.03	9.56	4.86	8.73	4.09	5.17	5.52			-	-
	NT2RP4000929	3.84	3.91	13.46	5.95	2.85	3.04	2.12	4.29	1.99			-	-
	NT2RP4000946	6.59	6.92	14.08	8.15	4.03	3.77	3.48	3.97	1.29			-	-
	NT2RP4000947	3.36	4.07	10.59	4.84	0.29	0.97	0.36	0.58	0			-	-

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	NT2RP4000949	10.71	9.2	16.65	6.86	2.65	3.74	2.78	1.39	2.41	*	*	-	-
	NT2RP4000955	5.81	4.35	6.4	6.28	2.77	1.08	2.31	3.19	3.37	*	*	-	-
5	NT2RP4000959	46.28	46.79	57.49	28.43	49.02	25.11	20.47	30.52	16.93	**	*	-	-
	NT2RP4000962	11.98	9.47	12.39	11.59	10.69	8.83	6.01	4.92	5.77	**	*	-	-
	NT2RP4000973	21.72	16.11	23.28	13.29	14.47	13.18	9.73	13.42	15.34	*	*	-	-
	NT2RP4000975	12.7	11.46	22.76	9.51	5.19	6.19	5.82	10.95	9.25	*	*	-	-
	NT2RP4000979	15.15	9.34	21.99	15.27	12.98	9.04	9.28	10.97	8.24	*	*	-	-
	NT2RP4000984	6.41	8.08	14.46	6.57	1.97	3.73	2.22	3.31	3.09	*	*	-	-
10	NT2RP4000986	6.86	5.41	12.86	6.12	4.31	1.27	1.5	2.5	1.16	*	*	-	-
	NT2RP4000988	17.65	11.88	13.93	10.42	7.43	7.63	9.24	12.28	11.72	*	*	-	-
	NT2RP4000989	4.65	7.43	5.1	6.61	2.52	1.81	2.98	2.09	3.85	*	*	-	-
	NT2RP4000990	6.25	7.92	5.23	9.42	4.63	4.12	5.36	2.51	2.44	*	*	-	-
	NT2RP4000994	8.9	9.21	16.92	10.87	4.94	9.69	11.79	23.69	21.99	*	*	-	-
	NT2RP4000996	77.3	49.17	79.6	45.61	34.69	39.35	32.71	38.95	46.1	*	*	-	-
15	NT2RP4000997	122.55	129.24	107.05	94.09	70.8	26.94	46.25	80.17	57.14	**	*	-	-
	NT2RP4001001	12.46	18.44	15.8	14.39	8.88	9.17	8.14	8.28	5.33	*	*	-	-
	NT2RP4001004	5.22	3.76	7.06	6.01	1.06	2.64	1.83	1.39	1.05	*	*	-	-
	NT2RP4001006	13.89	13.25	17.25	8.9	7.61	7.07	7.25	6.36	7.3	**	*	-	-
	NT2RP4001009	16.48	20.86	24.07	12.83	13.33	10.38	13	7.19	7.56	*	*	-	-
20	NT2RP4001010	12.07	13.64	9.65	9.47	5.84	7.62	5.8	4.44	3.25	**	*	-	-
	NT2RP4001013	109.49	147.49	90.54	50.6	80.74	63.83	38.95	52.28	51.67	*	*	-	-
	NT2RP4001029	20.54	17.68	29.5	9.58	9.72	9.68	7.27	4.7	8.7	*	*	-	-
	NT2RP4001036	9.27	12.23	13.79	8.52	7.63	4.92	8.03	6.75	4.44	*	*	-	-
	NT2RP4001041	36.4	40.27	32.69	14.35	15.64	11.72	23.48	9.92	16.78	**	*	-	-
	NT2RP4001042	15.67	10.3	17.88	10.18	7.53	8.42	5.86	5.84	7.9	*	*	-	-
25	NT2RP4001046	36.69	45.09	54.4	22.18	26.84	16.1	31.95	24.71	14.49	*	*	-	-
	NT2RP4001050	14.02	22.04	12.83	10.97	2.91	3.84	9.37	3.59	3.94	*	*	-	-
	NT2RP4001051	21.06	26.13	23.41	17.4	11.41	16.25	15.66	11.32	18.06	*	*	-	-
	NT2RP4001057	5.02	3.25	6.98	7.18	2.13	3.82	4.33	2.83	3.14	*	*	-	-
	NT2RP4001063	6.13	4.37	7.2	7.29	2.91	4.39	2.87	3.18	3.35	*	*	-	-
30	NT2RP4001064	9.3	9.96	15.17	12.02	5.98	5.07	7.19	9.48	7.97	*	*	-	-
	NT2RP4001067	10.58	14.37	13.96	6.93	4.54	4.48	7.26	9.16	8.36	**	*	-	-
	NT2RP4001078	4	5.51	5.6	4.49	1.94	2.06	3.66	2.7	1.04	*	*	-	-
	NT2RP4001079	8.77	14.47	11.97	8.98	3.49	1.98	7.36	2.56	7.44	*	*	-	-
	NT2RP4001080	8.56	8.71	5.39	7.24	5.74	5.86	5.43	5.54	6.58	*	*	-	-
	NT2RP4001086	8.1	13.85	11.2	8.73	5.59	7.65	7.59	3.27	6.54	*	*	-	-
35	NT2RP4001095	21.9	10.2	20.98	20.1	8.21	22.42	25.97	28.91	25.72	*	*	-	-
	NT2RP4001098	9.87	7.14	14.73	8.69	4.17	6.42	4.56	7.67	4.16	*	*	-	-
	NT2RP4001100	87.64	83.13	87.53	54.87	47.17	71.93	63.14	104.74	100.86	*	*	-	-
	NT2RP4001105	4.62	5.85	6.18	8.6	3.1	3.62	2.72	2.96	3.35	**	*	-	-
	NT2RP4001110	4.35	3.52	3.95	6.4	1.65	2.19	2.86	1.95	2.46	*	*	-	-
	NT2RP4001115	9.9	15.92	16.54	12.73	4.3	5.05	12.1	7.78	11.14	*	*	-	-
40	NT2RP4001117	47.61	50.63	46.56	30.24	19.2	17.67	37.4	37.77	12.69	**	*	-	-
	NT2RP4001122	7.49	13.49	11.17	8.93	3.06	4.64	5.55	4.07	4.81	*	*	-	-
	NT2RP4001123	15.99	10.87	15.29	13.96	11.8	8.64	4.92	11.31	11.27	*	*	-	-
	NT2RP4001126	32.2	22.75	27.43	23.25	13.48	17.12	8.86	11.87	13.23	**	*	-	-
	NT2RP4001127	5.7	5.54	5.37	7.61	3.72	4.66	3.57	2.2	3.61	**	*	-	-
	NT2RP4001138	6.95	3.88	7.12	9.78	5.66	5.09	4.09	4.44	3.91	*	*	-	-
45	NT2RP4001143	12.5	11.65	11.43	11.35	7.29	7.76	9.34	8.18	11.45	*	*	-	-
	NT2RP4001148	6.15	6.48	10.09	9.88	3.88	5.87	3.55	2.98	4.94	*	*	-	-
	NT2RP4001149	10.58	12.29	14.62	14.76	6.44	4.57	8.21	6.46	7.23	*	*	-	-
	NT2RP4001150	2.08	2.58	2.6	5.53	2.21	2.02	2.86	2.61	5.29	*	*	-	-
	NT2RP4001159	28.55	18.66	30.75	17.14	15.33	13.97	7.91	12.84	18.83	*	*	-	-
	NT2RP4001162	19.05	7.92	22.71	10.51	6.28	6.36	7.29	6.36	7.28	*	*	-	-
50	NT2RP4001170	4.82	3.9	7.97	5.23	1.81	3.87	2.53	3.13	2.09	*	*	-	-
	NT2RP4001174	28.66	24.87	30.19	18.62	12.05	22.33	28.65	25.07	34.84	*	*	-	-
	NT2RP4001175	41.57	44.74	48.16	32.54	33.99	41.64	26.8	24.72	38.38	*	*	-	-
	NT2RP4001176	940.52	839.83	1091.9	860.36	609.5	960.82	721.44	858.51	780.83	*	*	-	-
	NT2RP4001184	63.86	45.01	63.95	60.3	52	64.4	59.44	58.17	76.19	*	*	-	-
55	NT2RP4001198	36.14	14.18	33.12	25.99	15.11	24.84	10.23	17.15	15.95	*	*	-	-
	NT2RP4001199	7.47	5.66	10.86	10.65	3.07	4.16	4.96	7.07	8.52	*	*	-	-
	NT2RP4001206	64.73	49.7	69.67	51.07	49.14	54.08	37.12	41.91	43.36	*	*	-	-
	NT2RP4001207	7.32	3.58	10.38	7.77	2.4	3.4	3.22	3.79	1.65	*	*	-	-
	NT2RP4001210	10.03	7.14	12.93	9.04	5.66	7.56	3.96	6.73	5.83	*	*	-	-

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Table 456

	NT2RP4001213	7.81	5.05	8.73	8.57	3.73	3.81	4.8	3.72	3.86			
	NT2RP4001214	3.93	5.31	4.9	6.79	4.2	2.68	6.35	2.95	4.56			
5	NT2RP4001219	16.88	22.36	19.11	23.96	11.89	15.23	12.2	5.76	8.23	*	-	
	NT2RP4001228	31.68	26.26	28.99	28.25	18.75	24.21	24.62	30.13	29.4			
	NT2RP4001235	19.17	16.01	20.65	14.75	7.88	8.31	4.98	7.75	11.6	*	*	-
	NT2RP4001256	7.87	5.89	15.98	8.52	4.59	3.98	3.22	7.66	6.44			
	NT2RP4001257	10.17	7.29	12.91	9.33	4.43	6.16	4.58	7.66	4.3			
	NT2RP4001260	9	7.35	9.45	7.52	2.82	3.63	1.87	4.5	2.81	**	-	
10	NT2RP4001261	14.73	14	19.92	14.97	13.67	11.83	31.07	30.65	37.38	**	+	
	NT2RP4001274	46.98	48.98	34.12	11.26	8.82	9.09	7.45	6.66	5.77	**	**	-
	NT2RP4001276	24.77	28.67	28.03	20.15	20.05	19.84	15.05	9.27	8.86	**	**	-
	NT2RP4001283	274.25	154.44	255.86	208.49	145.59	283.17	127.22	121.38	88.24			
	NT2RP4001299	70.57	64.2	62.96	46.39	43.31	37.19	12.59	32.14	14.83	**	**	-
	NT2RP4001313	1.97	3.19	11.08	5.06	1.72	1.96	1.4	3.15	1.49			
15	NT2RP4001315	13.31	15.88	15.77	13.24	9.24	10.09	4.21	7.24	8.5	*	**	-
	NT2RP4001320	57.94	46.23	43.52	51.85	61.21	49.26	36.69	35.49	37.13	*	-	
	NT2RP4001325	218.13	214.83	355	324.95	260.73	208.15	240.45	201.7	209.88			
	NT2RP4001336	66.24	37.07	61.11	58.79	61.6	67.7	54.66	37.6	43.21			
	NT2RP4001339	6.71	9.24	9.26	9.34	4.49	4.79	2.82	4.96	4.68	*	-	
20	NT2RP4001343	117.66	66.55	122.62	134.91	97.85	136.86	58.06	81.43	87.93			
	NT2RP4001344	93.3	59.49	108.06	106.25	89.38	122.67	65.91	65.77	78.19			
	NT2RP4001345	8.99	7.64	17.74	11.99	4.82	6.81	4.98	6.9	5.71			
	NT2RP4001351	19.43	14.61	27.02	22.21	10.47	17.51	14.3	12.05	12.26			
	NT2RP4001353	3.32	5.15	8.01	5.72	0.75	1.22	1.09	1.47	0.82	*	-	
	NT2RP4001355	4.79	4.23	4.91	4.97	2.19	1.13	2.63	2	2.13	**	-	
25	NT2RP4001367	14.2	16.94	22.96	11.42	11.61	7.99	7.87	8	4.49	*	-	
	NT2RP4001372	4.19	2.77	5.41	7.79	3.55	1.91	2.83	1.62	2.32			
	NT2RP4001373	51.47	33.24	43.9	16.16	26.86	13.77	10.57	24.44	16.81	*	*	-
	NT2RP4001375	4.45	4.59	11.77	7.62	2.36	2.63	2.14	3.81	2.97			
	NT2RP4001379	5.44	4.91	12.41	7.76	2.24	3.26	2.93	5.12	3.63			
30	NT2RP4001381	28.02	25.15	21.15	23.38	16.12	13.96	17.03	26.57	24.23			
	NT2RP4001386	29.66	19.44	36.04	29.56	18.78	18.25	18.75	24.44	26.66			
	NT2RP4001389	11.24	11.58	9.67	9.26	6.9	5.34	3.69	2.72	3.74	*	**	-
	NT2RP4001396	5.21	4.67	8.34	6.72	2.25	1.78	3.47	3.22	1.99			
	NT2RP4001407	5.66	5.49	6.51	7.81	4.54	1.79	3.65	1.8	5.23			
	NT2RP4001409	8.48	7.57	16.74	7.93	2.96	5.53	4.77	6.78	4.46			
35	NT2RP4001410	76.31	89.86	99.62	25.06	52.86	47.85	42.92	82.06	57.7	*	-	
	NT2RP4001414	30.84	57.5	63.9	31.08	20.37	24.44	13.71	23.74	21.51	*	-	
	NT2RP4001424	11.24	11.55	15.27	11.2	4.99	6.97	6.22	6.82	6.88	**	-	
	NT2RP4001433	19.8	14.14	16.87	12.54	11.03	6.56	10.55	8.89	6.43	*	-	
	NT2RP4001438	69.21	52.84	81.07	58.91	49.01	54.6	39.37	44.33	43.61	*	-	
	NT2RP4001442	7.93	5.58	7.34	6.34	2.77	3.09	4.34	2.59	3.24	*	-	
40	NT2RP4001447	7.95	6.53	5.53	6.92	3.73	3.72	3.38	1.74	2	**	-	
	NT2RP4001466	26.98	30.25	30.96	13.22	11.9	17.04	5.41	8.17	9.81	**	**	-
	NT2RP4001467	56.03	66.43	78.02	42.37	52.35	39.87	17.7	35.75	26.38	*	**	-
	NT2RP4001472	23.78	41.35	30	13.57	13.9	13.93	11.58	12.27	10.38	*	*	-
	NT2RP4001474	7.87	8.46	14.35	7.2	5.31	5.23	4.32	3.7	3.69	*	-	
	NT2RP4001483	6.68	4.49	11.62	7.08	3.5	3.8	3.02	2.79	3.04			
45	NT2RP4001488	25.21	54.85	68.99	28.07	36.56	22.06	36.35	46.46	23.9			
	NT2RP4001492	10.33	5.85	8.11	7.33	2	4.79	7.35	5.55	5.24			
	NT2RP4001498	7.69	4.58	4.14	7.14	3.13	3.73	4.3	3.05	2.12			
	NT2RP4001502	209.76	206.24	150.31	118.11	105.88	95.3	44.44	56.95	57.25	*	**	-
	NT2RP4001503	7.44	8.32	13.64	9.66	7.22	6.9	4.97	6.76	6.61			
	NT2RP4001507	13.79	9.83	18.56	10.78	5.48	8.77	10.23	16.21	17.48			
50	NT2RP4001510	5.75	3.91	6.87	6.33	3.38	4.41	4.72	4.9	4.63			
	NT2RP4001516	8.14	6.69	9.41	7.53	2.26	3.8	4.88	3.25	3.25	*	-	
	NT2RP4001520	131.31	173.55	237.05	131.12	129.89	116.61	94.53	82.4	103.86			
	NT2RP4001523	33.88	38.97	38.29	18.41	8.08	12.46	21.96	12.77	13.03	**	**	-
	NT2RP4001524	21.05	28.36	29.26	13.82	9.16	8	8.02	5.86	9.68	**	**	-
	NT2RP4001529	19.64	17.51	18.7	21.14	10.37	22.92	12.83	17.42	17.09			
55	NT2RP4001531	12.2	10.44	17.59	14.87	8.44	10.35	9.15	12.78	10.56			
	NT2RP4001546	200.55	317.08	217.26	217.42	252.35	233.58	165.76	290.78	247.68			
	NT2RP4001547	50.85	72.72	70.29	50.48	41.66	51.65	70.8	75.31	63.14			
	NT2RP4001551	5.28	7.23	6.07	6.96	2.03	2.81	2.74	2.79	2.73	**	-	

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Table 457

	NT2RP4001555	5.61	4.66	4.4	6.85	1.41	2.54	5.43	2.64	2.46			
	NT2RP4001567	14.43	18.57	12.18	9.17	4.93	4.07	5.01	3.84	5.68	*	**	-
	NT2RP4001568	20.92	33.87	32.23	19.47	17.65	14.08	25.04	13.01	8.31			
5	NT2RP4001569	38.32	29.49	40	37.57	26.2	39.13	21.18	30.23	30.47			
	NT2RP4001571	15.01	7.71	15.89	14.4	7.44	9.88	7.38	9.18	8.27			
	NT2RP4001574	25.53	25.21	25.8	22.48	16.52	21.02	13.78	20.38	15.43	*	*	-
	NT2RP4001575	5.89	6.11	13.99	11.72	4.86	9.13	5.91	5.72	3.19			
	NT2RP4001578	138.32	156.83	176.17	106.73	98.03	117.94	140.07	117.64	162.41	*		-
10	NT2RP4001592	9.9	23.21	17.14	17.16	3.08	11.08	13.53	10.53	12.39			
	NT2RP4001593	39.07	48.78	46.75	25.68	17.84	15.12	20.23	20.2	20.66	**	**	-
	NT2RP4001605	8.89	11.75	9.28	6.36	2.98	4.4	4.38	3.06	5.09	*	**	-
	NT2RP4001606	18.77	11.14	16.78	12.15	11.21	15.99	4.83	13.12	16.6			
	NT2RP4001607	6.86	5.47	8.59	11.52	4.98	6.05	4.83	4.03	5.51			
	NT2RP4001610	3.61	1.38	4	7.17	1.24	4.9	2.72	3.85	3.06			
15	NT2RP4001614	9.32	7.4	5.36	10.94	2.88	8.46	8.3	5.56	6.1			
	NT2RP4001623	4.1	3.9	7.53	8.2	4.59	6.06	6.02	5.72	5.27			
	NT2RP4001626	25.96	32.39	24.45	30.25	8.64	19.85	8.25	9.34	7.78		**	-
	NT2RP4001634	5.5	5.13	5.73	8.25	3.86	4.21	6.58	3.67	4.85			
	NT2RP4001638	6.66	10.41	10.2	8.73	4.08	5.57	10.07	5.59	6.69			
20	NT2RP4001644	54.14	31.27	53.8	60.84	32.15	47.2	22.38	29.74	30.92			
	NT2RP4001646	19.49	10.73	26.93	21.07	12.28	14.22	11.82	16.28	16.41			
	NT2RP4001656	13.27	8.07	17.13	8.91	6.79	8.31	7.24	7.86	6.43			
	NT2RP4001666	5.12	4.37	7.8	6.14	1.29	4.07	3.21	5.08	2.86			
	NT2RP4001670	3.87	4.22	8.36	10.93	2.63	2.89	3.57	4.05	2.82			
	NT2RP4001677	60.48	67.97	86.27	37.88	33.85	40.42	60.13	40.04	66.44	*		-
25	NT2RP4001679	63.4	46.03	74.85	69.08	70.96	72.54	80.35	59.3	58.1			
	NT2RP4001695	25.41	48.09	50.45	43.83	20.99	24.93	40.69	28.74	39.61			
	NT2RP4001696	10.8	7.02	11.48	9.54	3.39	6.61	2.58	6.02	6.23			
	NT2RP4001699	7.34	4.14	12.45	8.78	2.82	5.44	4.48	5.75	8.17			
	NT2RP4001717	14.1	8.06	13.01	8.07	5.02	5.29	6.3	4.01	4.24	*		-
	NT2RP4001719	12.35	7.72	11.2	8.9	5.51	7.17	4.84	7.79	6.21			
30	NT2RP4001725	3.63	2.94	5.27	5.13	1.69	2.36	2.09	2.38	2.12			
	NT2RP4001726	27.43	19.04	36.39	17.49	15.05	17.67	16.15	9	13.24			
	NT2RP4001730	17.07	14.23	28.12	18.8	22.34	22.39	15.23	16.15	19.5			
	NT2RP4001739	13.08	27.52	18.78	28.99	19.24	16.38	17.13	15.51	14.38			
	NT2RP4001741	36.21	33.9	43.76	24.77	17.24	19.76	19.65	43.11	31.46	**		-
	NT2RP4001753	17.2	14.59	16.48	7.48	4.99	6.73	3.91	7.96	13.47	**		-
35	NT2RP4001760	8.36	7.54	12.21	7.55	2.73	5.75	3.77	6.5	5.81			
	NT2RP4001787	449.13	318.48	382.02	579.25	624.67	556.76	483.34	493.96	418.4	**	+	
	NT2RP4001790	7.47	3.89	8.52	8.8	3.39	5.62	4.59	3.58	5.07			
	NT2RP4001795	63.42	46.97	73.29	43.26	32.42	28.05	20.69	20.32	20.73	*	**	-
	NT2RP4001803	8.84	7.88	10.54	9.34	4	5.93	4.96	3.55	3.59	**		-
40	NT2RP4001805	5.95	5.69	10.38	8.15	3.79	5.46	9.95	6.17	7.95			
	NT2RP4001809	55.79	43.66	54.44	43.11	38.36	44.76	37.5	36.54	53.86			
	NT2RP4001817	34.65	23.28	22.77	22.82	15.26	16.99	9.01	16.13	16.73	*		-
	NT2RP4001822	6.52	3.81	10.26	6.23	2.19	2.7	2.67	9.77	2.8			
	NT2RP4001823	3.6	2.46	7.23	4.29	1.65	1.68	0.91	2.7	2.37			
	NT2RP4001827	92.63	82.48	90.1	26.32	25.71	23.6	20.01	17.73	25.06	**	**	-
45	NT2RP4001828	61.47	38.75	56.29	48.73	63.93	48.7	40.24	45.94	36.84			
	NT2RP4001836	44.8	31.89	48.09	43.58	41.3	52.3	39.14	27.95	48.98			
	NT2RP4001838	6.15	7.83	5.55	9.67	6.83	6.27	7.38	14.64	4.59			
	NT2RP4001841	120.68	83.99	187.16	139.43	130.99	191.28	92.44	82.4	82.84			
	NT2RP4001849	5.44	4.67	11.88	5.66	3.18	2.21	2.03	4.71	2.38			
50	NT2RP4001861	120.57	86.96	121.65	102.03	95.48	118.7	109.17	140.23	134.58			
	NT2RP4001877	47.77	41.26	29.9	28.86	24.84	22.31	17.4	14.34	21.88	*		-
	NT2RP4001879	28.67	26.1	20.85	19.88	15.94	14.99	7.59	15.66	4.85	*	*	-
	NT2RP4001889	38.95	24.39	36.19	23.27	20.66	27.73	35.61	41.13	33.21			
	NT2RP4001893	6.77	9.6	11.58	7.5	6.4	5.73	3.91	4.94	4.11	*		-
	NT2RP4001896	20.14	21.68	20.53	23.47	19.99	18.99	15.61	11.88	13.51	**		-
	NT2RP4001898	54.69	54.01	78.1	65.64	57.05	63.77	28.3	45.74	52.57			
55	NT2RP4001901	17.19	14.63	24	14.51	10.05	13.25	15.49	18.92	20.72			
	NT2RP4001910	121.38	105.48	128.54	129.33	152.14	104.65	69.31	116.85	87.82			
	NT2RP4001925	17.35	19.33	26.78	14.34	7.91	7.52	5.99	7.67	6.41	*	**	-
	NT2RP4001926	13.94	13.08	14.09	14.02	5.92	2.48	4.72	6.01	4.66	**		-

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Table 458

	NT2RP4001927	22.95	20.54	20.03	14.02	11.73	7.04	7.86	6.56	6.03	*	**	-	-
	NT2RP4001931	31.71	30.66	39.53	15.12	11.86	11.1	6.42	8.14	7.84	**	**	-	-
	NT2RP4001933	124.92	135.92	123.56	117.23	83.52	79.43	61.4	54.06	63.46	*	*	-	-
5	NT2RP4001938	21.23	9.61	28.3	17.33	8.99	14.74	12.02	19.38	17.02			-	-
	NT2RP4001942	40.71	46.99	41.11	32.73	26.67	27.19	19.11	35.23	32.36	**		-	-
	NT2RP4001945	3.45	3.93	9.62	6.08	1.55	2.05	2.15	2.81	1.6			-	-
	NT2RP4001946	10.3	8.04	13.38	10.29	3.79	3.79	3.46	4.08	3.41	*	*	-	-
	NT2RP4001947	16.45	15.77	21.11	11.34	9.6	7.02	4.68	3.24	4.94	*	**	-	-
10	NT2RP4001950	5.04	4.87	6.27	6.87	2.41	1.7	3	2.63	1.3	*	*	-	-
	NT2RP4001953	26.47	19.18	22.05	22.48	9.35	15.94	17.83	14.03	17.8			-	-
	NT2RP4001966	6.74	6.56	3.55	6.86	3.2	2.07	1.97	1.5	1.8	*	*	-	-
	NT2RP4001970	7.84	6.46	14.19	9.16	3.49	5.37	2.96	4.43	3.21			-	-
	NT2RP4001975	16.36	22.03	28.3	17.31	12	7.09	9.7	16.29	13.08			-	-
	NT2RP4001988	38	36.95	48.12	29.2	31.09	30.9	21.07	21.03	23.16	*	**	-	-
15	NT2RP4001996	24.73	23.55	24.27	15.39	14.66	5.03	8.32	9.1	9.68	*	**	-	-
	NT2RP4002014	11.39	15.95	16.62	10.15	7.55	6.98	8.4	7.61	5.52	*	*	-	-
	NT2RP4002018	16.73	14.11	11.76	12.16	9.31	11.09	15.09	12.65	8.98			-	-
	NT2RP4002035	5.82	5.03	4.44	7.72	3.9	4.37	5.69	2.8	2.78			-	-
	NT2RP4002043	18.95	25.2	14.18	17.22	10	14.87	15.39	7.04	10.89			-	-
20	NT2RP4002046	24.11	28.29	25.84	19.27	12.78	20.33	11.41	17.55	17.78	*	*	-	-
	NT2RP4002052	12	15.65	20.88	9.3	9.08	6.85	4.02	3.61	4.24	*	**	-	-
	NT2RP4002056	153.48	150.03	95.32	64.65	34.92	59.97	51.1	38.55	53.86	*	*	-	-
	NT2RP4002057	40.68	39.2	39.83	19.31	30.56	26.73	27.83	37.55	52.18	*	*	-	-
	NT2RP4002058	17.65	14.46	13.17	10.87	3.28	4.52	5.26	2.89	2.9	*	**	-	-
	NT2RP4002064	5.15	7.64	7.19	5.68	1.88	1.94	2.62	1.16	2.09	**	**	-	-
25	NT2RP4002071	19.67	23.04	16.87	12.91	7.48	6.56	8.07	4.85	9.75	*	**	-	-
	NT2RP4002075	4.49	2.91	8.1	6.42	3.43	5.27	3.76	2.11	2.28			-	-
	NT2RP4002078	19.28	11.77	21.52	11.04	6.62	7.49	7.2	13.73	14.2	*	*	-	-
	NT2RP4002081	26.93	23.83	24.19	19.25	16.65	23.73	20.7	21.48	20.63	*	*	-	-
	NT2RP4002083	12.48	9.47	12.44	9.18	6.34	7.57	7.79	10.15	9.98	*	*	-	-
	NT2RP4002099	4.69	4.27	5.09	6.55	1.89	1.66	2.86	2.04	1.79	**	**	-	-
30	NT2RP4002106	48.22	85.51	111.5	22.9	29.06	16.21	28.91	8.21	26.28	*	*	-	-
	NT2RP4002111	21.8	28.93	25.95	13.09	13.73	11.32	21.21	10.01	16.62	**	*	-	-
	NT2RP4002112	18.8	22.05	20.04	17.73	8.26	13.72	15.37	6.12	8.09	*	*	-	-
	NT2RP4002116	131.42	129.9	145.31	124.89	86.8	130.87	116.59	193.03	130.26			-	-
	NT2RP4002122	9.21	7.05	12.08	10.75	5.68	5.1	3.65	7.4	5.23			-	-
35	NT2RP4002126	16.25	10.45	26.23	9.01	12.04	10.44	10.14	17.51	8.7			-	-
	NT2RP4002133	59.92	73.72	76.92	61.59	43.1	56.16	80.78	84.66	86.01			-	-
	NT2RP4002136	12.24	16.73	29.34	16.04	8.23	7.86	20.93	16.43	17.62			-	-
	NT2RP4002139	65.39	168.51	135.79	98.21	29.79	27.09	86.97	65.15	29.84			-	-
	NT2RP4002174	10.15	13.02	11.19	12.5	4.36	7.32	8.88	11.55	11.53			-	-
	NT2RP4002185	23.38	25.82	19.72	13.23	6.3	10.39	10.9	7.33	11.09	**	**	-	-
40	NT2RP4002186	16.88	7.65	12.65	11.9	7.3	14.74	12.63	14.19	17.64			-	-
	NT2RP4002187	28.59	22.57	36.35	26.74	19.36	12.02	11	23.37	23.58			-	-
	NT2RP4002188	5.08	7.53	8.31	11.66	6.59	7.86	4.55	4.87	6.3			-	-
	NT2RP4002199	5.25	3.74	5.62	11.93	2.92	3.8	2.79	4.05	2.9			-	-
	NT2RP4002206	3.81	1.86	2.83	8.57	1.99	1.73	3.4	4.64	3.09			-	-
	NT2RP4002210	5.45	3.2	5.65	5.42	1.97	2.88	3.71	3.22	3.36			-	-
45	NT2RP4002222	6.38	6.14	7.04	6.83	3.57	3.25	6.5	5.55	8.67			-	-
	NT2RP4002241	19.38	17.71	14.08	18.19	11.3	8.8	22.47	17.63	22.91			-	-
	NT2RP4002248	35.82	21.31	27.47	30.46	20.08	26.03	19.35	24.1	27.06			-	-
	NT2RP4002250	1.58	1.78	7.25	3.8	1.3	0.25	0.61	0.65	1.92			-	-
	NT2RP4002259	5.84	5.18	13.48	7.69	2.79	5.42	4.19	2.88	3.6			-	-
50	NT2RP4002268	35.43	25.77	32.22	22.21	30.41	16.71	15.9	32.72	23.26			-	-
	NT2RP4002288	22.95	20.57	22.28	19.59	16.95	19.16	16.63	15.69	17.98	*	**	-	-
	NT2RP4002290	13.7	13.76	25.96	11.44	11.61	14.66	7.05	8.48	10.18			-	-
	NT2RP4002298	10.23	12.39	16.74	11.6	8.3	6.18	9.56	4.97	3.02			-	-
	NT2RP4002306	15.16	15.97	20.14	18.18	10.48	11.51	13.4	11.06	13.62			-	-
	NT2RP4002308	8.45	5.65	13.02	8.55	4	9.83	3.47	4.84	5.83			-	-
55	NT2RP4002336	36.27	19.86	28.94	13.28	11.25	15.46	7.56	12.49	16.8	*	*	-	-
	NT2RP4002340	2.84	2.81	9.7	4.27	0.88	0.87	1.22	1.79	3.04			-	-
	NT2RP4002361	9.6	7.94	13.29	10.99	5.46	5.57	5.78	8.11	5.48			-	-
	NT2RP4002367	2.79	2.98	7.18	5.28	1.95	2.56	3.24	1.85	1.33			-	-
	NT2RP4002368	24.08	18.92	33.22	37.31	27.57	13.68	19.74	22.15	15.46			-	-

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	NT2RP4002377	39.07	34.91	52.74	47.19	54.21	38.25	54.01	36.88	39.01			
	NT2RP4002408	8.23	10.17	7.33	8.55	4.11	5.54	5.29	2.67	3.53	*		
	NT2RP4002425	16.72	9.87	22.95	18.36	10.72	16.61	14.74	22.3	29.56			
5	NT2RP4002432	134.52	97.55	162.62	149.32	142.05	170.39	110.43	102.21	77.71			
	NT2RP4002447	15.99	16.51	16.61	15.14	7.55	8.09	7.58	13.4	16.29			
	NT2RP4002451	15.11	13.46	19.12	12.6	10.1	7.99	7.15	14.07	11.51			
	NT2RP4002461	94.61	109.24	116.21	78.57	91.21	74.75	80.34	65.93	74.08	*	*	-
	NT2RP4002486	16.89	12.32	16.5	14.11	11.37	5.17	6.32	4.06	4.53	**		-
10	NT2RP4002517	13.38	14.55	13.22	12.72	9.03	11.46	10.8	6.18	8.61	*		-
	NT2RP4002556	14.42	18.7	14.04	18.8	13.59	13.31	16.09	6.06	5.52			
	NT2RP4002569	16.26	11.41	27.18	13.33	6.98	10.11	3.13	6.78	11.56			
	NT2RP4002587	4.28	5.9	13.49	5.9	21.35	3.55	2.37	3.48	4.03			
	NT2RP4002591	11.21	8.73	16.81	10.63	3.25	5.39	2.62	6.98	4.42	*		-
	NT2RP4002607	7.19	4.54	8.62	7.82	4.54	6.78	3.93	3.64	3.85			
15	NT2RP4002627	129.04	84.31	131.91	123.08	121.1	113.29	100.69	103.33	117.09			
	NT2RP4002628	23.42	19.42	25.54	15.3	10.07	9.36	10.28	14.93	5.74	*	*	-
	NT2RP4002630	34.52	45.14	38.61	24.65	19.47	21.97	38.2	24.12	21.41	**		-
	NT2RP4002639	69.58	58.92	77.5	92.97	83.99	82.67	76.62	44.55	74.09	*		+
	NT2RP4002641	10.87	7.59	20.93	9.6	5.64	6.42	5.77	9.03	8.9			
20	NT2RP4002658	167.82	202.75	171.29	210.71	275.39	155.29	113.71	313.1	177.93			
	NT2RP4002669	11.89	14.59	18.31	13.81	8.54	6.37	6.6	13.8	11.32			
	NT2RP4002677	38.73	39.84	49.87	21.84	19.97	14	8.4	12.92	7.79	**	**	-
	NT2RP4002715	60.14	28.66	66.85	78.28	49.48	49.64	41.22	48.79	51.15			
	NT2RP4002750	5.11	4.54	6.02	5.02	2.86	2.29	1.61	2.5	1.93	**		-
	NT2RP4002784	13.9	15.39	21.97	16.43	16.29	10.56	10.51	11.54	8.19			
25	NT2RP4002791	19.14	16.24	15.43	15.81	11.98	5.79	6.28	6.12	6.25	**		-
	NT2RP4002811	7.07	4.03	15.62	8.02	4.02	6.88	1.73	4.87	5.66			
	NT2RP4002830	22.24	23	26.1	14.14	12.81	9.89	5.49	12.55	7.49	**	**	-
	NT2RP4002832	6.62	7.2	10.83	9.33	4.27	5.54	7.23	5.78	6.45			
	NT2RP4002850	120.8	112.69	112.51	87.95	73.32	75.57	95.07	111.13	108.7	**		-
	NT2RP4002874	8.25	8.24	13.89	8.67	2.89	3.54	1.21	3.45	2.95	*		-
30	NT2RP4002884	89.55	83.99	93.99	87.7	70.28	83.78	63.11	54.66	68.06	**		-
	NT2RP4002888	6.66	8.16	10.03	7.45	4.69	3.72	4.86	3.64	2.94	*		-
	NT2RP4002891	19	20.18	21.15	16.8	8.39	11.91	12.08	8.99	11.53	*	**	-
	NT2RP4002894	39.86	38.92	34.99	21.18	29.78	22.86	11.88	16.42	39.6	*		-
	NT2RP4002896	7.81	11.66	17.8	10.13	3.4	6.5	5.01	4.37	5.08			
35	NT2RP4002905	5.89	3.63	14.35	7.98	3.09	2.98	3	5.21	1.93			
	NT2RP4002907	14.82	12.9	19.78	10.14	7.04	6.74	11.86	12.75	9.47	*		-
	NT2RP5003459	437.62	468.29	451.9	449.8	544.78	414.46	466.17	464	478.98			
	NT2RP5003461	21.93	17.54	18.05	12	9.18	10.65	7.44	6.63	4.58	**	**	-
	NT2RP5003471	52.72	62.97	42.21	31.11	21.1	25.12	46.83	20.37	35.04	*		-
	NT2RP5003477	5.7	3.4	3.74	5.93	3.44	2.66	3.17	2.23	2.28			
40	NT2RP5003487	1749.6	1957.3	1778.8	1241.4	1573.1	1807.7	1562.4	2343.9	2243.6			
	NT2RP5003492	6.08	6.5	15.88	6.67	3.98	3.96	2.59	3.25	1.92			
	NT2RP5003500	4.26	2.52	9.75	6.65	2.34	2.66	2.29	2.53	3.57			
	NT2RP5003506	10.49	9.24	16.38	12.74	9.52	9.22	9.69	9.29	9.27			
	NT2RP5003512	6.99	7.06	8.63	5.95	2.46	3.36	2.76	2.88	3.49	*	**	-
	NT2RP5003522	10.07	9.26	8.55	5.18	3.12	3	5.35	1.85	3.07	**	**	-
45	NT2RP5003524	6.44	9.05	5.63	7.13	1.41	1.72	4.66	2.23	3	*		-
	NT2RP5003527	117.46	141.32	115.3	136.41	95.19	117.09	134.61	57.44	67			
	NT2RP5003531	24.59	24.67	34.31	22.85	17.67	26.56	12.06	25.82	35.99			
	NT2RP5003534	6.96	7.88	13.1	6.91	5.36	2.92	2.47	4.02	3.38	*		-
	NT2RP6000020	19.43	27.72	47.01	19.42	30.65	12.46	29.24	22.48	15.27			
	NT2RP6000022	13.58	7.81	13.25	8.64	4.5	5.83	7.1	5.5	4.05	*		-
50	NT2RP6000050	5.27	8.58	7.67	6.81	3.59	4.26	5.19	3.06	5.18			
	NT2RP6000063	5.9	4.93	5.56	6.03	1.07	1.6	2.56	2.13	3.15	**		-
	NT2RP6000074	10.12	8.88	7.2	8.89	3.35	3.32	4.76	3.03	4.96	*		-
	NT2RP6000083	36.48	50.53	36.06	34.94	19.9	25.84	29	16.57	36.99			
	NT2RP6000100	9.33	8.85	11.79	8.7	3.93	5.47	3.33	5.54	5.88	*		-
	NT2RP6000123	7.59	5.31	8.35	10.56	5.66	4.44	3.17	5.91	3.98			
55	NT2RP6000129	4.7	6.51	7.04	5.86	2.6	3.34	4.3	7.17	3.53			
	NT2RP6000147	23.98	19.21	18.37	28.9	18.17	21.68	18.73	17.92	16.85			
	NT2RP6000163	6.02	5.5	6.17	6.66	2.33	2.81	2.76	2.24	3.12	**	**	-
	NT2RP6000181	31.82	37.36	38.55	11.76	5.01	6.27	13.35	6.28	18.64	**	**	-

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	NT2RP6000182	11.67	12.98	10.81	11.27	4.67	4.19	7.63	8.13	8.65	**	-
	OVARC1000001	10.18	10.98	7.82	10.48	3.67	5.27	8.05	6.3	4.32		
	OVARC1000003	18.46	16.04	21.53	24.56	18.39	28.35	24.31	27.93	25.27	*	+
5	OVARC1000004	154.65	161.68	111.37	257.56	204.62	269.89	148.7	142.43	153.8	*	+
	OVARC1000006	8.96	9.17	13.23	12.36	9.89	7.09	8.46	11.94	16.91		
	OVARC1000013	12.84	15.42	21.83	13.5	7.52	11.75	8.01	7.31	7.45	*	-
	OVARC1000014	9.51	5.51	9.75	8.67	3	2.57	4.2	4.5	5.23		
	OVARC1000017	7.8	10.89	11.1	9.23	5.72	5.56	7.08	8.83	7.59		
10	OVARC1000026	39.87	98.56	58.17	35.12	21.04	21.52	23	21.16	19.52		
	OVARC1000035	53.62	63.74	56.85	49.18	30.89	52.6	44.01	25.83	35.4	*	-
	OVARC1000037	44.18	27.1	33.64	21.27	17.7	36.96	22.76	28.28	23.56		
	OVARC1000058	21.2	16.03	18.93	19.43	6.93	18.25	18.85	19.08	20.93		
	OVARC1000060	8.69	7.53	9.42	11.74	4.69	15.1	7.86	12.81	10.28		
	OVARC1000068	11.63	6.29	9.06	11.58	8.06	9.18	6.71	8.97	7.36		
15	OVARC1000069	130.28	91.82	110.55	138.44	48.02	81.99	34.87	114.87	91.52		
	OVARC1000071	4.7	2.59	5.56	6.14	1.28	3.78	7.5	3.79	3.09		
	OVARC1000075	608.15	715.16	979.97	596.89	401.8	521.41	1505.9	1295.8	1454	**	+
	OVARC1000083	31.41	22.53	32.47	28.89	10.2	12.73	23.7	17.6	16.65		
	OVARC1000085	150.84	132.35	115.14	65.66	79.36	104.26	57.87	55.95	46.39	*	-
20	OVARC1000086	21.41	22.84	29.16	11.19	16.67	9.71	14.87	19.23	16.21	*	-
	OVARC1000087	5.75	4.1	5.37	4.05	5.46	2.99	2.78	3.2	3.4	*	-
	OVARC1000090	32.43	34.99	39.46	22.05	34.29	19.79	30.39	42.7	35.58		
	OVARC1000091	19.21	16.58	18.4	9.39	12.78	9.69	3.97	5.82	3.09	**	-
	OVARC1000092	12.38	12.28	20.09	9.9	9.89	8.91	11.14	12.55	9.97		
25	OVARC1000105	143.72	148.63	164.07	88.33	70.71	97.62	141.54	139.36	177.6	**	-
	OVARC1000106	56.13	50.31	43.64	33.71	26.64	28.64	25.97	22.43	26.91	**	-
	OVARC1000109	41.67	37.23	42.5	18.44	22.06	21.86	20.05	26.41	16.1	**	-
	OVARC1000113	24.72	16.19	25.29	12.07	22.86	8.51	9.56	13.5	7.9	*	-
	OVARC1000114	20.78	17.23	18.89	9.6	15.6	9.38	19.16	20.46	17.77	*	-
	OVARC1000133	17.57	29.71	58.68	7.88	21.62	13.9	11.06	7.62	51.45		
30	OVARC1000137	26.29	21.24	32.71	19.41	23.84	21.06	17.64	15.76	21.29		
	OVARC1000139	159.47	147.34	170.25	146.09	161.46	121.94	114.2	86.17	91.75	**	-
	OVARC1000146	5.46	5.11	5.9	4.05	7.97	2.4	2.98	4.01	3.61	**	-
	OVARC1000148	26.75	26.35	26.82	10.67	7.97	11.29	11.04	13.8	10.7	**	-
	OVARC1000151	10.96	7.69	7.49	4.61	6.76	7.44	5.23	9.46	5.82		
	OVARC1000157	131.87	72.71	159.16	28.64	46	29.09	32.55	30.3	35.03	*	-
35	OVARC1000162	5.48	6.74	10.68	5.09	8.45	3.6	3.17	7.57	4.35		
	OVARC1000168	20.5	23.24	26.19	11.56	15.79	12.79	11.3	16.45	13.91	**	-
	OVARC1000169	67.7	69.5	69.91	59.55	32.42	51.67	35.89	25.97	33.69	**	-
	OVARC1000178	7.01	7.74	9.93	3.35	8.16	5.02	5.67	3.4	4.49	*	-
	OVARC1000182	6.26	2.63	4.45	2.72	4.87	3.13	2.7	3.24	3.81		
	OVARC1000186	14.26	11.19	12.68	6.9	8.25	3.97	5.99	5.56	7.72	*	-
40	OVARC1000188	19.42	11.08	15.15	6.26	7.14	4.44	6.66	6.47	9.02	*	-
	OVARC1000191	10.3	6.61	7.55	5.45	7.49	3.47	4.08	6.65	4.21		
	OVARC1000198	22.01	20.32	21.51	13.28	15.24	8.22	13.24	17.04	19.28	*	-
	OVARC1000208	131.85	125.05	141.2	106.48	130.32	109.42	107.54	141.64	112.43		
	OVARC1000209	37.5	42.42	46.9	35.76	48.15	33.79	26.69	26.98	20.75	**	-
45	OVARC1000212	14.17	16.96	15.84	10.34	14.11	8.11	6.32	5.07	5.47	**	-
	OVARC1000216	7.5	5.29	9.53	2.31	4.11	1.95	4.22	3.32	1.87	*	-
	OVARC1000240	30.72	25.44	20.48	13.87	16.01	11.11	15.84	21.45	17.35	*	-
	OVARC1000241	9.83	9.47	8.6	4.52	5.75	4.08	4.87	6.55	6.44	**	-
	OVARC1000249	12.5	10.38	14.17	6.99	8.18	4.94	7.53	30.07	10.99	*	-
	OVARC1000254	211.04	164.08	171.72	162.84	218.18	173	104.59	109.93	114.49	**	-
50	OVARC1000255	8.62	6.5	15.01	2.8	3.3	2.22	1.58	8.88	3.88	*	-
	OVARC1000267	41.48	57.68	54.05	22.69	31.39	23.55	19.25	29.77	21.42	*	-
	OVARC1000275	6.58	9.72	13.14	1.2	3.21	1.15	3.78	4.58	2.47	*	-
	OVARC1000287	20.12	19.59	19.09	8.41	13.5	9.21	9.7	16.66	9.51	**	-
	OVARC1000288	34.41	32.21	34.44	10.93	20.1	12.59	9.34	11.6	15.85	**	-
	OVARC1000298	37.89	35.05	40.4	28.93	41.61	26.19	16.03	19.69	20.76	**	-
55	OVARC1000302	10.27	8.52	8.63	3.64	6.33	2.17	4.38	8.26	6.64	*	-
	OVARC1000304	13.52	8.67	11.83	6.89	9.55	6.81	7.04	9.75	5.89		
	OVARC1000307	9.2	9.65	13.33	4.99	7.9	7.07	7.34	4.85	4.2	*	-
	OVARC1000309	10.77	7.81	10.14	3.65	4.52	3.3	3.45	4.14	3.51	**	-
	OVARC1000312	38.52	63.36	48.96	16.29	39.99	22.16	11.44	23.2	11.33	*	-

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	OVARC1000313	31.08	25.28	22.97	16.65	33.34	16.32	7.95	14.64	16.92	*	-
	OVARC1000321	95.57	70.17	108.42	49.21	78.85	36.91	71.72	84.76	66.41	*	-
5	OVARC1000326	9.36	7.55	9.19	5.69	4.73	3.83	2.8	4.95	2.81	**	**
	OVARC1000327	9.64	6.54	7.7	4.58	5.69	4.67	3.24	3.34	3.39	*	**
	OVARC1000331	31.51	26.56	17.69	20.2	32.18	25.32	7.77	12.73	9.94	*	*
	OVARC1000335	10.5	10.92	9.98	3.56	6.12	5.55	3.62	2.51	3.12	**	**
	OVARC1000347	22.28	19.59	19.77	14.38	17.51	15.31	11.64	10.94	10.7	*	**
	OVARC1000348	9.03	9.66	11.56	3.27	3.92	2.72	2.5	3.43	2.51	**	**
10	OVARC1000363	17.67	18.03	15.99	8.09	14.09	9.86	7.93	4.93	7.38	*	**
	OVARC1000377	9.05	5.89	9.25	3.23	6.62	3.71	2.88	2.47	4.83	*	-
	OVARC1000382	11.38	10.29	10.44	4.87	5.92	3.1	5	4.78	5.93	**	**
	OVARC1000384	15.04	16.77	12.96	3.9	4.19	3.88	3.11	4.29	3.9	**	**
	OVARC1000401	12.88	8.81	11.8	7.36	8.78	6.88	5.26	4.94	4.67	**	-
	OVARC1000406	452.57	396.91	414.58	242.32	241.63	222.43	202.53	242.65	184.03	**	**
15	OVARC1000407	11.18	13.52	12.76	4.82	6.15	3.43	3.77	3.81	3.74	**	**
	OVARC1000408	143.25	152.71	130.24	110.8	163.58	95.03	87.98	95.98	86.83	**	-
	OVARC1000410	12.11	11.07	15.74	6.71	11.27	6.87	6.11	5.6	3.42	**	-
	OVARC1000411	11.28	8.14	7.71	4.73	4.82	3.45	4.09	4.41	4.68	*	*
	OVARC1000414	15.72	17.28	11.48	7.59	8.9	10.02	14.36	14.47	14.88	*	-
20	OVARC1000420	11.3	11.1	10.67	5.43	7.49	5.25	8.15	6.28	6.64	**	**
	OVARC1000421	21.51	18.12	14.96	8.46	10.6	6.1	8.22	6.83	7.06	*	**
	OVARC1000427	255.84	237.66	229.09	230.15	286.16	201.09	155.75	128.13	139.78	**	-
	OVARC1000431	86.97	107.76	104.05	53.83	76.2	48.18	31.1	18.06	18.56	*	**
	OVARC1000437	18.7	18.85	16.29	10.2	15.26	9.01	9.96	5.69	8.45	*	**
	OVARC1000439	14.55	21.25	13.48	9.92	17.37	9.21	5.86	5.66	4.06	*	-
25	OVARC1000440	37.93	36.45	33.24	14.99	19.86	14.94	10.14	8.93	10.09	**	**
	OVARC1000442	47.65	39.77	34.86	17.92	25.44	19.14	36.52	26.4	37.91	*	-
	OVARC1000443	9.63	12.52	9.02	8.56	33.14	5.66	16.38	5.13	9.47	*	-
	OVARC1000461	8.43	5.22	4.46	4.04	5.64	3.64	3.41	4.7	3.49	*	-
	OVARC1000465	13.05	12.4	8.82	5.16	5.82	3.89	4.59	3.18	2.41	*	**
	OVARC1000466	22.78	19.36	18.72	10.66	17.86	12.45	11.65	7.24	8.12	**	-
30	OVARC1000467	8.03	5.77	8.99	2.45	3.8	2.2	3.29	2.29	3.38	*	*
	OVARC1000470	15.96	13.65	10.41	7.96	9.91	7.26	9.53	10.16	10.25	*	-
	OVARC1000473	12.49	10.05	10.69	6.2	7.49	6.37	10.6	7.2	9.15	**	-
	OVARC1000479	24.56	30.78	25.75	8.77	13.76	7.96	8.07	9.81	9.07	**	**
	OVARC1000484	41.23	29.61	25.62	15.32	17.14	13.32	29.7	26.23	34.72	*	-
	OVARC1000486	15.8	17.22	17.4	11.06	13.85	9.12	14.13	11.53	12.18	*	*
35	OVARC1000496	6.74	8.5	5.88	2.96	8.22	5.46	2.84	3.93	3.9	*	-
	OVARC1000520	8.86	5.17	6.53	2.16	5.01	3.05	4.06	3.97	5.92	*	-
	OVARC1000522	35.51	29.95	29.3	26.12	30.21	22.71	22.42	16.55	18.06	**	-
	OVARC1000526	25.75	25.79	19.89	12.38	14.14	8.6	32.78	19.39	27.42	**	-
	OVARC1000529	17.7	16.61	13.49	7.72	9.26	6.61	12.03	7.5	12.39	**	-
40	OVARC1000533	31.08	27.41	22.88	25.25	24.54	12.97	18.02	13.21	18.14	*	-
	OVARC1000543	11.04	5.87	5.45	4.07	4.48	2.25	3.68	3.22	4.84	*	-
	OVARC1000550	9.45	7.02	5.98	3.29	4.46	2.66	4.35	2.47	4.43	*	*
	OVARC1000553	34.95	36.44	34.04	16.33	24.77	21.97	31.22	31.95	33.2	**	*
	OVARC1000556	22.37	23.81	26.15	14.72	11.54	9.38	19.99	16.63	22.58	**	-
	OVARC1000557	11.61	9.78	7.49	2.51	3.89	2.24	6.45	4.03	5.39	**	*
45	OVARC1000561	67.36	70.57	52.24	30.14	35.45	26.39	87.82	47.67	77.14	**	-
	OVARC1000564	79.74	89.59	94.8	35.3	37.73	54.01	49.59	52.84	37.26	**	**
	OVARC1000573	11.41	12.83	14.29	6.97	10.13	6.51	5.93	10.17	8.55	*	*
	OVARC1000576	235.06	210.51	199.48	203.8	258.47	200.46	142.26	126.19	115.56	**	-
	OVARC1000578	15.29	13.44	14.45	8.15	12.93	8.56	9.81	12.76	11.9	*	-
50	OVARC1000581	5.46	3.63	4.65	3.12	3.25	1.85	1.84	1.64	2.35	**	-
	OVARC1000586	99.11	90.08	96.7	58.86	53.54	48.9	78.17	82.33	62.01	**	*
	OVARC1000588	5.04	6.16	5.9	2.73	4.3	3.79	4.96	4.69	3.2	*	-
	OVARC1000605	11.72	9.54	8.96	6.4	6.63	6.02	4.7	4.72	5.55	*	**
	OVARC1000622	86.95	79.96	78.79	29.56	66.79	40.9	71.63	93.74	75.18	*	-
	OVARC1000636	9.18	7.82	11.99	5.56	8.68	4.67	5.37	6.74	3.7	*	*
	OVARC1000640	9.32	12.02	12.8	8.63	10.33	8.57	6.08	8.89	7.4	*	-
55	OVARC1000649	137.37	159.82	123.65	116.33	170.6	128.38	91.38	85.12	81.65	**	-
	OVARC1000661	14.89	15.01	20.86	11.94	15.89	11.61	9.31	9.27	13.9	*	-
	OVARC1000677	42.34	38.62	28.23	30.67	34.02	28.61	19.25	22.35	28.93	*	-
	OVARC1000678	18.66	21.84	18.64	9.55	15.51	8.53	9.3	11.98	8.4	*	**

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	OVARC1000679	17.17	15.32	16.17	8.84	11.11	9.51	8.07	11.07	12.27	**	*	-	-
	OVARC1000681	8.2	7.24	6.7	4.69	3.61	5.03	3.58	6.1	3.97	**	*	-	-
	OVARC1000682	113.12	97.53	93.09	104.53	135.81	99.85	59.24	48.57	73.95	*	-	-	-
5	OVARC1000689	57.01	42.21	46.96	44.44	54.09	47.18	30.34	27.71	26.26	*	-	-	-
	OVARC1000700	15.99	15.69	20.71	10.16	14.93	8.67	10.07	14.65	13.84	*	-	-	-
	OVARC1000703	26.78	29.43	35.22	14.83	20.62	12.69	19.45	19.63	21.91	*	*	-	-
	OVARC1000722	101.86	85.68	116.52	89.03	99.63	84.39	90.99	59.44	79.26	*	-	-	-
	OVARC1000726	14.33	9.39	12.54	8.8	8.89	8.63	5.72	6.56	7.04	*	-	-	-
	OVARC1000727	10.18	7.75	13.09	5.79	7.58	4.18	6.38	6.81	6.67	*	-	-	-
10	OVARC1000730	29.15	29.95	31.68	12.76	10.82	12.92	11.85	21.92	19.46	**	*	-	-
	OVARC1000741	29.33	29.17	34.55	13.03	37.4	9.12	12.19	21.98	17.49	*	-	-	-
	OVARC1000746	7.78	5.19	7.05	4.39	4.32	3.45	2.05	2.62	3.13	*	-	-	-
	OVARC1000764	38.05	40.13	44.9	31.76	33.36	24.43	25.99	25.42	30.04	*	**	-	-
	OVARC1000769	15.32	19.03	26.3	6.54	8.47	6.17	10.92	9.44	11.01	*	-	-	-
15	OVARC1000771	12.14	10.36	12.36	5.65	9.59	2.99	5.56	6.75	5.39	**	-	-	-
	OVARC1000773	208.54	178.97	168.4	156.38	229.88	197.98	120.99	98.51	115.59	**	-	-	-
	OVARC1000775	34.96	28.91	27.77	13.91	16.38	12.88	14.63	18.43	17.02	**	**	-	-
	OVARC1000778	16.25	14.26	17.29	7.71	11.77	9.22	9.21	13.13	13.25	*	-	-	-
	OVARC1000779	5.51	4.08	7.92	1.14	3.76	1.42	1.72	21.49	16.55	*	-	-	-
20	OVARC1000781	14.72	11.11	14.65	7.53	10.61	4.88	3.59	7.19	4.56	*	**	-	-
	OVARC1000787	16.08	11.69	22.35	5.66	7.21	5.45	9	11.11	9.91	*	-	-	-
	OVARC1000789	23.78	29.78	21.78	12.72	20.51	12.99	10.1	11.61	10.12	**	-	-	-
	OVARC1000800	37.24	52.19	47.92	15.44	23.62	15.47	18.1	25.22	22.47	**	**	-	-
	OVARC1000802	10.69	12.79	19.22	5.61	8.97	4.92	12.57	10.26	7.88	*	-	-	-
	OVARC1000810	41.47	36.61	45.9	14.82	21.04	14.45	26.69	32.64	43.34	**	-	-	-
25	OVARC1000811	19.55	15.32	20.3	9.11	11.03	10.04	5.82	8.76	8.16	**	**	-	-
	OVARC1000814	47.61	40.61	47.27	21.78	30.43	20.51	28.06	40.57	35.2	**	-	-	-
	OVARC1000816	30.44	36.85	45.82	25.26	35.08	20.13	15.73	10.27	23.79	*	-	-	-
	OVARC1000817	7.44	5.99	13.01	2.4	3.28	3.96	1.6	3.36	1.57	*	-	-	-
	OVARC1000834	9.2	11.08	10.6	3.33	5.92	2.58	4.12	4.4	2.95	**	**	-	-
	OVARC1000846	33.2	36.76	34.02	15.54	20.84	16.18	25.4	21.7	22.13	**	-	-	-
30	OVARC1000850	10.1	9.46	13.94	3.02	6.63	4.93	5.97	6.78	5.46	*	-	-	-
	OVARC1000853	124.13	83.82	117.1	50.7	94.43	68.32	58.07	66.46	64.96	*	-	-	-
	OVARC1000862	9.58	7.61	8.86	6.22	4.52	5.06	2.49	2.85	3.78	*	**	-	-
	OVARC1000873	22.12	9.86	11.25	3.95	10.2	7.01	4.33	4	5.66	*	-	-	-
	OVARC1000875	25.32	18.88	20.49	9.43	11.13	12.13	10.43	9.71	12.19	**	**	-	-
	OVARC1000876	14.43	11.76	13.8	4.33	8.64	6.48	3.87	5.38	3.7	**	**	-	-
35	OVARC1000883	16.65	14.83	22.63	10.71	10.46	10.25	4.07	3.52	3.44	*	**	-	-
	OVARC1000885	14.94	15.72	15.2	7.47	13.49	6.08	8.84	6.87	4.31	**	-	-	-
	OVARC1000886	13.43	12.39	14.55	7.87	12.43	7.38	15.33	6.54	7.36	*	-	-	-
	OVARC1000890	238.12	222.49	244.97	168.11	248.06	165.63	120.4	102.6	108.39	**	-	-	-
	OVARC1000891	14.84	13	11.09	4.07	5.36	4.55	3.08	4.38	3.01	**	**	-	-
40	OVARC1000897	5.52	4.78	5.55	2.64	2.48	2.49	2.14	2.77	2.38	**	**	-	-
	OVARC1000912	18.82	12.83	16.34	8.16	8.42	8.22	8.21	8.74	10.52	*	-	-	-
	OVARC1000914	14.59	8.15	9.14	3.85	5.26	5.95	4.68	5.3	4.1	*	-	-	-
	OVARC1000915	17.53	15.34	14.44	6.42	7.74	4.39	7.85	11.07	8.04	**	**	-	-
	OVARC1000916	15.19	18.72	21.06	9.85	20.11	11.22	12.02	12.35	10.4	*	-	-	-
	OVARC1000924	11.12	12.86	14.01	5.55	9.51	4.44	3.13	4.61	3.65	*	**	-	-
45	OVARC1000928	46.27	37.28	34.31	5.2	8.81	6.65	4.93	6.15	5.85	**	**	-	-
	OVARC1000936	10.09	10.55	9.33	5.2	9.07	4.74	3.02	5.31	5.15	**	-	-	-
	OVARC1000937	7.99	8.04	6.58	4.25	5.19	2.94	3.85	3.95	5.45	*	*	-	-
	OVARC1000945	15	14.88	13.39	5.71	5.62	7.78	3.1	4.11	2.76	**	**	-	-
	OVARC1000948	7.88	5.06	4.83	2.65	3.28	2.79	2.69	2.39	2.47	*	-	-	-
	OVARC1000956	14.88	11.07	13.93	5.15	8.05	6.51	8.38	4.46	6.46	**	*	-	-
50	OVARC1000959	16.85	16.96	14.18	9.84	10.41	6.42	15.3	9.78	14.01	**	-	-	-
	OVARC1000960	47.32	52.37	41.49	22.16	32.89	19.82	46.28	34.15	44.56	*	-	-	-
	OVARC1000964	306.84	272.77	304.89	274.01	264.01	211.54	160.52	108.2	102.39	**	-	-	-
	OVARC1000971	7.74	6.08	3.76	3.85	7.47	4.63	2.45	4.82	2.32	*	-	-	-
	OVARC1000975	109.05	95.15	91.82	89.45	126.14	83.84	54.44	48.09	54.61	**	-	-	-
	OVARC1000976	6.41	7.34	5.63	3.4	4.98	2.89	5.48	3.56	2.85	*	-	-	-
55	OVARC1000981	24.82	24.19	24.61	14.13	15.11	11.79	18.79	11.54	16.77	**	*	-	-
	OVARC1000982	21.37	12.18	12.3	7.66	16.73	9.68	5.67	4.54	5.45	*	-	-	-
	OVARC1000984	10.44	9.85	10.17	2.64	4.79	2.24	2.88	2.32	3.54	**	**	-	-
	OVARC1000995	27.57	24.28	19.39	14.42	17.35	10.4	23.31	17.65	22.26	*	-	-	-

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	OVARC1000996	12.75	15.42	13.22	7.58	7.82	4.86	10.5	9.45	10.8	**	*	-	-
	OVARC1000999	77.92	64.11	52.33	34.61	41.57	26.78	51.13	38.47	53.84	*	-	-	-
	OVARC1001000	34.25	25.88	23.55	13.32	17.72	11.08	24.85	23.48	28.11	*	-	-	-
5	OVARC1001004	4.45	4.47	4.74	3.56	4.7	2.11	3.94	2.09	3.24	*	*	-	-
	OVARC1001010	7.8	4.93	6.92	2.94	3.81	2.97	3.34	2.1	2.69	*	*	-	-
	OVARC1001011	10.56	5.96	7.28	2.55	4.47	3.01	5.82	4.52	6.68	*	-	-	-
	OVARC1001030	135.15	261.75	227.94	119.93	118.81	67.28	114.11	94.32	117.34	**	*	-	-
	OVARC1001032	10.53	7.53	10.42	4.6	4.01	3.78	8.13	6.94	7.33	**	*	-	-
10	OVARC1001034	10.83	11.24	8.27	5.28	4.2	4.55	7.53	5.89	7.35	**	*	-	-
	OVARC1001038	36.07	37.32	30.24	14.88	24.71	11.8	14.41	10.88	16.24	*	**	-	-
	OVARC1001040	40.95	33.02	36.27	20.4	24.74	15.2	38.11	31.08	34.73	**	*	-	-
	OVARC1001041	28.88	24.51	24.41	14.12	19.17	10.91	20.98	17.34	23.83	*	-	-	-
	OVARC1001044	8.66	8.02	6.34	3.74	2.76	3.79	6.52	3.05	4.17	**	*	-	-
	OVARC1001049	23.67	22.64	22.97	8.16	12.73	9.28	19.46	22.57	21.53	**	*	-	-
15	OVARC1001051	381.08	484.89	350.06	354.62	546.22	323.29	741.7	383.07	703.22			-	-
	OVARC1001054	6.6	5.59	5.17	3.06	5.01	2.19	3.89	3.27	2.79	**	*	-	-
	OVARC1001055	14.4	14.98	14.95	7.9	10.31	6.02	5.76	7.98	6.8	**	*	-	-
	OVARC1001062	17.06	13.11	19.77	9.47	7.02	5.92	5.47	7.54	3.76	*	**	-	-
	OVARC1001065	58.8	47.67	46.94	41.39	58.25	31.45	28.27	24.21	23.74	**	*	-	-
20	OVARC1001068	12.24	9.85	10	9.05	10.45	10.03	4.46	8.42	5.6	*	-	-	-
	OVARC1001072	5.2	5.85	5.86	2.66	7.45	1.74	3.96	4.57	2.54	*	-	-	-
	OVARC1001073	7.5	8.58	12.65	4.78	6.4	4.65	5.22	6.96	5.47	*	-	-	-
	OVARC1001074	4.7	5.22	6.88	3.02	6.61	3.48	7.1	3.06	2.4	*	-	-	-
	OVARC1001078	12.05	11.95	9	4.67	9.88	3.56	7.61	7.71	7.4	*	-	-	-
	OVARC1001085	11.18	10.66	13.33	5.34	5.76	6.26	7.62	7.57	5.14	**	*	-	-
25	OVARC1001086	9.39	8.11	10.75	4.2	10	3.47	6.76	8.44	4.74	*	-	-	-
	OVARC1001091	241.22	186.8	193.81	163.03	271.86	178.86	140.22	106.42	112.84	*	+	-	-
	OVARC1001092	18.15	15.63	18.59	22.78	28.04	21.17	13.63	16.45	14.87	*	-	-	-
	OVARC1001104	8.1	6.77	10.2	3.75	7.44	6.44	3.73	7.33	6.12	*	-	-	-
	OVARC1001107	107.49	92.87	112.02	98.9	125.4	90.42	58.37	49.66	59.61	**	*	-	-
30	OVARC1001113	4.26	4.3	6.18	3.48	7.31	2.59	2.8	2.95	2.48	*	-	-	-
	OVARC1001117	14	17.53	15.78	9.22	10.42	7.27	18.6	16.88	12.72	**	*	-	-
	OVARC1001118	28.39	26.32	27.08	13.26	13.63	13.64	14.58	18.84	21.16	**	*	-	-
	OVARC1001125	15.09	9.24	18.28	5.27	6.72	6.58	3.81	6.47	3.35	*	*	-	-
	OVARC1001129	8.66	7.06	12.46	3.03	6.25	3.24	5.49	10.45	5.05	*	-	-	-
	OVARC1001132	9.08	13.23	15.1	8.86	15.2	9.07	5.57	13.13	8.52	*	-	-	-
35	OVARC1001138	155.24	193.79	160.3	115.39	149.38	101.68	122.48	164.58	137.03	**	*	-	-
	OVARC1001141	12.99	10.8	12.94	7	9.03	7.57	7.48	10.75	7.3	*	-	-	-
	OVARC1001154	128.63	107.01	106.33	119.46	158.63	83.66	81.42	78.16	83.39	*	-	-	-
	OVARC1001161	17.68	27.92	21.1	11.55	22.82	12.42	16.84	15.27	15.42	**	**	-	-
	OVARC1001162	21.74	16.75	19.82	10.26	11.33	9.72	10.1	12.69	11.14	**	*	-	-
40	OVARC1001163	10.91	8.03	10.73	4.37	5.95	4.38	3.95	7.35	4.62	**	*	-	-
	OVARC1001167	38.47	38	43.81	17.29	22.87	18.91	28.74	29.72	36.08	**	*	-	-
	OVARC1001169	11.94	7.48	10.4	5.85	13.24	4.72	3.88	5.51	4.65	*	-	-	-
	OVARC1001170	26.22	26.34	31.69	14.46	15.02	12.36	12.5	14.3	11.17	**	**	-	-
	OVARC1001171	143.81	236.48	129.81	114.4	117.18	158.91	77.44	54.36	128.19	**	*	-	-
	OVARC1001173	24.91	33.6	36.93	11.93	16.26	13.53	26.95	27.14	25.91	*	-	-	-
	OVARC1001176	209.32	244.43	234.51	205.75	340.26	228.89	167.09	179.74	200.74	**	*	-	-
45	OVARC1001180	67.2	61.17	66.56	30.38	32.42	26.76	42.84	47.13	54.33	**	*	-	-
	OVARC1001188	18.84	14.15	17.06	4.37	15.93	5.9	10.16	39.68	8.56	*	-	-	-
	OVARC1001200	14.51	7.89	14.82	6.11	7.72	3.65	4.16	15.56	6.11	*	-	-	-
	OVARC1001202	37.46	21.56	29.17	10.06	10.43	13.25	17.78	23.14	18.29	*	-	-	-
	OVARC1001206	6.83	6.97	11.31	3.06	5.96	2.9	2.03	8.52	4.3	*	-	-	-
50	OVARC1001209	56.31	51.58	60.2	57.91	69.04	54.41	36.32	29.24	28.87	**	*	-	-
	OVARC1001219	14.82	14.11	12.95	3.65	7.48	4.86	4.34	7.98	3.54	**	**	-	-
	OVARC1001222	17.11	17.29	18.38	6.61	16.42	9.64	6.56	7.21	5.56	**	*	-	-
	OVARC1001232	34.23	34.49	36.17	16.43	23.42	19.3	24.37	27.16	28.45	**	*	-	-
	OVARC1001240	22.68	22.79	23.45	11.83	13.49	10.07	14	20.54	14.23	**	*	-	-
	OVARC1001243	8.41	5.82	7.86	3.1	7.95	3.99	3.48	18.25	1.41	*	-	-	-
55	OVARC1001244	43.29	22.42	33.3	20.02	23.25	15.87	15.69	21.46	15.18	*	-	-	-
	OVARC1001246	191.8	262.18	216.69	139.76	292.92	181.43	261.49	147.46	197.54	**	*	-	-
	OVARC1001247	33.18	25.43	26.03	8.87	21.81	17.23	8.61	11	7	*	-	-	-
	OVARC1001260	10.58	9.81	13.5	4.35	12.46	3.56	7.06	8.38	13.07	*	**	-	-
	OVARC1001261	10.86	9.17	11.3	5.17	7	3.2	4.94	4.19	3.51	*	**	-	-

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	OVARC1001268	91.7	87.42	103.18	50.09	61.38	43.24	78.98	90.56	56.28	**	-	-
	OVARC1001270	7.04	6.65	7.37	4.89	4.4	3.37	2.36	3.78	2.58	**	**	-
	OVARC1001271	19.59	14.31	19.8	9.15	12.99	7.59	10.4	9.45	13.28	*	*	-
5	OVARC1001282	9.08	5.35	8.29	3.47	3.89	2.86	2.79	2.02	1.62	*	*	-
	OVARC1001296	8.37	7.88	7.76	3.73	3.83	3.51	3.2	2.52	1.42	**	**	-
	OVARC1001306	8.13	8.36	10.06	2.51	4.13	1.61	1.91	3.24	2.11	**	**	-
	OVARC1001314	6.35	7.88	10.42	5.15	6.88	5.6	5.8	2.73	3.16	*	*	-
	OVARC1001316	9.21	9.19	7.4	3.28	5.15	2.41	2.09	2	2.6	**	**	-
10	OVARC1001329	66.76	60.97	62.75	30.71	36.83	28.85	49.5	54.71	56.06	**	*	-
	OVARC1001330	6.94	7.09	6.08	3.83	3.92	2.72	1.52	3.71	2.62	**	**	-
	OVARC1001336	20.53	13.52	17.21	8.37	10.93	7.02	7.67	13.22	12.66	*	*	-
	OVARC1001338	9.67	3.35	7.39	3.31	2.87	2.49	3.22	2.79	2.03	*	*	-
	OVARC1001339	93.84	87.95	84.06	45.91	65.98	50.22	43.37	46.73	40	**	**	-
	OVARC1001340	6.83	5.17	8.34	3.19	3.73	1.7	2.64	3.21	3.16	*	*	-
15	OVARC1001341	30.38	40.21	33.21	15.81	17.56	16.77	23.98	16.89	14.16	**	*	-
	OVARC1001342	319.96	384.64	298.02	528.73	514.44	449.66	353.76	251.2	152.62	*	†	-
	OVARC1001344	24.05	19.69	20.03	8.91	10.1	7.96	16.66	12.81	15.35	**	*	-
	OVARC1001357	6.41	18.75	6.59	4.08	6.56	3.73	3.75	4.14	3.16	*	*	-
	OVARC1001359	59.32	54.06	31.23	23.17	43.75	45.21	51.59	26.81	37.78	*	*	-
20	OVARC1001360	5.67	4	3.9	1.82	2.67	1.87	1.59	2.07	1.71	*	**	-
	OVARC1001369	7.6	9.8	9.35	5.24	6.16	2.48	5.5	3.41	1.68	*	*	-
	OVARC1001372	9.97	8.14	5.06	1.49	5.79	2.2	2.9	3.07	0.96	*	*	-
	OVARC1001376	27	25.34	21.25	12.73	15.31	10.9	17.23	14.16	15.91	**	*	-
	OVARC1001381	39.84	52.86	35.2	18.78	31.21	17.84	39.83	32.09	35.47	*	*	-
	OVARC1001391	4.35	4.74	4.59	3.41	5.61	3.07	2.93	3.15	1.97	**	*	-
25	OVARC1001392	11.01	13.87	11.26	7.11	8.72	6.36	4.32	4.97	3.08	*	**	-
	OVARC1001399	7.11	9.27	5.73	3.62	4.78	3.62	4.04	3.29	4.7	*	*	-
	OVARC1001417	8.65	8.11	7.05	3.69	5.18	3.15	2.59	2.11	3.11	**	**	-
	OVARC1001419	9.55	7.34	7.59	3.69	5.75	3.4	4.52	2.92	1.58	*	**	-
	OVARC1001425	13.5	5.66	6.59	3.04	5.54	5.43	3.66	1.31	1.7	*	*	-
	OVARC1001436	14.91	13.09	11.35	5.12	5.94	3.89	4.56	3.69	3.48	**	**	-
30	OVARC1001442	5.57	6.26	6.22	3.11	6.56	2.54	5.62	2.71	2.72	*	*	-
	OVARC1001451	30.68	20.35	20.93	10.57	21.04	10.84	19.07	21.71	23.63	*	*	-
	OVARC1001452	16.95	14.67	11.44	7.52	6.15	5.24	7.7	11.36	6.64	**	*	-
	OVARC1001453	7.86	6.06	6.61	4.22	6.52	4.39	4.72	4.86	4.79	*	*	-
	OVARC1001476	20.63	24.57	30.44	15.92	22.32	7.34	11.05	12.16	16.07	*	*	-
	OVARC1001480	7.35	4.8	7.98	3.71	4.84	5.16	2.87	2.08	3.16	*	*	-
35	OVARC1001489	11.25	5.88	6.53	8.16	19.5	4.38	4.69	2.8	2.81	*	*	-
	OVARC1001493	15.28	11.36	13.67	4.88	4.94	2.76	9.11	6.21	8.31	**	*	-
	OVARC1001496	32.05	27.24	23.8	12.75	20.64	11	9.38	5.04	10.85	*	**	-
	OVARC1001499	5.67	6.05	4.7	2.72	3.78	1.85	2.85	4.6	2.57	*	*	-
	OVARC1001506	31.76	25.87	22.22	8.57	18.43	9.44	18.79	15.06	20.59	*	*	-
40	OVARC1001509	17.78	13.64	12.09	7.06	8.79	5.76	15.13	14.75	21.14	*	*	-
	OVARC1001510	8.59	5.24	6.08	3.07	5.95	3.22	7.27	7.67	4.5	*	*	-
	OVARC1001516	10.81	12.88	13.12	5.8	9.08	6.34	8.79	7.64	9.61	*	*	-
	OVARC1001525	7.75	5.51	6.34	3.13	4.32	3.66	4.26	3.77	3.8	*	*	-
	OVARC1001542	30.12	29.23	28.39	14.89	25.03	14.49	18.26	13.2	26.28	*	*	-
	OVARC1001544	27.99	28.47	20.46	12.55	18.48	10.77	36.56	24.05	33.39	*	*	-
45	OVARC1001546	6.07	8.98	10.22	3.38	5.35	8.68	3.38	3.45	4.28	*	*	-
	OVARC1001547	4.36	6.21	6.19	3.96	3.95	1.63	2.77	2.7	2.24	**	*	-
	OVARC1001555	137.04	110.5	136.25	120.36	174.1	119.31	90.66	69.83	70.87	*	*	-
	OVARC1001560	10.54	9.21	9.05	6.2	10.38	4.19	4.33	6.13	2.34	*	*	-
	OVARC1001569	28.34	25.69	28.31	17.71	19.82	21.58	15.15	17.9	15.82	**	**	-
	OVARC1001570	9.57	12.59	13.54	7.21	9.92	6.14	6.01	6.08	8.45	*	*	-
50	OVARC1001577	10.2	13.78	13.09	13.59	16.75	9.11	10.56	8.87	5.25	*	*	-
	OVARC1001578	0	0.27	1.12	0.09	2	0.48	1.37	0.77	0	*	*	-
	OVARC1001596	18.44	38.66	31.49	14.48	23.49	16.88	13.34	13.82	12.27	*	*	-
	OVARC1001600	12.84	12.05	12.79	8.39	9.83	7.52	7.16	10.38	7.31	**	*	-
	OVARC1001607	17.69	15.72	17.94	10.9	18.71	12.05	10.18	16.33	11.6	*	*	-
	OVARC1001610	7.42	7.24	11.17	5.09	7.94	4.34	2.78	4.22	3.55	*	*	-
55	OVARC1001611	3.52	5.78	9.33	2.82	5.44	3.47	2.68	4.9	2.76	*	*	-
	OVARC1001615	7.22	4.15	9.71	3.66	4.51	3.88	4.88	4.91	5.78	*	*	-
	OVARC1001636	5.13	4.74	6.26	4.34	6.6	4.17	6.58	6.24	9.12	*	*	-
	OVARC1001668	40.93	55.07	40.85	20.99	33.29	18.89	40.58	43.41	37.28	*	*	-

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	OVARC1001702	9.4	5.63	9.29	4.18	2.13	4.1	3.32	3.32	2.46	*	*	-	-
	OVARC1001703	7.15	7.4	12.31	4.47	5.7	4.5	5.85	8.24	3.65				
	OVARC1001710	18.66	12.34	27.68	8.37	10.17	11.06	8.89	17.12	13.23				
5	OVARC1001711	18.7	15.2	21.81	10.78	18.26	9.63	7.19	14.6	8.6	*	*	-	-
	OVARC1001713	106.12	95.89	110.84	111.33	127.16	96.1	59.14	62.39	67.07	**	*	-	-
	OVARC1001725	7.41	8.41	15.02	6.01	22.46	3.17	4.32	4.47	6.9				
	OVARC1001726	9.14	11.76	13.16	5.3	10.91	4.63	7.72	5.13	7.08	*	*	-	-
	OVARC1001727	6.13	4.36	5.44	2.42	3.92	3.64	2.37	4.79	3.09	*	*	-	-
10	OVARC1001731	326.35	314.92	333.21	240.06	116.88	168.02	275.41	235.36	284.79	*	*	-	-
	OVARC1001735	10.45	7.4	10.3	3.26	6.6	5.16	2.85	50.48	3.58	*	*	-	-
	OVARC1001741	51.89	35.06	44.69	30.3	40.05	30.18	29.82	27.49	31.74	*	*	-	-
	OVARC1001745	48.03	48.42	50.14	20.26	24.89	18.25	35.38	41.14	42.19	**	*	-	-
	OVARC1001759	8.58	9.79	14.25	4.9	9.68	2.54	3.21	5.87	3.66	*	*	-	-
	OVARC1001762	15.44	18.76	16.88	4.99	8.2	5.87	5.45	4.57	3.61	**	**	-	-
15	OVARC1001766	83.39	85.91	87.93	59.55	79.17	53.32	53.78	49.12	57.96	**	*	-	-
	OVARC1001767	7.04	5.21	8.42	2.96	5.88	2.78	2.97	1.63	2.74	*	*	-	-
	OVARC1001768	14.52	13.49	18.22	6.31	12.6	7.55	3.97	6.24	6.88	**	*	-	-
	OVARC1001770	26.33	28.28	29.2	13.86	20.54	11.13	6.52	15.1	8.61	*	**	-	-
	OVARC1001776	7.09	4.63	7.55	4.18	5.49	2.76	2.6	3.29	2.71	*	*	-	-
	OVARC1001791	10.39	7.82	10.63	6.37	4.38	3.31	3.58	4.2	5.4	*	**	-	-
20	OVARC1001795	7.98	5.23	12.47	1.59	4.12	3.1	3.31	4.76	7.14				
	OVARC1001798	40.84	44.26	46	20.27	29.31	16.26	30.23	32.18	29.44	**	**	-	-
	OVARC1001802	21.47	24.32	21.73	9.56	17	10.13	13.8	16.34	14.18	*	**	-	-
	OVARC1001805	21.41	25.19	22.93	13.01	23.64	11.53	6.55	5.13	2.96	**	*	-	-
	OVARC1001807	9.03	4.95	8.69	4.35	5.41	3.66	4.23	6.47	5.73				
25	OVARC1001809	149.46	129.89	172.57	133.13	197.68	130.62	61.18	73.6	73.85	**	*	-	-
	OVARC1001812	14.81	11.9	18.98	7.06	7.79	6.77	7.18	8.19	7.69	*	*	-	-
	OVARC1001813	16.16	13.4	12.96	5.79	9.88	6.64	9.17	11.83	7.83	*	*	-	-
	OVARC1001820	13.24	13.12	21.66	6.46	7.84	7.81	9.43	11.92	8.26	*	*	-	-
	OVARC1001828	7.36	8.18	15.13	2.53	4.46	3.16	2.97	2.27	1.93	*	*	-	-
	OVARC1001833	7.55	8	10.4	3.73	5.88	2.72	2.14	3.67	2.55	*	**	-	-
30	OVARC1001839	9.51	8.23	9.47	3.48	6.12	2.44	2.33	1.23	3.33	*	**	-	-
	OVARC1001846	10.75	6.47	12.96	4.44	5.49	4.43	2.19	5.18	4.87	*	*	-	-
	OVARC1001849	21.23	22.64	18.18	12.84	14.77	8.26	9.88	17.09	10.17	*	*	-	-
	OVARC1001861	14.15	12.35	14.96	7.86	9.2	6.06	6.33	6.39	8.07	**	**	-	-
	OVARC1001873	10.37	9.13	10.41	3.08	3.81	3.28	3.75	2.72	3.55	**	**	-	-
	OVARC1001879	12.35	13.47	14.5	4.79	6.62	4.85	9.81	8.26	4.82	**	*	-	-
35	OVARC1001880	17.95	16.04	17.13	6.7	12.3	6.25	9.7	7.19	8.89	*	**	-	-
	OVARC1001883	10.68	7.64	9.62	5.66	5.31	4.96	4.5	5.37	3.66	*	**	-	-
	OVARC1001900	21.57	23.04	21.79	9.35	13.16	8.64	4.93	5.9	5.98	**	*	-	-
	OVARC1001901	6.1	3.23	6.27	3.76	3.35	2.44	2	2.36	2.55	*	*	-	-
	OVARC1001911	5.85	6.08	5.24	3.87	3.1	3.23	3.29	4.37	2.41	**	*	-	-
40	OVARC1001916	15.55	14.04	13.05	10.21	8.26	9.44	6.7	7.73	11.27	**	*	-	-
	OVARC1001928	4.28	4.17	5.98	2.82	2.37	1.14	3.65	1.6	1.43	*	*	-	-
	OVARC1001937	25.6	15.71	13.44	9.48	11.18	11.27	11.49	12.97	7.51				
	OVARC1001940	8.76	8.78	8.37	2.83	3.28	2.84	2.16	2.96	2.02	**	**	-	-
	OVARC1001942	20.24	15.16	17.14	7.55	9.31	5.48	5.3	6.71	7.34	**	**	-	-
	OVARC1001943	29.68	32.41	20.55	12.97	22.62	15.27	4.34	4.72	5.72	**	*	-	-
45	OVARC1001949	14.19	11.75	10.33	3.19	5.85	4.46	2.89	6.47	5.47	**	*	-	-
	OVARC1001950	13.94	15.9	10.94	6.19	9.29	6.75	8.04	7.58	9.81	*	*	-	-
	OVARC1001952	122.9	130.05	103.73	90.55	135.58	102.89	79.11	70.36	72.15	**	*	-	-
	OVARC1001954	7.45	6.81	6.15	3.11	3.63	2.91	2.32	2.33	2.18	**	*	-	-
	OVARC1001963	12.44	11.79	17.61	6.04	6.32	5.28	6.38	9.47	7.04	*	*	-	-
50	OVARC1001983	25.71	30.08	25.81	12.15	15.68	10.47	16.02	11.31	11.87	**	**	-	-
	OVARC1001987	13.81	15.75	12.25	6.15	7.8	4.37	5.37	6.61	4.93	**	**	-	-
	OVARC1001989	18.41	16.89	13.96	7.74	13.38	8.71	14.94	11.39	11.29	*	*	-	-
	OVARC1001991	12.31	10.21	10.74	6.47	8.3	7.41	6.69	6.19	5.31	*	**	-	-
	OVARC1002005	33.83	38.39	35.62	17.89	27.06	20.01	28.16	23.73	27.11	**	**	-	-
	OVARC1002044	25.13	24.53	23.58	14.08	17.38	11.27	23.29	17.04	24.49	**	*	-	-
55	OVARC1002046	79.06	107.27	86.51	49.53	77.97	65.8	68.65	65.46	67.43	*	*	-	-
	OVARC1002050	9.22	6.62	10.19	4.05	4.76	4.15	4.13	2.81	4.5	*	*	-	-
	OVARC1002058	18.18	16.91	17.55	13.19	18.87	6.99	24.17	22.71	28.4	*	*	-	-
	OVARC1002058	67.02	72.72	47.65	37.79	39.59	35.74	62.17	50.77	51.33	*	*	-	-
	OVARC1002062	24.4	33.12	24.78	17.13	27.63	15.59	48.32	29.05	33.16				

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	OVARC1002091	18.78	19.82	15.43	10.02	4.76	6.56	9.66	6.62	10.94	**	**	-	-
	OVARC1002092	11.35	7.73	4.3	3.87	5.5	2.76	3.85	4.56	3.79			-	-
5	OVARC1002093	11.71	8.5	20.66	4.96	14.44	7.82	5.85	5.4	7.08			-	-
	OVARC1002094	6.29	6.49	6.65	2.69	4.04	2.24	4.34	3.07	3.08	**	**	-	-
	OVARC1002107	13.48	8.34	12.83	6.06	7.84	6.33	9.41	7.18	12.5	*	*	-	-
	OVARC1002112	26.38	33.01	27.23	12.79	21.35	12.35	12.54	9.82	14.29	*	**	-	-
	OVARC1002126	65.16	69.33	51.38	44.56	51.62	38.84	65.71	52.52	60.89			-	-
	OVARC1002127	6.15	6.37	5.32	1.95	4.41	3.09	5.22	3.46	3.37	*	*	-	-
10	OVARC1002138	5.22	5.32	3.68	5.16	3.08	2.95	2.56	2.26	2.94	*	*	-	-
	OVARC1002143	7.3	4.6	3.7	3.29	5.14	1.8	3.79	3.64	5.8			-	-
	OVARC1002156	14.33	13.86	13.02	10.03	12.28	6.78	8.59	6.29	5.67	**	*	-	-
	OVARC1002158	9.15	5.03	4.65	3.18	3.11	2.41	3.88	2.86	4.37			-	-
	OVARC1002165	67.03	61.86	54.25	23.78	36.97	31.97	46.19	44.24	42.15	**	*	-	-
	OVARC1002176	10.61	13.89	9.02	5.22	6.29	4.46	9.03	7.11	8.09	*	*	-	-
15	OVARC1002178	11.02	11.22	6.01	3.16	5.47	2.82	6.17	3.48	3.57	*	*	-	-
	OVARC1002182	6.32	5.52	5.4	2.92	5.92	3.91	6.46	4.29	5.82			-	-
	OVARC1002185	13.32	14.59	15.01	5.81	10.11	6.86	7.78	7.13	8.82	**	**	-	-
	PLACE1000004	9.74	9.21	11.61	4.85	7.73	5.01	4.83	8.27	4.93	*	*	-	-
	PLACE1000005	27.12	18.01	21.46	13.29	16.54	9.78	14.01	13.75	13.04	*	*	-	-
20	PLACE1000006	91.12	57.04	55.23	34.88	52.28	43.96	6.98	11.96	13.8	**	*	-	-
	PLACE1000007	7.26	8.75	8.28	8.37	10.72	8.06	3.04	5.48	2.7	*	*	-	-
	PLACE1000014	2.23	2.04	4.15	1.42	4	3.02	1.88	2.43	1.7			-	-
	PLACE1000031	25.49	34.88	32.13	13.67	27.22	11.3	27.49	25.37	24.47			-	-
	PLACE1000033	18.11	15.97	17.95	12.01	14.01	16.72	14.29	10.78	15.77			-	-
	PLACE1000040	8.82	8.21	10.8	5.78	10.45	6.53	3.91	7.12	4.69	*	*	-	-
25	PLACE1000048	20.38	17.3	18.51	15.36	23.63	12.54	8.78	9.57	6.66	**	*	-	-
	PLACE1000050	5.4	7.04	6.5	2.42	4.86	4.46	3.72	6.27	1.7			-	-
	PLACE1000061	9.33	8.61	17.28	5.67	11.39	8.55	3.23	9.76	4.54			-	-
	PLACE1000066	6.66	5.77	17.49	7.42	6.83	5.75	5.92	4.2	3.99			-	-
	PLACE1000075	12.56	13.3	14.47	10.46	23.06	11.81	12.58	8.36	7.76			-	-
	PLACE1000078	16.43	18.48	16.12	10.89	9.95	8.28	13.59	13.8	12.7	**	*	-	-
30	PLACE1000081	10.24	9.79	10.46	3.99	5.51	5	3.34	5.78	6.89	**	*	-	-
	PLACE1000086	24.93	18.78	23.44	11.66	12.45	12.8	14.85	17.83	16.54	**	*	-	-
	PLACE1000094	9.77	8.35	20.14	5.83	7.13	8.45	9.11	6.86	4.47			-	-
	PLACE1000101	13.24	13.69	14.14	7.47	11.68	8.08	3.54	8.15	5.57	*	**	-	-
	PLACE1000121	13.12	18.46	20.42	15.19	20.27	14.52	7.88	10.58	8.77	*	*	-	-
	PLACE1000133	9.91	9.72	12.83	7.9	8.22	8.5	5.09	6.11	8.25	*	*	-	-
35	PLACE1000142	9.88	8.89	10.42	4.19	7.46	3.72	7.05	4.74	5.82	*	**	-	-
	PLACE1000146	26.84	30.96	24.74	12.94	22.4	10.59	30.36	28.2	29.92	*	*	-	-
	PLACE1000163	7.41	5.19	10.36	3.1	5	4.08	3.16	3.43	3.29	*	*	-	-
	PLACE1000172	27.22	20.45	29.16	10.4	14.2	9.22	8.64	12.45	11.02	**	**	-	-
	PLACE1000181	113.9	71.51	73.22	49.28	64.78	42.83	38.76	53.7	55.02			-	-
40	PLACE1000184	17.72	15.27	19.8	11.79	14.01	13.85	9.11	9.87	10.76	*	**	-	-
	PLACE1000185	16.19	14.48	17.72	7.66	7.1	6.34	4.1	6.59	4.27	**	**	-	-
	PLACE1000198	9.65	11.81	15.71	11.09	11.55	8.4	6.38	19.65	7.03			-	-
	PLACE1000213	6.26	6.05	11.46	4.09	6.38	3.94	3.17	3.29	3.78			-	-
	PLACE1000214	9.15	11.17	11.68	8.73	8.08	4.64	3.79	6.02	5.34	**	*	-	-
	PLACE1000220	25.57	22.54	23.7	11.03	13.14	7.79	10.18	10.81	12.09	**	**	-	-
45	PLACE1000231	14.42	18.43	23.26	5.64	9.79	6.68	7.36	7.88	9.82	*	*	-	-
	PLACE1000236	7.58	6.02	8.68	1.98	6.24	5.31	3.56	10.92	5.78			-	-
	PLACE1000245	26.52	25.91	22.56	9.19	16.74	15.36	8.75	9.5	10.2	*	**	-	-
	PLACE1000246	45.69	36.58	50.55	14.83	17.16	15.14	8.9	11.47	10.62	**	**	-	-
	PLACE1000258	9.85	11.52	11.33	3.16	7.63	3.08	2.46	5.51	4.37	*	**	-	-
	PLACE1000268	14.3	14.29	20.76	4.5	8.13	8.1	4.73	7.76	5.77	*	*	-	-
50	PLACE1000292	22.65	21.9	21.53	9.54	18.93	11.23	12.98	16.24	12.38	*	**	-	-
	PLACE1000302	24.34	18.15	25.79	8.82	16.47	8.9	10.89	16.25	19.37	*	*	-	-
	PLACE1000304	9.25	6.15	7.74	5.54	8.18	3.68	3.39	11.18	2.7			-	-
	PLACE1000308	15.07	8.66	14.03	6.88	10.38	7.58	8.62	8.08	9.22			-	-
	PLACE1000309	50.33	32.12	45.32	24.2	31.82	23.11	35.7	38.12	29.88			-	-
	PLACE1000312	7.8	7.45	13.99	4.65	6.15	3.95	7.1	6.14	4.22			-	-
55	PLACE1000330	37.2	43.13	26.2	23.56	30.84	17.96	20.8	28.35	14.01			-	-
	PLACE1000332	19.72	22.93	22.77	9.1	18.25	13.71	15.08	10.86	13.37	*	**	-	-
	PLACE1000347	18.65	20.7	25.21	9.08	28.96	11.34	16.06	14.13	12.46	*	*	-	-
	PLACE1000351	4.55	3.12	7.2	2.8	3.17	2.14	6.68	4.21	4.87			-	-

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	PLACE1000374	4.36	4.25	6.34	4.3	3.67	2.84	1.94	3.1	1.77	*	-
	PLACE1000380	16.1	6.91	17.82	9.8	10.53	4.49	5.18	5.02	6.92	*	-
	PLACE1000383	6.36	4	6.16	2.37	2.92	2.52	2.89	0.95	0.87	*	-
5	PLACE1000397	11.59	7.26	11.9	2.79	5.06	5.01	6.09	6.59	6.48	*	-
	PLACE1000401	9.04	6.59	7.42	3.23	3.26	3.54	3.28	2.6	2.94	**	-
	PLACE1000406	13.08	8.33	14.95	2.59	5.95	3.66	6.86	10.26	6.27	*	-
	PLACE1000412	8.51	7.48	7.35	3.42	4.96	3.44	3.84	4.02	2.52	**	-
	PLACE1000420	18.93	23.33	27.28	7.24	14.78	9.32	4.07	6.78	6.75	*	-
10	PLACE1000421	17.83	12.09	14.21	5.67	5.38	4.01	4.24	5.77	6.73	**	-
	PLACE1000423	9.91	10.66	9.25	5.17	5.46	3.16	3.23	3.33	2.82	**	-
	PLACE1000424	6.41	4.46	8.86	3.52	3.38	1.84	2.63	2.91	2.34	*	-
	PLACE1000430	9.9	7.48	10.47	5.49	5	3.45	3.57	3.09	3.55	*	-
	PLACE1000433	8.1	6.1	7.11	1.95	4.44	2.14	2.34	1.88	2.11	*	-
	PLACE1000435	28.95	26.53	24.32	14.09	14.79	9.09	16.84	11.65	12.23	**	-
15	PLACE1000437	13.7	9.76	13.69	6.32	11.96	9.08	8.69	6.76	4.42	*	-
	PLACE1000442	4.21	4.33	5.54	1.97	3.93	1.28	2.62	4.3	2.3	*	-
	PLACE1000444	8.39	8.02	5.47	3.23	8.73	7.32	3.64	5.13	5.23	*	-
	PLACE1000453	8.24	8.08	7.4	2.64	6.34	3.96	5.87	6.05	5.1	*	-
	PLACE1000456	9.14	8.93	7.88	4.6	6.83	3.55	4.93	5.65	3.15	*	-
20	PLACE1000465	29.59	27.02	24.71	10.66	16.38	9.53	7.25	7.03	4.61	**	-
	PLACE1000481	10.19	8.45	9.18	6.24	5.2	4.46	5.55	2.41	2.95	**	-
	PLACE1000492	14.54	13.99	15.18	6.98	17.38	5.81	5.24	4	6.05	**	-
	PLACE1000508	8.74	6.29	6.02	2.46	6.75	1.48	4.68	3.01	3.04	*	-
	PLACE1000512	4.85	3.74	3.65	2.37	3	3.01	2.27	2.44	1.75	*	-
	PLACE1000540	12.96	8.47	7.79	4.5	9.85	7.03	5.75	9.5	3.54	*	-
25	PLACE1000541	10.16	15.98	11.44	6.25	17.26	10.37	7.65	6.38	9.85	*	-
	PLACE1000546	13.1	11.96	11.32	7.18	10.25	10.48	6.08	5.2	6.25	**	-
	PLACE1000547	8.49	5.52	7.86	5.49	10.6	14.98	5.43	2.62	3.64	*	-
	PLACE1000560	22.37	15.31	18.14	8.36	10.85	7.86	6.26	3.35	3.9	*	-
	PLACE1000562	8.22	7.18	9	4.62	4.33	3.02	4.18	2.13	2.7	**	-
	PLACE1000564	17.41	14.24	11.35	10.42	10.44	10.34	8.72	6.17	6.09	*	-
30	PLACE1000583	11.44	8.04	7.49	4.72	4.9	3.91	5.24	5.95	5.26	*	-
	PLACE1000587	7.15	6.59	3.7	3.14	3.88	4.15	3.78	3.64	4.07	*	-
	PLACE1000588	18.91	11.92	8.8	5.65	7.81	8.36	8.6	5.83	6.87	*	-
	PLACE1000596	11.7	13.56	11.65	8.47	13.84	9.08	10.58	5.53	9.44	*	-
	PLACE1000599	9.76	11.08	9.94	6.95	10.5	6.09	4.81	2.43	3.16	**	-
35	PLACE1000605	16.65	12.34	15.55	9.49	9.68	6.14	6.32	3.07	5.49	*	-
	PLACE1000610	13.13	11.57	11.01	8.74	7.05	4.41	9.69	6.2	4.65	*	-
	PLACE1000611	44.34	42.43	32.52	26.13	31.67	19.73	63.56	39.23	50.7	**	-
	PLACE1000626	7.16	6.36	6.63	3.54	3.14	2.93	5.25	5.57	5.32	**	-
	PLACE1000633	7.75	6.07	5.61	4.09	5.95	4.33	4.51	3.72	5.54	*	-
	PLACE1000636	9.18	4.57	3.73	3.4	5.99	3.07	2.89	4.22	5.33	*	-
40	PLACE1000653	13.52	15.36	9.28	7.56	11.63	7.5	6.22	4.09	7.58	*	-
	PLACE1000656	16.45	24.27	20.78	6.6	13.98	8.95	13.7	10.63	9.13	*	-
	PLACE1000663	17.59	14.23	11.72	6.71	8	7.43	15.75	11.07	16.5	*	-
	PLACE1000706	22.58	27.08	16.29	14.32	16.15	9.77	10.6	7.13	11.87	*	-
	PLACE1000712	15.91	18.32	12.16	10.41	18.03	9.89	15.21	13.33	14.12	*	-
	PLACE1000716	9.51	6.38	10.32	4.38	8.28	5.91	5.52	6.18	6.28	*	-
45	PLACE1000740	62.65	63.87	75.82	66.13	88.56	67.41	54.02	47.28	39.42	*	-
	PLACE1000748	21.69	20.13	21.77	15.61	19.67	14.26	16.35	17.23	19.62	*	-
	PLACE1000749	8.09	6.77	9.49	5.21	7.14	4.97	2.01	3.41	3.49	**	-
	PLACE1000751	5.85	6.89	7.76	3.42	4.79	3.39	2.03	3.31	2.82	*	-
	PLACE1000755	17.27	23.58	23.84	13.28	21.64	9.25	15.55	10.98	9.19	*	-
	PLACE1000769	3.3	5.09	3.02	3.66	5.56	3.4	3.76	2.68	2.93	*	-
50	PLACE1000773	43.25	43.09	44.83	22.77	18.03	27.54	20.87	24.08	21.65	**	-
	PLACE1000785	31.35	17.11	31.03	9.35	9.07	8.25	11.86	8.82	7.46	*	-
	PLACE1000786	5.99	3.18	7.12	2.4	4.01	1.88	2.45	4.94	6.92	*	-
	PLACE1000793	62.95	70.84	86.12	74.56	80.1	68.58	59.03	72.61	48.69	*	-
	PLACE1000795	170.82	165.32	165.81	123.39	175.42	137.1	104.41	82.02	95.27	**	-
	PLACE1000798	34.34	30.96	28.31	19.04	23.22	14.81	22.05	22.97	28.25	*	-
55	PLACE1000812	16.41	17.23	19.15	11.98	12.41	10.24	15.41	13.57	12.8	**	-
	PLACE1000823	25.51	22.51	19.45	15.2	17.94	10.61	13.45	15.88	12.99	*	-
	PLACE1000825	9.78	4.9	7.94	5.02	3.89	3.88	4.94	3.55	4.1	*	-
	PLACE1000838	37.15	32.03	40.12	17.98	18.59	17.35	19.92	15.21	15.97	**	-

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	PLACE1000841	7.87	7.94	8.8	7.6	12.23	10.86	5.33	4.89	4.56	**	-	-
	PLACE1000843	16.04	20.1	24.44	8.07	13.38	10.98	7.02	9.18	7.59	*	**	-
	PLACE1000849	5.43	7.23	9.29	4.99	5.8	4.19	3.26	3.96	2.16	*	-	-
5	PLACE1000856	209.98	229.07	253.03	209.39	256.66	183.75	147.93	119.29	119.6	**	-	-
	PLACE1000863	16.12	16.52	27.27	10.41	12.7	10.18	13.62	16.56	12.54	*	-	-
	PLACE1000876	16.98	21.81	24.49	11.69	18.7	12.24	19.45	15.76	20.21	*	-	-
	PLACE1000899	225.37	148.25	253.61	106.96	112.25	68.21	130.08	130.64	120.26	*	-	-
	PLACE1000907	11.9	9.88	11.62	4.52	6.53	6.56	4.58	7.2	4.58	**	**	-
10	PLACE1000909	219.81	187.78	224.87	129.92	144.43	97.69	209.39	207.09	231	**	-	-
	PLACE1000912	4.53	4.31	6.11	1.98	4.16	2.65	2.79	1.25	1.4	*	-	-
	PLACE1000914	13.65	11.52	16.16	6.76	9.53	7.59	5.22	5.53	2.91	*	**	-
	PLACE1000918	13.18	11.98	16.82	5.88	9.64	8.52	8.09	14.67	8.16	*	-	-
	PLACE1000927	6.93	7.22	10.54	4.38	6.32	3.11	4.55	3.47	4.34	*	-	-
	PLACE1000931	9.5	7.15	10.84	7.43	6.57	4.4	3.12	4.27	3.39	**	-	-
15	PLACE1000944	12.44	7.29	10.38	5.9	6.11	4.93	5.15	6.79	5.9	*	-	-
	PLACE1000948	15.03	15	16.76	7.56	11.29	7.62	5.5	9.31	6.83	**	**	-
	PLACE1000958	5.27	4.99	7.38	2.51	5.7	3.99	1.85	6.23	4.43	*	-	-
	PLACE1000972	8.38	5.92	10.49	3.65	7.53	4.25	3.77	5.86	4.19	*	-	-
	PLACE1000977	11.29	8.32	15.95	5.04	5.25	7.02	2.5	10.48	3.14	*	-	-
	PLACE1000979	13.89	7.86	9.86	3.34	7.43	5.36	4.42	5.93	8.8	*	-	-
20	PLACE1000986	30.12	30.53	34.37	25.05	28	23.07	15.94	15.63	18.52	*	**	-
	PLACE1000987	19.26	23.97	21.74	13.41	21.5	10.91	16.26	13.02	12.47	*	-	-
	PLACE1001000	4.37	7.15	10.87	3.42	3.04	2.14	2.69	2.93	3.43	*	-	-
	PLACE1001007	6.61	2.96	5.44	2.81	6.08	3.04	2.78	3.89	2.07	*	-	-
	PLACE1001010	9.46	6.18	10.43	5.02	5.52	3.2	5.18	3.73	3.91	*	-	-
25	PLACE1001015	7.99	5.3	8.03	6.19	7.65	4.6	3.26	3.31	2.3	*	-	-
	PLACE1001016	17.51	11.26	16.44	6.61	7.04	6.42	3.95	3.27	2.38	*	**	-
	PLACE1001022	14.42	12.9	14.76	4.97	7.37	5.56	7.11	8.21	7.4	**	**	-
	PLACE1001024	11.18	12.76	12	5.14	10.39	4.2	4.43	3.88	2.99	**	-	-
	PLACE1001036	105.59	109.4	58.51	52.8	114.22	89.89	113.54	86.02	137.21	*	-	-
	PLACE1001038	9.63	8.86	10.53	4.68	5.51	5.33	2.98	5.92	7.98	**	-	-
30	PLACE1001048	7.22	3.94	6.41	5.19	5.21	3.49	3.25	3.01	2.83	*	-	-
	PLACE1001054	17.12	18.15	23	21.95	14.11	11.96	6.57	6.82	6.81	**	-	-
	PLACE1001062	7.69	5.86	7.49	3.03	6.18	4.98	5.6	1.77	1.91	*	-	-
	PLACE1001063	11.82	13.23	13.09	8.34	8.29	7.45	3.15	3.88	2.78	**	**	-
	PLACE1001076	17.46	15.27	22.58	9.61	12.22	10.09	9.5	6.93	10.2	*	-	-
	PLACE1001081	8.04	6.12	10.01	3.34	3.8	3.43	2.11	2.93	3.84	*	-	-
35	PLACE1001088	1077.5	1434.9	897.35	706.08	898.84	874	835.46	1189	1173.1	*	-	-
	PLACE1001092	41.3	35.7	38.59	14.58	20.22	12.39	28.15	30.94	33.71	**	*	-
	PLACE1001098	27.39	22.29	18.87	5.94	11.11	13.11	8.05	8.36	7.66	*	**	-
	PLACE1001100	12.04	12.72	14.57	7.69	8.66	8.94	7.95	8.39	9.98	**	*	-
	PLACE1001104	10.26	8.03	11.29	7.1	4.81	4.72	5.84	4.16	5.12	*	-	-
40	PLACE1001114	19.87	21.11	13.11	5.44	7.05	8.22	2.52	3.44	2.49	*	**	-
	PLACE1001116	15.04	15.17	13.54	9.49	13.49	10.14	5.69	6.26	3.99	**	-	-
	PLACE1001123	11.13	9.28	10.37	3.01	8.71	7.98	2.59	2.22	5.96	**	-	-
	PLACE1001136	9.63	8.36	10.4	4.16	7.83	10.1	11.4	6.43	4.95	*	-	-
	PLACE1001144	22.24	18.89	18.24	5.11	10.59	8.11	16.88	14.03	17.77	**	-	-
	PLACE1001147	9.73	14.79	11.54	7.5	5.73	6.98	3.33	4.01	4.07	*	**	-
45	PLACE1001148	16.26	12.46	13.41	8.25	12.02	6.54	11.91	10.71	11.91	*	-	-
	PLACE1001159	5.83	2.18	9.14	5.55	4.85	2.75	3.37	5.16	1.28	*	-	-
	PLACE1001168	6.64	5.38	5	2.78	4.75	2.95	4.38	2.12	2.36	*	-	-
	PLACE1001171	17.87	14.63	16.06	9.77	9.8	9.82	9.4	7.26	9.58	**	**	-
	PLACE1001183	24.74	23.48	20.67	15.23	15.9	11.49	12.71	7.91	11.36	**	**	-
	PLACE1001185	8.91	7.62	8.02	4.21	7.14	4.11	5.56	3.21	2.94	*	**	-
50	PLACE1001201	16.85	15.12	18.88	10.04	10.01	9	9.33	10.2	8.94	**	**	-
	PLACE1001229	15.21	12.61	13.94	9.57	11.26	12.86	8.81	8.47	8.63	**	-	-
	PLACE1001231	13.31	19.61	12.2	8.58	26.11	14.91	13.39	13.43	8.59	*	-	-
	PLACE1001238	6.16	6.8	5.78	3.46	6.45	5.07	3.57	1.84	3.63	**	-	-
	PLACE1001241	7.81	12.55	8.77	4.56	8.8	2.29	6.75	1.69	5.45	*	-	-
	PLACE1001242	15.15	9.43	9.57	6.93	8.62	5.05	5.42	2.88	4.67	*	-	-
55	PLACE1001247	18.19	25.95	17.43	7.95	13.13	8.09	9.19	7.53	8.42	*	-	-
	PLACE1001250	27.19	16.6	15.62	14.1	21.99	16.23	13.87	8.35	7.98	*	-	-
	PLACE1001257	5.07	4.07	3.3	6.21	3.6	2.05	3.64	3.01	2.82	*	-	-
	PLACE1001272	11.61	5.34	6.33	4.73	5.73	6.35	5.18	6.02	6.39	*	-	-

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	PLACE1001279	20.66	18.57	13.78	9.04	11.1	8.58	6.47	4.72	6	*	**	-	-
	PLACE1001280	13.73	13.22	15.63	11.44	10.47	6.22	11.2	7.22	13.37	*	*	-	-
	PLACE1001294	6.1	5.02	7.03	2.98	5.24	4.37	4.18	2.25	4.36	*	*	-	-
5	PLACE1001295	9.52	6.34	5.73	4.11	5.38	4.8	4.66	3.72	5.16	*	*	-	-
	PLACE1001300	110.16	136.11	96.73	55.88	77.8	69.78	127.86	93.28	123.22	*	*	-	-
	PLACE1001304	22.83	23.36	19.82	13.09	11.18	12.56	8.64	8.3	14.22	**	**	-	-
	PLACE1001311	22.93	29.08	18.33	13.63	11.98	8.91	18.15	14.72	19.17	*	*	-	-
	PLACE1001323	5.15	4.73	4.73	2.24	3.77	2.07	2.58	2.19	2.91	*	**	-	-
	PLACE1001325	6.51	4.36	2.66	3.73	4.01	0.79	3.09	1.19	1.69	*	*	-	-
10	PLACE1001340	12.71	9.9	7.91	5.93	10.17	3.62	8.49	5.49	7.3	*	*	-	-
	PLACE1001344	7.26	5.61	6.3	3.22	4.87	2.35	5.26	3.25	5.47	*	*	-	-
	PLACE1001351	10.82	9.34	9.06	4.54	4.04	2.83	5.68	5.94	6.17	**	**	-	-
	PLACE1001366	16.46	16.32	12.21	7.96	10.61	8	10.02	6.25	6.08	*	*	-	-
	PLACE1001377	10.72	11.21	8.12	8.14	11.01	6.18	7.03	5.07	5.96	*	*	-	-
15	PLACE1001383	8.47	7.74	7.34	7.01	7.31	9.16	4.38	4.51	5.67	**	*	-	-
	PLACE1001384	5.51	3.13	4.87	2.26	4.64	2.12	1.25	1.77	2.28	*	*	-	-
	PLACE1001387	3.71	2.66	5.28	2.18	4.13	3.15	1.31	2.35	1.76	*	*	-	-
	PLACE1001395	2.97	1.83	2.95	0.9	3.39	0.94	2.26	2.27	0.93	*	*	-	-
	PLACE1001399	43.48	36.95	39.47	25.54	39.02	28.91	11.4	22.35	12.37	**	*	-	-
	PLACE1001401	8.85	12.13	13.82	4.1	7.84	5.28	5.15	5.58	4.43	*	*	-	-
20	PLACE1001407	6.42	8.95	6.88	3.19	5.6	3.04	3.23	2.38	2.93	*	**	-	-
	PLACE1001412	4.65	3.97	3.56	2.52	8.46	2.63	3.1	2.07	4.54	*	*	-	-
	PLACE1001414	10.05	7.04	8.23	5.26	7.99	5.53	4.37	7.32	4.41	*	*	-	-
	PLACE1001416	18.05	14.76	21.75	8.21	15.69	7.54	12.66	14.94	10.13	*	*	-	-
	PLACE1001433	10.35	9.53	10.38	6.47	9.26	5.35	4.33	6.8	5.78	**	*	-	-
25	PLACE1001440	15.78	8.2	12.06	9.97	10.51	7.97	4.11	5.02	3.17	*	*	-	-
	PLACE1001456	5.95	5.2	7.6	4.32	4.51	3.68	3.46	5.83	4.09	*	*	-	-
	PLACE1001464	7.17	7.13	12.08	4.46	13.26	4.47	2.92	3.59	4.74	*	*	-	-
	PLACE1001468	5.87	5.89	7.51	4.49	7.19	3.15	4.98	3.89	5.45	*	*	-	-
	PLACE1001484	1.93	2.72	3.26	3.17	5.24	2.3	3.27	1.7	4.61	*	*	-	-
	PLACE1001500	5.55	5.43	7.47	3.4	4.88	4.91	3.43	5.41	4.22	*	*	-	-
30	PLACE1001502	10.13	6.73	10.36	4.95	5.09	3.9	4.24	7.4	4.55	*	*	-	-
	PLACE1001503	18.94	15.22	23.11	6.62	14.6	9.42	9.19	12.06	11.69	*	*	-	-
	PLACE1001505	14.33	11.5	15.08	6.94	9.91	8.35	5.05	5.21	4.29	*	**	-	-
	PLACE1001513	9.76	7.84	14.27	4.51	12.01	5.72	4.02	6.18	4.23	*	*	-	-
	PLACE1001516	12.33	10.13	14.29	6.5	8.85	7.91	5.4	6.92	6.78	*	*	-	-
	PLACE1001517	22.78	28.63	26.65	15.6	22.43	12.49	25.55	23.34	19.3	*	*	-	-
35	PLACE1001523	4.85	4.2	4.25	1.46	3.64	2.44	3.61	4.37	5.02	*	*	-	-
	PLACE1001526	15.63	6.8	12.63	5.9	5.99	8.7	6.38	8.18	11.68	*	*	-	-
	PLACE1001534	13.26	10.83	12.93	4.83	7.66	4.05	5.45	22.34	4.41	**	*	-	-
	PLACE1001536	12.35	10.07	11.17	5.95	10.51	7.42	7.47	10.57	7.69	*	*	-	-
	PLACE1001545	7.78	9.31	13.04	5.48	7.28	3.94	2.6	3.19	3.02	*	*	-	-
40	PLACE1001551	11.64	13.9	20.49	7.15	9.98	9.21	7.74	8.57	7.76	*	*	-	-
	PLACE1001564	5.33	7.01	11.33	5.64	6.02	6.32	3.9	3.45	6.93	*	*	-	-
	PLACE1001570	8.81	7.17	13.9	5.61	7.77	3.89	5.34	9.04	4.82	*	*	-	-
	PLACE1001571	30.16	29.44	29.76	18.26	25.49	9.78	12.94	16.78	20.12	**	**	-	-
	PLACE1001595	49.16	53.02	65.48	26.84	29.86	29.28	20.63	17.19	22.48	**	**	-	-
	PLACE1001602	17.93	20.86	26.59	9.8	15.66	12.03	25.23	43.22	27.97	*	*	-	-
	PLACE1001603	16	11.85	13.84	6.26	7.5	6.17	10.37	25.06	14.43	**	*	-	-
45	PLACE1001608	313.79	262.26	299.49	248.62	194.58	212.51	255.55	259.42	224.33	*	*	-	-
	PLACE1001610	34.83	33.4	50.14	21.2	19.91	21.09	16.25	16.43	15.58	*	*	-	-
	PLACE1001611	16.58	14.57	13.52	8.27	15.57	6.53	5.96	3.97	4.4	**	*	-	-
	PLACE1001629	15.86	14.27	16.52	6.92	12.73	5.97	9.05	9.4	8.15	*	**	-	-
	PLACE1001632	15.6	14.68	11.95	5.15	11.43	6.76	4.77	3.59	2.95	*	**	-	-
50	PLACE1001634	10.26	9.24	12.21	4.71	7.41	4.15	3.93	4.97	4.63	*	**	-	-
	PLACE1001637	29.75	28.67	35.48	16.79	19.46	16.75	23.41	26.79	22.84	**	*	-	-
	PLACE1001640	28.95	18.03	24.89	16.93	21.97	12.71	8.91	11.62	9.32	*	*	-	-
	PLACE1001655	8.24	5.56	6.83	4.09	4.25	2.93	2.13	3.7	1.34	*	*	-	-
	PLACE1001672	8.94	18.15	13.66	4.81	11.29	4.01	5.1	4.86	14.47	*	*	-	-
	PLACE1001676	39.58	47.75	47.96	23.16	26.28	21.98	31.5	32.99	28.58	**	**	-	-
55	PLACE1001683	7.64	6.2	11.62	2.16	4.9	3.68	2.93	3.43	3.72	*	*	-	-
	PLACE1001691	10.4	6.5	11.03	4.05	13.34	5.07	4.28	5.31	2.34	*	*	-	-
	PLACE1001692	3.74	6.24	4.95	3.58	3.97	3.4	3.88	3.22	2.42	*	*	-	-
	PLACE1001705	11.04	7.84	13.66	10.64	5.83	6.51	5.2	5.34	3.62	*	*	-	-

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	PLACE1001716	13.89	6.26	12.85	5.68	7.61	3.53	6.17	4.09	5.84				
	PLACE1001720	20.23	23.86	21.86	17.41	19.42	17.41	10.68	9.34	8.72	*	**	-	-
	PLACE1001728	21.97	14.68	15.36	7.87	10.67	10.96	10.39	5.46	5.25	*	*	-	-
5	PLACE1001729	7.28	8.78	9.32	4.24	3.8	3.29	3.96	2.03	2.64	**	**	-	-
	PLACE1001739	18.08	18.75	18.08	11.34	16.38	11.72	10.55	8.26	8.75	*	*	-	-
	PLACE1001740	60.6	61.56	51.85	52.21	47.26	48.19	41.09	28.81	37.51	**	**	-	-
	PLACE1001745	155.43	121.46	146.04	80.69	92.15	78.37	106.17	102.99	100.25	**	*	-	-
	PLACE1001746	12.07	9.53	11.89	5.08	6.32	6.38	6.4	7.42	7.33	**	**	-	-
10	PLACE1001748	20.09	15.85	13.57	8.98	10.94	8.77	6.58	3.28	8.51	*	*	-	-
	PLACE1001753	8	5.61	7.17	2.42	2.42	2.08	3.13	1.99	2.1	**	**	-	-
	PLACE1001760	16.81	13.89	14.09	5.89	6.99	11.7	8.68	6.91	7.81	*	**	-	-
	PLACE1001767	7.75	5.83	9.04	3.14	5.58	2.6	2.92	2.72	1.2	*	**	-	-
	PLACE1001771	6.86	8.78	6.5	5.1	22.6	7.92	6.68	3.61	1.79			-	-
	PLACE1001775	10.25	8.72	8.89	5.62	4.98	4.94	5.79	4.51	5.33	**	**	-	-
15	PLACE1001777	55.87	33.24	46.38	19.69	26.37	22.71	26.45	22.89	29.83	*		-	-
	PLACE1001781	7.62	4.99	5.26	2.61	3.65	3.27	2.46	2.47	3	*	*	-	-
	PLACE1001783	8.67	3.54	4.17	1.75	1.71	2.1	2.79	1.87	2.94			-	-
	PLACE1001786	10.13	7.03	6.19	5.28	7.53	4.48	4.3	2.57	2.1	*		-	-
	PLACE1001788	9.62	8.2	7.79	2.13	3.02	3.67	3.87	1.93	2.04	**	**	-	-
20	PLACE1001795	12.86	13.57	11.91	3.76	6.82	4.77	2.63	4.68	2.65	**	**	-	-
	PLACE1001799	15.19	12.46	11.73	6.44	10.22	5.84	11.66	9.72	12.14	*		-	-
	PLACE1001810	19.9	17.99	15.3	8.61	16.81	15.9	19.42	15.41	19.52			-	-
	PLACE1001817	9.2	10.03	10.24	5.73	12.6	6.09	4.49	4.6	5.41	**		-	-
	PLACE1001821	8.12	9.65	9.24	5.34	5.81	5.22	5.09	4.7	3.49	**	**	-	-
25	PLACE1001836	14.74	10.74	8.7	7.59	8.81	4.93	6.55	5.02	5	*		-	-
	PLACE1001844	8.12	5.11	7.16	1.96	5.82	2.85	3.18	2.67	1.5	*		-	-
	PLACE1001845	13.24	11.82	8.77	7.59	7.48	3.74	4.84	2.2	2.42	**		-	-
	PLACE1001858	9.06	7.62	7.23	4.16	3.93	3.22	7.66	3.49	3.91	**		-	-
	PLACE1001869	5.88	6.08	4.84	3.37	6.33	2.79	3.14	2.33	2.54	**		-	-
	PLACE1001890	14.71	9.13	7.02	7.27	10.27	7.92	6.48	7.41	7.67			-	-
	PLACE1001897	21.63	13.66	12.13	7	10.58	7.47	6.17	7.42	7.81	*		-	-
30	PLACE1001902	25.9	24.36	23.51	11.89	19.02	13.01	23.32	19.87	28.51	*		-	-
	PLACE1001904	4.8	4.58	4.71	4.2	4.02	2.48	4	1.2	3.18			-	-
	PLACE1001907	11.99	11.09	12.77	4.36	7.42	4.55	5.4	2.81	6.4	**	**	-	-
	PLACE1001910	17.55	13	11.78	10.79	10.86	3.78	8.75	3.34	6.51	*		-	-
	PLACE1001912	16.99	20.76	18.01	10.56	10.89	7.91	12.99	8.39	12.1	**	*	-	-
	PLACE1001918	10.35	11.16	9.4	5.64	8.81	4.76	8.14	4.97	7.28	*	*	-	-
35	PLACE1001920	3.62	1.84	1.09	2.06	2.78	2.12	0.89	2.37	2.67			-	-
	PLACE1001928	33.91	29.31	26.67	16.07	24.12	10.81	21.1	17.01	25.49	*		-	-
	PLACE1001930	13.35	8.41	9.7	5.16	9.65	8.14	5.7	4.65	9.73			-	-
	PLACE1001949	83.24	64.21	68.53	50.5	75.89	66.37	92.93	85.41	92.12	*		-	-
	PLACE1001959	8.04	5.93	10.64	4.56	6.1	3.95	4.33	5.06	5.07			-	-
40	PLACE1001969	8.52	5.51	4.9	2.62	4.36	2.04	3.84	2.43	3.2			-	-
	PLACE1001974	16.8	19.43	17.28	9.77	10.54	5.8	6.98	5.43	6.49	**	**	-	-
	PLACE1001981	11.42	11.82	8.18	7.19	8.78	5.34	7.9	5.15	5.59	*		-	-
	PLACE1001983	9.22	8.71	12.62	5.54	7.95	6.32	7.39	5.63	6.5			-	-
	PLACE1001989	27.47	22.77	28.46	13.3	18.78	12.49	12.35	16.17	10.35	*	**	-	-
45	PLACE1002004	8.73	7.48	9.33	6.79	9.77	5.49	6.57	6.13	4.33	*		-	-
	PLACE1002008	10.54	8.97	12.2	6.77	11.46	10.25	3.74	7.33	3.11	*		-	-
	PLACE1002015	12.37	10.1	13.36	6.64	10.58	8.15	7.89	14.69	9.22			-	-
	PLACE1002044	18.51	15.04	21.28	6.21	11.74	9.02	6.6	10.2	12.21	*	*	-	-
	PLACE1002046	3.16	4.19	5.33	2.46	6.56	3.13	3.41	1.95	2.73			-	-
	PLACE1002052	4.29	2.34	2.47	1.89	4.94	1.55	4.09	3.83	3.62			-	-
	PLACE1002066	4.5	3.49	6.01	2.29	3.79	2.93	3.54	3.65	2.92			-	-
50	PLACE1002072	6.4	5.54	6.91	3.66	5.16	4.7	3.95	6.12	2.07	*		-	-
	PLACE1002073	12.89	11.8	16.36	10.66	11.47	7.97	5.88	5.64	4.74	**		-	-
	PLACE1002080	18.63	22.97	23.1	12.21	18.28	13.9	13.6	15	15.2	*	*	-	-
	PLACE1002081	23.13	27.18	27.3	14.91	18.06	14.86	16.14	20.45	20.82	**	*	-	-
	PLACE1002090	11.49	14.13	12.79	4.54	7.24	4.65	4.29	3.51	5.75	**	**	-	-
55	PLACE1002095	5.46	5.54	4.46	5.08	11.47	7.41	4.99	5.27	7.8			-	-
	PLACE1002102	8.22	13.54	14.09	8.11	14.1	7.74	9.04	16.2	14.08			-	-
	PLACE1002109	17.45	10.93	19.35	12.82	7.15	7.61	9.22	12.81	9.47			-	-
	PLACE1002115	6.48	5.79	9.09	2.86	4.39	3.56	3.32	3.75	3.44	*	*	-	-
	PLACE1002119	3.98	5.58	7.03	2.87	6.47	3.2	3.72	4.12	4.62			-	-

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Table 471

	PLACE1002140	8.54	9.5	15.02	4.83	8.98	6.88	2.91	6.38	4.28	*	*	-
	PLACE1002150	27.18	33.61	30.05	18.28	25.09	23.98	12.7	14.95	15.29	*	**	-
	PLACE1002153	173.25	217.95	284.37	422.44	424.65	291.99	262.39	242.27	220.74	*	+	-
5	PLACE1002157	7.42	5.99	8.84	3.16	6.59	2.52	3.59	2.5	5.34	*	*	-
	PLACE1002163	9.5	10.33	17.51	4.81	9.35	4.71	6.61	8.07	8.46	*	*	-
	PLACE1002168	406.19	407.62	562.52	187.65	80.86	161.78	377.56	231.11	429.49	**	-	-
	PLACE1002170	23.07	18.68	22.02	9.58	14.95	10.12	4.39	9.86	5.14	*	**	-
	PLACE1002171	118.3	86.27	82.5	107.58	135.49	96.73	60.2	59.88	56.63	*	*	-
10	PLACE1002180	12.53	12.02	17.4	11.66	15.77	12.8	11.61	13.11	10.84	*	*	-
	PLACE1002184	76.94	90.34	67.89	42.12	70.86	43.23	20.87	27.8	29.07	**	-	-
	PLACE1002200	5.64	6.44	11.56	2.73	4.37	3.29	2.8	2.86	3.48	*	*	-
	PLACE1002205	5.47	5.6	9.09	2.28	6.05	2.28	3.51	2.6	1.9	*	*	-
	PLACE1002213	11	9.68	7.88	3.37	8.5	3.33	5.73	2.26	4.33	*	*	-
15	PLACE1002219	30.67	24.88	33.1	11.7	18.03	17.11	5.85	10.58	12.01	*	**	-
	PLACE1002227	5.38	6.1	6.51	3.19	5.95	3.48	3.48	8.52	2.37	*	*	-
	PLACE1002253	7.93	4.46	10.74	3.51	5.52	2.84	4.18	3.76	3.24	*	*	-
	PLACE1002256	10.19	4.49	11.42	3.66	5.44	3.17	1.81	4.48	5.21	*	*	-
	PLACE1002259	6.68	9.14	16.04	2.32	8.56	3.26	2.76	5.45	13.61	*	*	-
	PLACE1002285	15.21	20.2	16.69	10.84	18.4	10.19	8.14	7.95	6.12	**	-	-
20	PLACE1002301	11.84	7.92	13.87	3.5	5.75	4.91	3.98	8.04	4.04	*	*	-
	PLACE1002310	9.3	8.21	7.36	1.56	5.25	3.56	3.57	2.81	3.34	*	**	-
	PLACE1002311	6.47	4.93	7.42	3.5	5.65	2.75	2.49	2.97	1.32	*	*	-
	PLACE1002319	23.43	17.43	19.83	7.96	14.77	10.74	10.78	13.23	11.96	*	*	-
	PLACE1002329	7	4.89	6.25	3.06	3.73	2.65	1.68	2.85	1.64	*	**	-
	PLACE1002333	16.35	14.3	13.78	9.29	11.1	10.53	8.49	6.32	5.51	**	**	-
25	PLACE1002342	14.18	15.16	20.35	5.96	11.78	6.24	4.58	8.15	6.84	*	**	-
	PLACE1002343	9.54	8.56	16.64	3.45	4.23	3.21	2.86	1.85	3.18	*	*	-
	PLACE1002355	8.47	11.34	12.23	4.32	8.27	5.65	2.98	2.78	4.19	*	**	-
	PLACE1002358	6.25	5.01	7.85	2.33	4.09	1.66	2.63	1.27	2.04	*	**	-
	PLACE1002359	94.59	64.3	78.26	42.47	26.68	29.68	51.17	53.76	59.14	**	-	-
30	PLACE1002374	11.64	7.08	11.73	4.84	7	4.57	3.23	3.62	3.66	*	*	-
	PLACE1002376	10.84	6.42	7.57	6.56	6.2	4.93	8.79	6.04	6.62	*	*	-
	PLACE1002379	14.26	10.82	12.17	6.95	8.14	6.98	5.34	4.44	3.6	**	**	-
	PLACE1002386	7.89	3.52	7.76	1.91	2.26	2.95	2.4	2.03	2.94	*	*	-
	PLACE1002395	17.68	20.65	22.77	6.45	9.6	7.04	4.3	2.63	2.39	**	**	-
	PLACE1002399	9.59	8.59	10	4	5.08	4.5	2.83	2.8	3.46	**	**	-
35	PLACE1002407	14.84	17.54	12.15	4.78	9.29	6.64	5.32	3.95	6.87	*	**	-
	PLACE1002433	18.89	14.68	17.11	8	12.47	6.81	12.74	12.61	16.41	*	*	-
	PLACE1002437	6.94	5.04	7.88	4.77	3.72	3.8	1.97	3.5	4.81	*	*	-
	PLACE1002438	8.47	9.76	8.93	6.11	6.03	2.52	3.69	3.74	4.55	*	**	-
	PLACE1002446	61.22	60.91	53.35	35.08	40.23	34.18	52.04	54.81	48.63	**	-	-
	PLACE1002447	50.06	38.25	48.75	30.92	38.93	28.36	26.38	23.5	18.47	**	-	-
40	PLACE1002450	8.68	4.18	8.14	2.56	3.07	3.06	3.45	3.27	1.66	*	*	-
	PLACE1002462	20.62	21.36	20.69	8.83	13.93	7.63	14.57	11.43	17.67	**	*	-
	PLACE1002465	6.3	10.21	4.45	2.37	6.62	4.25	3.41	1.81	3.99	*	*	-
	PLACE1002474	8.9	10.86	8.01	5.33	8.28	3.73	2.36	3.29	4.22	**	-	-
	PLACE1002477	10.23	12.91	13.31	8.45	8.55	11.89	12.5	6.6	14.96	*	*	-
	PLACE1002493	5.44	5.3	4.56	4.99	2.63	4.56	5.81	1.5	1.86	*	*	-
45	PLACE1002497	9.23	6.42	6.03	5.54	3.94	3.18	4.77	3.01	2.42	*	*	-
	PLACE1002499	28.78	23.91	22.93	13.59	10.19	9.79	16.45	7.7	12.71	**	*	-
	PLACE1002500	9.83	6.14	9.08	4.34	6.18	2.49	5.4	1.41	3.42	*	*	-
	PLACE1002514	57.39	61.96	51.39	31.16	36.96	26.56	53.37	39.47	40.85	**	-	-
	PLACE1002518	7.97	7.12	4.14	3.92	5.36	3.52	3.58	1.82	2.65	*	*	-
50	PLACE1002529	14.15	10.84	8.84	6.09	12.13	6.95	3.37	3.6	3.7	**	-	-
	PLACE1002532	6.92	6.97	5.35	4.94	5.47	4.76	4.62	5.36	3.19	*	*	-
	PLACE1002536	9.3	12.32	10.38	5.35	4.64	5.41	7.12	5.91	4.59	**	*	-
	PLACE1002537	7.11	8.85	6.37	5.99	5.45	6.3	4.25	3	3.53	**	-	-
	PLACE1002539	7.92	6.45	7.28	2.97	5.46	7.97	2.07	2.63	4.82	*	*	-
	PLACE1002547	14.65	14.48	12.7	9.78	11.89	6.33	5.01	4.47	6.38	**	-	-
55	PLACE1002571	27.85	40.71	17.49	15.84	14.71	12.01	13.72	7.48	9.31	*	*	-
	PLACE1002578	11.7	10.9	10.03	8.42	11.59	6.31	11.22	5.24	9.68	*	*	-
	PLACE1002589	12.45	8.98	8.93	4.7	6.58	5.37	8.92	7.31	10.13	*	*	-
	PLACE1002591	14.95	9.64	30.65	14.99	14.6	1.99	10.65	10.99	7.37	*	*	-
	PLACE1002598	134.77	135.3	115.7	105.05	127.67	81.8	77.51	75.71	89.77	**	-	-

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Table 472

	PLACE1002604	8.27	3.87	5.87	4.56	4.62	4.03	4.08	2.97	4.32			
	PLACE1002612	7.74	6.07	5.48	4.79	5.04	4.26	2.87	1.84	4.68	*		
	PLACE1002625	8.98	7.38	5.26	3.91	6.23	4.29	4.63	2.42	5.37			
5	PLACE1002638	10.71	6.82	9.31	4.39	4.89	3.67	4.86	2.91	4.12	*	*	-
	PLACE1002655	20.05	17.22	10.12	8.15	9.62	8.61	4.45	4.4	4.69	*		-
	PLACE1002665	2.85	2.11	1.16	1.34	3.18	0.77	1.36	1.74	1.47			
	PLACE1002685	40.11	36.95	37.09	21.27	32.67	18.25	35	28.12	33.61	*		-
	PLACE1002692	10.4	8.99	7.49	3.22	6.32	3.77	7.61	3.76	6.83	*		-
10	PLACE1002714	16.77	11.38	9.27	6.42	9.93	4.45	11.48	11.6	13.87			
	PLACE1002721	75.97	53.95	40.28	41.2	57.12	33.39	36.52	34.39	33.55			
	PLACE1002722	22.13	17.93	14.21	5.69	15.15	8.22	22.92	15.1	22.19			
	PLACE1002726	7.85	7.95	6.76	3.03	4.47	1.55	5.1	2.92	3.72	**	**	-
	PLACE1002756	11.64	12.77	9.75	6.41	12.37	7.42	9.89	7.27	9.98			
15	PLACE1002768	14.14	13.66	17.41	6.96	8.91	8.35	8.23	12.96	13.43	**		-
	PLACE1002772	11.58	12.05	13.28	5.34	9.18	5.42	7.04	6.7	6.74	*	**	-
	PLACE1002775	3.87	3.22	3.82	4.05	3.19	0.98	1.6	5	2.48			
	PLACE1002780	8.73	8.1	8.81	2.91	6.16	2.92	3.15	6.37	4.26	*	*	-
	PLACE1002782	15.09	16.8	18.22	6.13	9.37	3.95	11.73	13.03	12.96	**	*	-
	PLACE1002794	41.39	43.8	46.4	31.76	35.79	20.44	25	22.44	21	*	**	-
20	PLACE1002795	26.08	25.22	25.57	11.54	12.89	13.19	17.32	17.1	14.49	**	**	-
	PLACE1002811	45.78	45.63	45.46	25.72	32.56	23.15	17.78	22.39	22.66	**	**	-
	PLACE1002815	15.82	13.42	19.22	7.58	7.46	5.69	11.61	7.34	8.29	**	*	-
	PLACE1002816	4.86	2.68	5.34	8.68	10.83	8.75	3.44	3.56	2.71	**	+	-
	PLACE1002822	12.2	11.93	11.07	6.15	11.75	10.16	7.41	12.24	8.12			
	PLACE1002833	9.14	11.66	12.33	5.57	7.46	7.07	4.75	8.35	4.08	*	*	-
25	PLACE1002834	6.07	5.81	8.84	3.09	3.53	4.27	1.8	2.98	2.41	*	*	-
	PLACE1002835	58.22	46.91	63.08	49.95	62.63	44.56	42.91	35.34	35.49	*		-
	PLACE1002839	20.38	22.46	21.91	8.31	11	7.79	15.07	14.42	13.25	**	**	-
	PLACE1002851	24.75	15.11	15.09	7.91	14.09	8.63	20.69	22.56	25.92			
	PLACE1002853	17.64	15.34	22.8	5.52	6.45	6.1	6.28	8.18	4.17	**	**	-
30	PLACE1002881	24.86	14.92	26.75	13.38	16.28	13.04	14.2	20.46	17.04			
	PLACE1002901	14.25	14.06	17.74	6.8	8.96	8.66	8.78	4.53	4.12	**	**	-
	PLACE1002904	18.88	26.12	22.33	14.53	22.41	13.83	9.21	13.95	10.54	*		-
	PLACE1002905	4.41	8.93	12	2.54	8.87	4.07	3.83	5.83	4.18			
	PLACE1002908	13.22	16.1	15.63	15.4	12.99	11.14	8.47	5.63	8.35	**		-
	PLACE1002911	10.97	9.2	9.02	6.7	11.96	7.89	5.04	4.71	5.5	**		-
35	PLACE1002941	15.88	10.4	17.73	6.14	8.22	5.77	14.58	18	12.89	*		-
	PLACE1002950	23.65	20.5	17.79	16.96	17.44	5.49	24.31	14.61	17.93			
	PLACE1002955	5	5.58	7.97	3.29	6.71	3.81	3.06	3.96	2.19	*		-
	PLACE1002958	88.1	92.98	103.56	90.74	91.81	78.41	59.31	53.18	47.63	**		-
	PLACE1002962	3.13	4.33	9.15	0.9	4.01	2.47	0.8	0.76	1.87			
	PLACE1002967	35.4	50.14	51.41	21.55	34.48	29.97	31.98	26.21	37.19			
40	PLACE1002968	4.93	4.01	6.65	3.18	3.05	1.93	2.74	2.46	2.95	*	*	-
	PLACE1002976	59.32	76.52	110.97	52.57	103.04	77.15	42.49	35.2	48.8			
	PLACE1002991	6.88	4.41	7.57	2.11	5.56	3.18	2.77	5.13	6.66			
	PLACE1002993	13.31	16.98	19.44	6.54	17.73	10.56	9.53	20.73	7.89			
	PLACE1002996	33.54	26.83	25.33	24.84	36.88	25.62	15.5	28.74	20.59			
	PLACE1003010	5.97	5.37	8.7	4.68	3.28	4.88	3.8	4.41	3.12			
45	PLACE1003025	19.13	20.65	29.6	10.42	22.81	11.62	14.02	22.04	12.57			
	PLACE1003027	4.81	4.57	8.94	2.3	4.47	0.55	3.14	5.14	2.31			
	PLACE1003044	13.45	13	13.59	5.33	7.16	6.74	3.17	4.52	2.59	**	**	-
	PLACE1003045	16.2	13.12	16.27	11.21	14.83	10.08	8.58	7.66	5.73	**		-
	PLACE1003052	15.26	13.65	16.48	5.57	12.75	6.74	15.39	12.34	13.31	*		-
	PLACE1003083	26.86	32.06	29.46	16.75	26.42	15.92	23.57	20.32	20.14	*		-
50	PLACE1003085	11.46	7.5	13.4	5.76	9.36	4.66	6.66	6.58	5.57			
	PLACE1003092	13.44	11.78	13.5	8.16	11.43	7.08	8.07	7.87	6.9	*	**	-
	PLACE1003097	6.17	6.46	18.32	3.05	5.89	3.08	3.13	5.88	4.77			
	PLACE1003100	36.23	40.39	38.56	32.04	32.87	28.75	26.62	23.05	18.02	*	**	-
	PLACE1003108	11.34	8.75	20.83	7.36	13.72	5.15	3.96	4.75	4.82			
	PLACE1003115	7.34	6.75	7.41	3.32	6.32	2.75	1.65	0.73	1.92	**		-
55	PLACE1003120	12.49	11.78	16.03	7.63	9.21	4.76	11.87	11.32	7.77	*		-
	PLACE1003135	7.08	5.05	7.89	3.8	2.81	2.79	2.64	3.42	1.44	*	*	-
	PLACE1003136	68.81	77.15	81.76	65.96	72.38	60.39	44.74	38.52	47.1	**		-
	PLACE1003141	9.02	4.98	11.12	4.59	4.76	5.17	4.62	5.32	3.84			

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Table 473

	PLACE1003145	12.65	9.94	12.43	3.74	5.65	4.53	6.94	8.05	4.35	**	*	-	-
	PLACE1003147	26.48	26.41	26.84	11.9	16.38	12.11	16.22	18.19	14.71	**	**	-	-
5	PLACE1003153	10.51	10.55	11.78	2.97	6.22	4.35	5.52	7.01	3.61	**	**	-	-
	PLACE1003163	8.08	7.83	4.23	1.17	6.16	2.64	1.92	2.39	2.29	*	*	-	-
	PLACE1003172	11.82	10	15.87	-6.77	13.23	9.45	7.97	8.79	7.46			-	-
	PLACE1003174	15.37	9.05	12.28	9.12	4.76	2.9	4.07	4.06	4.97	*	*	-	-
	PLACE1003176	5.18	3.89	6.16	2.81	3.31	2.68	2.96	3.04	2.06	*	*	-	-
	PLACE1003181	9.36	6.29	8.52	1.78	2.48	3.42	2.28	1.97	1.19	**	**	-	-
10	PLACE1003184	23.08	18.89	20.23	9.3	11.84	12.17	13.78	13.13	10.63	**	**	-	-
	PLACE1003190	8.27	8.79	9.4	3.25	4.54	3.59	4.27	2.82	4.68	**	**	-	-
	PLACE1003200	9.79	7.56	9.39	2.41	6.08	2.83	2.42	1.72	3.3	*	**	-	-
	PLACE1003205	126.72	130.26	137.95	113.01	122.92	109.79	99.16	86	89.92	*	**	-	-
	PLACE1003209	2.16	16.18	2.48	0.47	10.18	0.97	2.71	3.36	3.16			-	-
	PLACE1003214	22.58	19.76	20.17	11.54	15.74	15.47	11.96	12.4	14.5	*	**	-	-
15	PLACE1003229	11.83	11.81	10.65	4.92	4.84	3.94	7.34	5.53	5.38	**	**	-	-
	PLACE1003238	8.67	6.17	6.07	3.06	1.84	4.56	1.99	2.39	2.01	*	**	-	-
	PLACE1003249	64.47	55.31	48	33.64	42.61	31.3	33.47	28.86	18.94	*	*	-	-
	PLACE1003256	18.3	25.49	17.26	10.97	13.36	18.51	17.3	11.04	4.08			-	-
	PLACE1003258	49.07	49.35	44.47	34.46	50.32	29.75	23.51	18.19	23.43	**	*	-	-
	PLACE1003279	10.3	14.58	7.71	5.42	10.68	4.9	6.28	3.11	11.78			-	-
20	PLACE1003294	21.78	16.35	23.18	6.69	11.5	6.25	12.62	8.7	9.35	*	*	-	-
	PLACE1003296	42.17	40.86	35.97	38.78	41.16	32.25	23.79	17.48	17.34	**	*	-	-
	PLACE1003297	49.69	50.94	40.2	15.98	31.29	21.98	19.68	11.27	24.02	*	**	-	-
	PLACE1003302	25.32	31.25	29.06	9.93	15.98	12.55	24.23	16.15	20.93	**	*	-	-
	PLACE1003334	185.2	152.92	141.49	146.89	154.17	125.41	110.94	69.78	76.19	*	*	-	-
25	PLACE1003337	48.98	43.27	41.6	31.2	33.91	22.01	17.95	11.14	16.35	*	**	-	-
	PLACE1003342	33.19	37.72	34.03	17.42	45.69	20.1	23.58	17.03	23.28	**	*	-	-
	PLACE1003343	6.84	5.22	10.11	7.16	4.99	3.86	5.46	2.81	3.26			-	-
	PLACE1003344	11.02	7.76	2.99	1.99	8.29	3.43	7.57	2.34	3.75			-	-
	PLACE1003353	19.54	21.69	17.69	8.25	8.74	5.2	10.76	10.8	13.5	**	**	-	-
	PLACE1003361	44.83	37.64	33.66	33.83	37.42	32.13	26.59	20.73	23.72	*	*	-	-
30	PLACE1003366	12	18.42	15.82	7.6	12.12	4.37	10.36	5.92	5.45	*	*	-	-
	PLACE1003369	4.81	3.43	3.93	0.94	3.73	1.31	1.63	1.07	0.84	**	*	-	-
	PLACE1003372	13.64	7.8	10.54	3.88	10.47	3.36	4.52	1.77	3.52	*	*	-	-
	PLACE1003373	8.88	8.18	9.38	3.94	3.76	0.99	4.29	2.31	3.38	**	**	-	-
	PLACE1003375	22.91	23.46	16.65	11.55	17.67	11.28	29.27	13.77	19.27			-	-
	PLACE1003378	1.92	0.43	0.47	1.45	0.86	1.22	0.77	0.97	0.76			-	-
35	PLACE1003383	15.75	12.58	10.55	7.3	8.49	3.81	2.43	7.46	2.15	*	*	-	-
	PLACE1003394	19.46	13.29	10.26	6.3	12.66	5.09	11.98	10.6	17.14			-	-
	PLACE1003401	8.87	6	5.04	3.66	4.75	2.93	5.66	3.3	5.47			-	-
	PLACE1003405	7.6	8.07	5.91	3.39	5.27	4.58	4.12	1.47	2.3	*	*	-	-
	PLACE1003407	10.24	7.49	7.79	2.43	3.28	2.12	4.16	2.37	3.5	**	**	-	-
40	PLACE1003420	7.71	5.57	6.39	3.78	6.36	2.21	2.89	1.88	2.26	**	*	-	-
	PLACE1003428	6.55	5.9	4.45	2.19	4.16	0.9	3.49	2.31	8.87	*	*	-	-
	PLACE1003432	51.6	69.55	75.77	36.76	44.92	44.22	42.27	64.14	52.55	*	*	-	-
	PLACE1003438	1.98	2.35	1.48	2.21	4.73	1.43	4.08	0.93	0.7			-	-
	PLACE1003452	3.01	3.41	4.3	1.8	3.84	2.08	2.34	2.25	1.64	*	*	-	-
	PLACE1003454	3.87	4.87	5.58	2.54	4.5	3.92	2.57	2.43	1.33	*	*	-	-
45	PLACE1003455	2.92	2.41	4.04	1.6	1.9	1.64	1.75	0.8	1.88	*	*	-	-
	PLACE1003456	2.36	4.17	3.63	2.06	10.37	2.22	2.4	1.94	0.64			-	-
	PLACE1003460	4.76	5.09	4.73	4.08	6	2.64	6.38	3.46	2.92			-	-
	PLACE1003478	6.15	2.11	2.66	1.92	3.96	2	5.39	1.91	4.04			-	-
	PLACE1003484	6.84	8.17	8.98	4.36	6.73	3.1	4.12	4.68	4.63	**	*	-	-
	PLACE1003493	83.14	41.9	88.74	60.01	72.45	45.07	64.55	71.53	53.96			-	-
50	PLACE1003503	7.36	5.03	5.29	1.12	3.91	3.51	2.36	3.64	2.4	*	*	-	-
	PLACE1003505	32.2	45.22	38.51	20.24	36.17	23.66	24.44	34.5	27.01			-	-
	PLACE1003516	7.02	7.8	7.71	2.88	5.85	3.76	2.24	2.98	3.86	*	**	-	-
	PLACE1003519	4.06	1.81	5.55	3.83	3.85	1.91	2.58	1.64	0.34			-	-
	PLACE1003520	12.72	16.96	9.15	8.71	16.58	8.45	4.85	6.39	5.22	*	*	-	-
55	PLACE1003521	14.95	10.13	14.17	6.02	7.53	5.56	6.77	8.38	4.75	*	*	-	-
	PLACE1003525	20.17	19.13	25.59	15.85	14.55	12.63	20.97	18.71	22.36	*	*	-	-
	PLACE1003528	35.65	25.12	43.38	21.63	30.38	28.64	16.02	24.64	18.65			-	-
	PLACE1003529	11.19	16.69	21.6	20.8	16.66	31.76	18.24	15.7	15.44			-	-
	PLACE1003537	3.15	4.02	8.21	3.24	3.64	3.89	1.76	2.65	2.32			-	-

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	PLACE1003549	16.21	19.52	27.74	11.72	18.71	13.09	12.65	15.02	13.74			
	PLACE1003553	12.63	20.69	18.89	10.17	18.28	8.51	8.12	9.44	8.9	*	-	
	PLACE1003566	9.49	12.35	9.77	7.53	10.49	7.08	3.77	4.66	6.9	*	-	
5	PLACE1003568	5.3	4.9	19.78	3.8	7.59	3.87	5.3	6.3	4.21			
	PLACE1003573	32	27.25	37.46	17.52	23.28	16.23	15	18.28	19.13	* **	-	
	PLACE1003575	66.07	60.03	70.99	42.8	62.9	38.6	75.17	59.46	62.58			
	PLACE1003583	8.33	4.65	6.88	3.47	6.26	5.07	2.38	3.4	4.1	*	-	
	PLACE1003584	12.09	10.66	18.02	7.17	8.48	19.2	8.54	7.15	2.79			
10	PLACE1003592	29.77	33.55	28.89	21.34	26.31	15.85	12.59	8.49	12.12	* **	-	
	PLACE1003593	7.15	3.54	8.27	3.34	2.24	1.83	3.11	5.19	5.45			
	PLACE1003594	7.18	8.49	9.31	5.03	6.61	3.38	4.99	3.18	2.37	* **	-	
	PLACE1003596	5.11	3.13	4.25	2.82	5	3.14	3.75	4.1	3.76			
	PLACE1003598	31.57	29.75	31.55	14.81	20.6	17.31	5.31	17.81	7.34	** **	-	
	PLACE1003602	6.51	2.47	7.47	1.84	4.91	0.98	2.4	4.6	2.56			
15	PLACE1003605	10	6.14	7.29	5.28	8.85	3.75	6.45	5.07	2.93			
	PLACE1003611	15.94	16.54	24.25	11	9.1	12.46	10.14	10.62	12.83	*	-	
	PLACE1003618	7.78	7.74	12.1	3.49	6.12	2.68	4.58	5.29	6.93	*	-	
	PLACE1003625	14.19	21.53	18.27	11.53	22.81	17.82	13.8	9.54	11.86			
	PLACE1003626	11.55	14.38	14.6	5.94	11.97	7.26	4.57	4.49	2.04	**	-	
20	PLACE1003630	3.86	4.65	3	4.62	4.58	3.02	3.68	3.68	1.66			
	PLACE1003635	8.33	7.29	10.19	5.35	5.59	4.6	3.51	4.48	4.17	* **	-	
	PLACE1003638	4.33	3.09	4.93	3.86	6.02	2.38	2.01	3.6	1.35			
	PLACE1003644	35.03	24.77	24.25	19.14	20.11	17.95	8.77	10.6	6.97	**	-	
	PLACE1003654	75.56	74.57	74.52	77.61	72.17	67	35.39	33.92	31.06	**	-	
	PLACE1003656	7.81	5.19	8.37	3.06	4.32	3.8	1.16	1.63	2.96	* **	-	
25	PLACE1003660	16.25	21.8	21.11	12.32	17.1	13.06	14.44	12.72	12.99	*	-	
	PLACE1003669	12.05	8.79	12.65	4.93	9.33	7.48	3.9	4.69	4.41	**	-	
	PLACE1003670	110.15	83.05	76.99	55.55	52.05	50.36	48.6	63.39	52.6	* *	-	
	PLACE1003671	11.47	3.49	4.69	7.13	4.59	4.35	3.71	2.69	2.22			
	PLACE1003697	9.65	10.83	16.05	9.21	10.08	8.25	6.51	4.97	6.76	*	-	
	PLACE1003704	10.58	7.92	10.14	6.15	6.81	6.51	4.22	3.63	3.86	* **	-	
30	PLACE1003709	9.06	8.99	10.78	5.34	6.7	5.47	3.53	3.36	1.83	** **	-	
	PLACE1003711	28.05	31.28	32.33	21.12	31.77	27.07	16.12	16.73	14.21	**	-	
	PLACE1003723	27.32	34.97	28.91	18.16	26.8	21.24	17.63	17.4	10.81	**	-	
	PLACE1003724	29.33	36.12	25.65	19.94	34.26	21.71	26.66	13.83	15.71			
	PLACE1003737	8.24	6.31	9.31	2.89	4.06	2.72	3.31	2.56	3.28	** **	-	
	PLACE1003738	5.02	4.71	5.03	8.76	2.78	9.43	1.8	2.2	2.93	**	-	
35	PLACE1003742	17.85	18.69	20.82	14.24	7.57	8.14	10.49	8.98	8.16	* **	-	
	PLACE1003744	5.48	2.82	3.4	0.66	1.04	1.08	1.74	1.94	0.38	*	-	
	PLACE1003758	23.32	22.73	21.79	9.9	15.26	16.38	15.29	14.75	13.36	* **	-	
	PLACE1003760	40.1	57.96	44.54	28.85	37.15	22.14	11.09	14.54	11.41	**	-	
	PLACE1003762	65.35	58.09	77.98	35.3	88.27	46.92	46.48	32.75	38.3	*	-	
	PLACE1003765	93.01	107	70.69	55.75	97.14	46.35	33.33	44.53	44.51	*	-	
40	PLACE1003768	34.07	21.23	23.34	10.87	13.6	6.67	25.2	17.43	28.3	*	-	
	PLACE1003771	5.38	5.57	5.27	3.47	7.27	2.71	1.77	1.77	2.44	**	-	
	PLACE1003772	5.63	7.96	4.89	1.17	7.74	2.12	3.12	2.24	2.28	*	-	
	PLACE1003783	5.15	3.84	3.95	2.36	3.83	1.92	1.65	1.17	0.84	**	-	
	PLACE1003784	5.59	6.96	5.68	2.81	4.01	2.73	3.1	2.42	1.88	** **	-	
	PLACE1003788	34.98	33.59	27.31	19.49	15.1	21.27	12.2	5.92	10.73	* **	-	
45	PLACE1003795	26.48	33.02	23.72	12.5	28.84	12.28	23.33	16.94	16.45			
	PLACE1003827	9.74	8.51	10.55	21.41	16.48	10.33	5.7	3.14	1.91			
	PLACE1003833	14.14	10.78	12.27	5.74	8.62	5.66	5.59	6.29	7.37	* **	-	
	PLACE1003839	259.31	241.18	222.89	217.52	173.45	205.17	163.55	139.4	151.61	**	-	
	PLACE1003845	69.72	60.2	118.04	40.89	28.14	26.89	48.08	43.86	45.73			
50	PLACE1003850	9.53	11.45	9.42	3.3	8.43	5.88	6.51	3.87	5.97	*	-	
	PLACE1003852	32.49	28.32	26.73	21.76	30.69	26.63	18.45	14.12	17.92	**	-	
	PLACE1003858	19.9	13.83	13.86	8.03	12.82	5.24	7.08	4.19	7.71	*	-	
	PLACE1003861	40.22	66.3	33.51	12.47	57.37	18.72	33.23	18.67	19.13			
	PLACE1003864	34.51	84.76	122.59	61.83	70.16	55.03	69.32	56.31	42.37			
	PLACE1003870	9.43	6.5	5.9	2.94	3.32	3.4	5.69	3.86	5.74	*	-	
55	PLACE1003885	10.07	6.76	3.91	3.5	6.22	3.91	3.49	3.72	6.33			
	PLACE1003886	12.66	12.76	10.57	6.28	9.54	3.51	13.66	8.88	12.28	*	-	
	PLACE1003888	15.48	13.6	17.45	7.94	12.36	6.23	14.56	8.73	9.07	*	-	
	PLACE1003892	6.59	4.85	8.21	5.64	7.14	2.75	3.77	2.15	4.24			

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	PLACE1003900	9.05	5.59	5.53	3.41	9.33	4.49	4.41	6.87	4.79				
	PLACE1003902	9.43	6.06	7.46	2.35	3.67	1.76	3.96	1.76	3.05	*	*	-	-
	PLACE1003903	17.33	19.36	14.55	9.42	10.87	10.03	9.08	6.56	7.77	**	**	-	-
5	PLACE1003915	14.67	18	11.19	12.64	10.36	9.98	8.5	5.29	8.8	*		-	-
	PLACE1003918	10.58	6.62	8.73	7.34	5.29	3.45	7.05	5.69	4.94				
	PLACE1003923	11.24	8.95	4.47	2.95	4.6	4.65	4.65	3.26	3.87				
	PLACE1003932	9.02	5.88	4.39	2.18	9.39	4.8	6.3	4.31	5.14				
	PLACE1003936	11.92	7.46	8.85	2.47	4.23	4.36	9.51	9.11	10.65	*		-	-
10	PLACE1003966	11.6	10.3	9.01	5.2	6.1	4.37	6.77	5.83	6.22	**	**	-	-
	PLACE1003968	4.88	5.07	4.71	0.66	3.28	0.8	3.51	1.87	0.72	*	*	-	-
	PLACE1004018	4.89	2.45	2.55	4.7	8.1	2.19	2.99	1.85	1.89				
	PLACE1004020	12.24	14.87	17.86	7.54	8.19	5.65	7.35	9.99	10.06	*	*	-	-
	PLACE1004028	2.49	1.88	2.35	1.78	7.14	2.28	1.01	1.49	0.82	*		-	-
	PLACE1004034	6.5	4.91	7.64	2.7	5.45	2.86	3.71	3.07	1.75	*		-	-
15	PLACE1004042	5.94	2.98	4.53	2.04	4.08	3.55	3.58	3.9	2.95				
	PLACE1004078	6.26	4	5.13	2.35	3.57	1.92	1.94	3.66	4.31	*		-	-
	PLACE1004103	4.16	6.73	8.68	2.05	3.45	2.36	1.89	0.91	3.01	*	*	-	-
	PLACE1004104	0.6	1.12	3	1.89	7.2	1.01	1.88	2.79	1.52				
	PLACE1004113	0.85	1	0.69	0.62	4.18	1	1.54	0.77	1.59				
20	PLACE1004114	12.27	11.63	12.84	9.04	6.13	6.15	17.17	8.3	11.59	**		-	-
	PLACE1004118	25.56	29.6	34.14	10.69	22.13	12.84	16.2	19.15	19.4	*	*	-	-
	PLACE1004128	6.77	8.44	8.16	3.47	7.23	7.78	2.81	3.08	3.14	**		-	-
	PLACE1004130	9.36	4.88	10.96	8.2	7.53	9.87	4.28	6.71	6.1				
	PLACE1004149	2.51	2.43	6.21	2.78	5.35	2.6	3.3	3.26	2.01				
25	PLACE1004156	13.06	9.08	13.29	7.39	11.05	6.74	9.05	9.4	10.62				
	PLACE1004160	20.97	19.94	23.27	14.03	30.3	7.33	16.97	16.65	14.66	*		-	-
	PLACE1004161	7.06	8.18	8.06	5.83	7.98	4.77	4.77	4.44	4.99	**	**	-	-
	PLACE1004166	41.1	39.11	42.06	19.36	22.19	21.87	24.56	28.32	30.02	**	**	-	-
	PLACE1004168	32.92	30.07	31.55	16.2	15.66	13.35	21.23	25.32	27.11	**	*	-	-
	PLACE1004170	14.53	21.92	19.94	10.32	12.85	10.61	11.03	18.31	8.2	*		-	-
	PLACE1004178	2.75	3.62	3.97	2.55	6.19	3.35	0.34	1.55	0.72	**		-	-
30	PLACE1004183	38.95	43.53	45.99	27.78	51.84	25.82	21.25	25.43	23.92	**		-	-
	PLACE1004197	5.75	5.24	7.84	2.14	4.97	3.74	3.04	2.49	3.28	*		-	-
	PLACE1004199	21.75	27.66	12.12	12.42	24.13	11.64	10.47	10.88	12.46				
	PLACE1004203	11	13.62	10.81	4.23	10.81	6.59	10.74	11.32	12.32				
	PLACE1004242	20.49	16.48	21.11	6.81	6.93	13.71	6.23	11.27	9.24	*	**	-	-
35	PLACE1004249	6.73	11	11.25	4.47	10.26	6.2	5.79	8.22	6.09				
	PLACE1004255	32.98	36.35	38.9	17.52	26.48	21.84	27.95	27.86	29.02	*	*	-	-
	PLACE1004256	12.54	10.51	15.03	5.99	5.51	6.23	3.84	5.04	3.23	**	**	-	-
	PLACE1004257	3.25	14.27	11.31	3.36	8.12	8.15	2.7	9.49	4.03				
	PLACE1004258	11.89	26.37	21.62	8.76	18.18	12.25	12.69	13.44	9.66				
	PLACE1004270	8.17	8.34	11.88	6.47	6.77	11.76	8.27	3.74	6.39				
40	PLACE1004272	1.52	1.56	3.17	1.04	3.51	0.46	1.56	1.06	1.78				
	PLACE1004273	23.31	38.14	20.87	17.38	14.34	7.01	17.2	17.07	20.56				
	PLACE1004274	12.13	13.19	15.06	6.12	12.19	6.04	6.47	11.78	6.75				
	PLACE1004277	18.65	17.3	16.15	12.2	21.29	13	13.46	15.12	20.1				
	PLACE1004279	20.99	17.87	19.27	8.96	30.05	13	8.21	11.3	11.19	**		-	-
	PLACE1004282	12.65	12.53	16.59	4.95	9.12	5.25	6.7	6.34	5.89	*	**	-	-
45	PLACE1004284	9.58	14.66	15.53	8.95	7.35	5.65	6.2	6.82	3.1	*	*	-	-
	PLACE1004289	11.29	10.79	11.74	3.16	5.71	3.35	2.35	6.14	2.14	**	**	-	-
	PLACE1004299	19.52	18.15	16.36	8.87	22.44	9.43	11.73	8.62	8.57	**		-	-
	PLACE1004302	6.5	4.57	6.26	4.18	7	3.55	1.56	4.16	0.55	*		-	-
	PLACE1004305	7.16	4.88	7.78	4.02	11.98	4.38	3.44	4.62	2.94	*		-	-
50	PLACE1004316	21.08	20.32	25.43	14.83	15.07	12.7	13.59	13.17	12.8	*	**	-	-
	PLACE1004322	9.54	3.44	10.02	13.05	22.34	1.36	2.52	7.35	3.43				
	PLACE1004325	13.79	15.32	21.15	8.25	8.41	6.63	10.63	11.11	9.78	*		-	-
	PLACE1004332	13.76	26.81	27.83	10.52	16.97	4.86	9.28	8.37	7.2	*		-	-
	PLACE1004336	9.25	9.04	10.31	3.17	5.77	3.05	2.53	4.29	2.93	**	**	-	-
	PLACE1004346	11.14	15.86	16.19	8.6	6.7	8.17	14.67	2.81	3.65	*		-	-
55	PLACE1004358	4.9	6.6	5.3	4.66	3.48	2.52	2.87	2.07	1.85	**		-	-
	PLACE1004376	4.37	7.66	6.28	3.82	16.23	3.24	18.46	3.42	3.06				
	PLACE1004384	20.82	15.88	20.1	10.2	14.54	11.76	10.47	11.55	9.77	*	**	-	-
	PLACE1004385	18.21	25.32	29.3	6.24	11.85	7.12	18.49	9.57	9.67	*		-	-
	PLACE1004388	13.03	15.64	14.98	6.25	11.49	8.38	7.85	6.97	4.61	*	**	-	-

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	PLACE1004405	6.83	7.82	8.42	1.74	2.87	2.17	1.79	1.77	1.06	**	**	-	-
	PLACE1004407	11.75	11.43	14.16	6.35	10.59	6.28	6.13	6.07	6.47	*	**	-	-
	PLACE1004424	6.94	8.4	8.66	2.02	6.19	2.66	3.43	3.43	2.34	*	**	-	-
5	PLACE1004425	15.08	13.72	13.35	6.65	11.37	7.31	11.7	10.39	11.17	*	*	-	-
	PLACE1004427	9.79	7.13	8.53	5.79	4.82	4.58	2.31	1.96	2.72	*	**	-	-
	PLACE1004428	8.46	5.33	5.57	3.25	3.29	3.21	2.85	2.65	3.1	*	*	-	-
	PLACE1004433	6.57	5.12	7.26	2.15	3.61	2.86	2.76	2.36	3.32	*	**	-	-
	PLACE1004435	5.31	5.07	8.8	2.76	3.41	3.61	2.83	0.69	1.36	*	*	-	-
10	PLACE1004437	123.66	158.84	144.08	116.56	167.95	86.05	49.84	88.42	68.77	**	**	-	-
	PLACE1004441	10.02	12.73	11.55	5.63	11.08	5.24	5.14	4.56	2.63	**	*	-	-
	PLACE1004446	4.95	5.73	4.69	2.19	3.83	1.62	2.79	2.61	2.66	*	**	-	-
	PLACE1004450	17.21	13.77	11.35	7.43	9.82	10.35	13.72	15.81	15.38	*	*	-	-
	PLACE1004451	21.93	21.83	22.42	14.24	15.13	14.34	10.39	9.42	10.97	**	**	-	-
	PLACE1004456	5.66	3.89	4.79	2.22	5.14	3.7	4.95	1.66	2.31	*	*	-	-
15	PLACE1004458	6.57	4.16	7.77	2.1	5.75	2.16	2.41	3.03	1.54	*	*	-	-
	PLACE1004460	6.93	5.13	4.79	2.01	4.85	1.65	3.61	2.54	1.12	*	*	-	-
	PLACE1004467	10.11	11.82	9.53	2.74	4.49	5.1	3.12	1.44	1.55	**	**	-	-
	PLACE1004471	14.09	22.14	14.79	8.38	18.33	11.21	5.81	8.78	5.83	*	*	-	-
	PLACE1004473	8.27	14.31	9.86	3.42	8.92	3.77	4.46	5.47	8.39	*	*	-	-
20	PLACE1004475	4.2	2.67	2.47	2.6	8.42	6.68	3.42	2.58	2.7	*	*	-	-
	PLACE1004482	42.46	39.9	32.17	18.98	31.24	19.51	41.1	31.66	45.4	*	*	-	-
	PLACE1004491	3.4	5.37	4.92	2.26	2.87	1.21	3.11	1.77	1.09	*	*	-	-
	PLACE1004492	14.75	10.5	4.26	8.39	16.03	7.27	3.28	2.19	2.31	*	*	-	-
	PLACE1004506	18.11	19.82	21.23	12.46	23.49	16.62	17.33	12.61	13.21	*	*	-	-
25	PLACE1004507	14.62	14.01	19.19	12.21	20.75	13.12	5.25	3.93	6.09	**	*	-	-
	PLACE1004510	8.27	7.11	7.77	4.2	4.81	1.36	5.06	2.94	3.49	*	**	-	-
	PLACE1004516	5.75	6.67	3.83	4.51	8.48	2.72	4.69	2.56	3.06	*	*	-	-
	PLACE1004518	9.64	6.39	6.6	5.58	7.29	2.45	2.45	4.03	4.48	*	*	-	-
	PLACE1004519	45.05	38.06	29.43	16.22	21.37	17.38	37.02	29.03	42.7	*	*	-	-
	PLACE1004520	5.65	5.88	4.83	5	23.3	3.26	7.89	2.48	5.32	*	*	-	-
30	PLACE1004530	8.55	8.01	8.19	4.33	4.87	3.07	5.74	4.33	5.72	**	**	-	-
	PLACE1004545	16.35	9.42	10.89	5.28	6.16	4.82	7.69	5.29	6.88	*	*	-	-
	PLACE1004547	8.88	4.99	7.28	3.79	10.69	2.44	2.07	2.03	2.03	*	*	-	-
	PLACE1004548	8.06	7.34	7.17	1.99	3.55	1.53	3.36	1.74	4.09	**	**	-	-
	PLACE1004550	9.29	4.74	4.57	6.39	7.24	2.64	11.12	3.11	5.12	*	*	-	-
	PLACE1004551	28.29	24.92	17.22	13.36	20.97	8.68	22.61	16.23	21.2	*	*	-	-
35	PLACE1004559	38.64	25.35	19.12	16.44	15.14	16.5	25.43	24.95	33.62	*	*	-	-
	PLACE1004562	50.29	46.32	50.21	54.16	56.41	39.84	35.71	42.24	45.43	*	*	-	-
	PLACE1004564	12.01	9.86	9.29	4.62	9.04	5.79	9.27	6.54	10.21	*	*	-	-
	PLACE1004604	17.66	17.86	15.11	9.74	9.81	7.66	16.75	11.47	16.51	**	*	-	-
	PLACE1004611	6.51	3.64	4.04	1.34	7.9	1.38	3.77	0.9	3.89	*	*	-	-
	PLACE1004629	7.22	4.23	7.21	2.88	5.64	1.27	4	2.37	6.88	*	*	-	-
40	PLACE1004630	5.71	5.71	5.05	2.41	3.38	0.92	6.59	3.07	5.19	*	*	-	-
	PLACE1004637	15.22	15.19	15.73	4.5	6.73	18.68	5.83	11.18	5.64	*	*	-	-
	PLACE1004645	16.19	10.08	17.1	10.36	11.57	13.97	10.9	12.36	6.68	*	*	-	-
	PLACE1004646	4.97	5.64	4.39	4.13	5.71	3.39	2.58	3.34	2.67	**	*	-	-
	PLACE1004648	5.49	4.11	3.96	3.64	5.16	4.29	1.91	1.5	0.14	**	*	-	-
	PLACE1004655	3.31	1.36	2.13	1.15	3.39	0.72	0.74	1.06	1.47	*	*	-	-
45	PLACE1004658	61.58	67.15	67	38.54	49.97	38.25	52.62	54.12	65.08	**	*	-	-
	PLACE1004664	1.19	4.36	2.93	2.86	5.73	2.7	1.85	2.13	1.51	*	*	-	-
	PLACE1004672	28.88	30.42	25.6	16.98	20.16	13.59	16.28	11.87	13.82	**	**	-	-
	PLACE1004674	4.27	1.5	4.11	2.41	3.15	1.89	1.56	2.96	3.87	*	*	-	-
	PLACE1004681	6.54	6.41	13.08	7.27	21.72	12.91	4.64	4.9	3.36	*	*	-	-
	PLACE1004686	4.34	3.3	4.61	2.4	3.38	2.38	2.29	3.63	0.39	*	*	-	-
50	PLACE1004690	6.4	6.12	8.6	4.32	13.96	8.66	2.73	4.56	2.78	*	*	-	-
	PLACE1004691	12.44	14.52	17.78	7.94	13.42	7.13	8.04	12.14	11.56	*	*	-	-
	PLACE1004693	8.4	10.27	9.88	5.82	5.16	5.28	2.45	3.25	2.73	**	**	-	-
	PLACE1004701	144.88	196.16	97.68	190.88	167.91	84.32	88.33	73.95	139.9	*	*	-	-
	PLACE1004705	3.47	3.01	2.93	2.39	3.96	1.27	1.92	3.49	3.87	*	*	-	-
	PLACE1004708	48.88	43.13	45.03	31.98	28.55	23.56	15.06	39.44	11.77	**	*	-	-
55	PLACE1004716	20.04	14.83	24.39	8.19	12.11	8.27	8.37	8.78	9.57	*	*	-	-
	PLACE1004722	5.57	7.39	10	4.45	6.54	3.93	3.57	3.69	3.48	*	*	-	-
	PLACE1004736	16.71	17.15	24.67	12.34	13.91	6.89	9.19	22.16	13.53	*	*	-	-
	PLACE1004737	5.22	7.74	7.78	3.83	6.24	1.98	3.06	3.38	3.05	*	*	-	-

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	PLACE1004740	5.7	7.45	13.2	8.48	9.7	6.78	5.51	4.01	4.39				
	PLACE1004743	25.2	29.5	32.11	15.32	29.52	15.01	26.22	23.41	28.91				
	PLACE1004751	26.3	37.3	36.23	17.86	40.34	16.49	27.84	27.38	23.37				
5	PLACE1004757	27.21	29.89	35.01	20.07	11.76	13.22	19.63	14.54	16.78	*	**	-	-
	PLACE1004761	36.62	28.57	36.7	16.84	22.51	18.17	11.71	16.47	11.41	**	**	-	-
	PLACE1004773	6.34	3	4.53	3.16	3.36	2.2	2.15	2.55	2.95				
	PLACE1004775	6.98	4.5	11.09	2.47	5.26	2.58	2.74	2.24	1.32				
	PLACE1004777	22.12	29.48	36.12	13.38	18.93	13.39	17.54	20.58	18.98	*		-	-
10	PLACE1004793	38.61	50.6	39.99	29.77	37.64	25.63	24.47	24.63	21.5		**	-	-
	PLACE1004796	8.45	9.48	8.63	3.38	9.79	3.2	3.16	2.68	3.41		**	-	-
	PLACE1004804	5.96	3.66	3.88	1.07	6.07	2.59	2.15	2.35	2.21		*	-	-
	PLACE1004813	7.54	8.6	8.99	4.2	5.66	4.51	4.87	4.35	4.23	**	**	-	-
	PLACE1004814	4.13	4.9	5.89	3.27	11.52	2.25	2.11	31.08	4.24				
	PLACE1004815	5.57	3.05	6.31	3.48	4.55	1.54	4.88	2.03	1.26				
15	PLACE1004816	10.65	12.52	15.46	46.15	13.59	7.88	11.01	6.49	24.95				
	PLACE1004824	10.1	10.18	14.93	3.84	7.8	4.37	6.87	4.52	8.59	*		-	-
	PLACE1004827	6.33	6.31	10.2	1.77	3.73	0.89	1.94	4.36	3.45	*	*	-	-
	PLACE1004836	18.51	24.59	14.94	5.86	11.83	5.72	3.63	5.6	4.83	*	*	-	-
	PLACE1004838	32.68	37.85	26.97	17.25	33.96	16.53	18.4	22.65	17.82	*		-	-
20	PLACE1004840	26.67	33.84	24.99	11.9	21.32	10.63	17.68	19.77	20.11	*	*	-	-
	PLACE1004842	29.36	29.36	36.71	26.03	17.22	20.39	11.25	16.65	13.58	*	*	-	-
	PLACE1004850	12.96	12.93	15.16	9.69	10.5	6.77	8.83	9.34	8.77	*	**	-	-
	PLACE1004868	19.8	16.22	20.8	8.53	16.93	9.03	11.19	11.11	9.47	**	*	-	-
	PLACE1004885	7.93	7.22	6.94	1.5	3.78	3.6	1.94	2.3	1.73	**	**	-	-
	PLACE1004886	8.48	8.07	17.49	4.04	4.63	2.9	4.53	4.47	2.5				
25	PLACE1004887	11.79	13.7	11.52	6.38	10.2	7	3.69	4.3	5.52	*	**	-	-
	PLACE1004896	6.25	6.09	7.72	0.93	8.2	4.59	2.58	2.25	1.01	**	*	-	-
	PLACE1004900	11.28	8.08	8.69	8.58	6.42	4.7	4.96	5.45	3.62	*	*	-	-
	PLACE1004902	7.13	7.38	10.7	4.87	6.92	2.81	4.29	4.21	2.64	*		-	-
	PLACE1004904	23.08	23.38	37.33	15.52	22.71	12.92	16.1	22.74	25.02				
	PLACE1004911	11.74	10.67	12.36	7.47	12.66	7.84	6.28	5.55	4.09	**	*	-	-
30	PLACE1004913	12.82	12.15	14.37	4.58	7.86	4.67	7.24	7.07	6.68	**	**	-	-
	PLACE1004918	17.31	18.68	18.94	7.36	10.01	6.44	8.32	5.56	6.18	**	**	-	-
	PLACE1004930	6.79	6.06	5.6	1.3	2	3.65	2.19	1.6	1.33	**	**	-	-
	PLACE1004934	14.99	19.19	12.29	5.42	10.92	8.11	4.61	8.66	7.47	*	*	-	-
	PLACE1004937	18.93	13.85	13.4	11.81	10.98	11.51	15	13.14	16.45				
	PLACE1004949	5	5.22	6.64	5.79	3.31	3.09	4.44	4.05	3.5	*	*	-	-
35	PLACE1004969	13.91	13.85	11.55	11.71	12.45	9.25	4.82	9.25	5.58	*	*	-	-
	PLACE1004970	28.75	33.22	29.53	13.51	29.35	23.54	15.11	12.88	14.15	**	*	-	-
	PLACE1004972	13.26	11.27	10.14	5.85	6.98	5.82	4.89	3.42	1.54	**	**	-	-
	PLACE1004974	16.47	29.85	28.89	16.44	23.94	17.53	14.71	17.1	12.72				
	PLACE1004975	12.92	11.66	12.08	5.89	13.8	6.88	5.54	3.55	3.43	**	*	-	-
	PLACE1004979	7.78	7.47	6.98	3.07	7.65	3.76	4.2	4.56	6.5	*	*	-	-
40	PLACE1004982	30.58	23.61	26.29	14.3	19.23	11.42	16.82	24.16	30.51	*	*	-	-
	PLACE1004985	29.68	24.94	25.1	15.66	19.26	12.6	21.78	17.15	20.28	*	*	-	-
	PLACE1005003	16.43	14.5	16.78	6.69	10.88	11.47	1.79	5.8	6.41	*	**	-	-
	PLACE1005004	5.26	4.21	4.06	1.44	3.4	2.25	2.76	1.23	1.09	*	*	-	-
	PLACE1005005	17.79	13.99	18.79	11.99	10.57	8.86	7.49	5.3	5.99	*	**	-	-
45	PLACE1005011	10.94	14.04	9.8	3.35	9.24	6.44	3.46	2.32	0.6	**	*	-	-
	PLACE1005026	31.74	35.88	28.88	14.82	24.65	14.67	35.74	25.33	28.57	*	*	-	-
	PLACE1005027	26.29	29.23	15.87	7.97	19.55	9.09	25.84	19.81	24				
	PLACE1005031	38.12	16.05	14.24	9.18	25.55	17.12	7.22	9.47	10.36				
	PLACE1005036	13.86	12.84	17.42	8.68	15.64	10.29	11.23	7.16	6.77	*	*	-	-
	PLACE1005041	111.13	87.66	72.07	36.83	51	43.47	99.34	93.97	97.87	*	*	-	-
50	PLACE1005046	27.6	29	18.07	15.06	19.65	20.68	22.16	13.25	24				
	PLACE1005047	50.64	34.98	35.58	25.13	37.56	21.77	26.01	15.91	25.77	*	*	-	-
	PLACE1005052	10.39	12.55	10.8	4.67	15.46	6.61	10.9	9.05	16				
	PLACE1005058	24.31	33.8	18.61	16.75	10.79	11.1	19.54	11.46	10.17				
	PLACE1005066	7.67	8.41	7	12.21	61.68	20.27	25.44	4.84	8.48				
	PLACE1005077	9.62	6.97	5.62	4.44	4.68	3.2	5.42	5.71	7.8				
55	PLACE1005085	10.11	4.46	3.84	3.42	3.7	2.05	2.8	5.01	2.86				
	PLACE1005086	11.97	11.74	11.67	7.31	18.85	7.84	6.74	6.63	9.62	*	*	-	-
	PLACE1005088	86.57	83.56	74.65	79.4	89.3	75.33	56.8	52.44	57.53	**	*	-	-
	PLACE1005089	6.31	4.13	4.27	1.8	3.13	4.07	2.18	0.56	2.04	*	*	-	-

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	PLACE1005101	11.5	9.29	11.94	9.18	4.8	5.47	5.22	3.69	6.78	*	**	-	-
	PLACE1005102	22.17	25.98	27.54	6.07	7.69	6.94	7.15	5.65	7.82	**	**	-	-
5	PLACE1005108	10.15	7.73	6.02	2.99	6.05	3.33	4.8	7.23	6.47				
	PLACE1005110	3.97	2.39	3.45	3.59	3.78	1.51	2.14	1.33	2.15				
	PLACE1005111	23.94	21.69	16.98	14.04	21.5	8.57	20.32	16.74	23.71				
	PLACE1005123	16.94	14.46	12.96	5.45	9.5	5	6.89	4.29	5.82	*	**	-	-
	PLACE1005124	9.14	6.62	6.15	2.06	5.47	1.8	6.61	3.46	5.33	*		-	-
10	PLACE1005128	6.83	4.81	4.87	1.09	3.42	1.91	3.3	3.63	2.82	*	*	-	-
	PLACE1005130	12.43	17.68	12.68	4.58	11.05	5.79	12.55	5.44	10.87				
	PLACE1005141	6.07	3.99	5.18	6.23	2.88	1.1	9.65	2.17	2.82				
	PLACE1005146	10.52	9.7	6.88	6.24	10.69	5.88	5.25	8.14	5.49				
	PLACE1005152	91.15	76.64	75.79	51.06	95.95	52.59	42.4	38.1	38.75	**		-	-
	PLACE1005157	5.11	3.75	6.06	2.82	4.86	2.4	1.9	2.79	1.7	*		-	-
15	PLACE1005162	24.79	23.25	27.03	17.82	26.77	20.32	10.52	15.51	11.65	**		-	-
	PLACE1005170	9.55	7.54	6.99	11.08	19.85	14.4	3.82	8.2	5.94				
	PLACE1005176	5.55	5.17	6.85	2.52	4.13	3.01	2.09	2.54	1.26	*	**	-	-
	PLACE1005181	10.56	18.07	15.09	7.46	9.06	8.01	10.91	12.85	10.11	*		-	-
	PLACE1005184	3.64	4.4	5.5	5.28	11.77	4.26	3.84	3.69	3.06				
	PLACE1005186	5.96	5.07	5.66	2.88	2.54	3.26	3.64	4.33	4.72	**	*	-	-
20	PLACE1005187	20.53	14.71	18.55	9.5	10.66	10.36	12.23	12.87	7.61	*	*	-	-
	PLACE1005189	8.28	7.72	11.92	4.24	7.19	3.99	6.84	7.52	5.99				
	PLACE1005193	39.26	44.11	39.59	31.34	38.66	28.91	36.03	40.56	33.69				
	PLACE1005200	1391.4	1317.2	1202.3	1770.3	2457.3	1744.3	1189.8	1397.9	586.38	*		+	
	PLACE1005206	48.27	41.57	88.17	48.38	52.86	50.82	27.19	13.53	58.32				
25	PLACE1005216	10.1	9.74	10.26	5.79	10.41	5.95	3.4	3.26	4.05	**		-	-
	PLACE1005223	36.86	44.94	37.06	23.02	26.39	16.59	23.41	26.05	19.76	*	**	-	-
	PLACE1005225	5.34	5.81	6.83	4.25	3.02	5.27	2.59	3.79	3.7	*		-	-
	PLACE1005232	37.45	31.95	45.29	20.08	17.68	11.81	24.42	25.92	23.95	**	*	-	-
	PLACE1005239	7.93	6.66	12.45	5.29	3.66	4.36	3.81	3.89	4.86				
	PLACE1005243	16.13	27.58	27.13	19.28	15.8	19.25	6.8	13.48	9.67	*		-	-
30	PLACE1005250	5.37	6.75	7.77	5.96	4.93	3.55	3.78	5.49	3.24				
	PLACE1005261	61.12	61.95	56.67	47.53	36.14	42.92	20.88	23.52	21.14	**	**	-	-
	PLACE1005266	7.03	6.91	9.71	5.82	8.14	5.96	4.18	3.69	5.53	*		-	-
	PLACE1005271	8.47	8.61	6.86	4.77	7.74	3.27	3.65	3.57	3.35	**		-	-
	PLACE1005277	20.92	15.1	22.31	9.09	13.8	9.19	14.68	15.64	18.36	*		-	-
	PLACE1005287	15.1	8.12	14.31	5.25	6.44	6.19	5.01	4.78	3.02	*	*	-	-
35	PLACE1005299	10.04	6.09	8.79	4.5	5.75	7.77	4.03	4.98	7.58				
	PLACE1005305	8.97	7.38	9.77	4.47	3.45	4.18	3.14	3.99	3.81	**	**	-	-
	PLACE1005307	12.01	9.78	33.93	6.5	6.01	6.92	5.78	5.91	8.37				
	PLACE1005308	6.72	9.28	13.18	4.37	5.39	4.05	5.69	4.54	7.02				
	PLACE1005313	8.46	6.04	10.79	5.16	6.95	3.74	4.51	3	4	*		-	-
	PLACE1005320	9.29	12.54	14.31	7.32	9.29	5.14	4.92	4.65	5.56	**		-	-
40	PLACE1005327	31	25.4	35.29	16.09	17.4	11.88	9.82	14.36	14.83	**	**	-	-
	PLACE1005331	13.95	13.36	13.69	9.09	7.58	7.27	7.77	10.5	7.36	**	**	-	-
	PLACE1005335	11.38	7.64	13.28	5.94	7.87	3.65	8.18	25.07	9.78				
	PLACE1005336	29.59	23.88	23.59	14.99	18	12.79	23.63	28.14	27.34	*		-	-
	PLACE1005351	11.96	8.58	19.03	4.6	4.51	3.68	3.27	6.24	4.61	*		-	-
45	PLACE1005366	73.8	70.61	70.61	45.9	65.72	42.52	55.33	53.05	50.72	*	**	-	-
	PLACE1005373	9.8	6.9	15.51	3.87	3.73	2.69	2.9	3.58	2.99	*	*	-	-
	PLACE1005374	31.25	37.89	30.27	12.29	20.74	12.12	33.17	26.39	29.29	**		-	-
	PLACE1005383	9.15	7.91	6.27	5.38	5.79	4.82	3.77	5.77	7.02	*		-	-
	PLACE1005388	14.78	7.34	14.13	9.31	7.11	6.02	6.28	5.49	5.89				
	PLACE1005409	11.86	10.31	14.09	4.95	5.84	5.2	5.09	4.29	5.35	**	**	-	-
50	PLACE1005410	13.35	9.74	14.55	5.14	6.18	4.53	6.86	5.79	5.13	**	*	-	-
	PLACE1005426	10.65	4.8	11.31	4.23	3.51	3	2.46	6.49	1.78				
	PLACE1005431	8.27	7.3	10.2	3.04	3.82	2.32	3.59	3.79	5.31	**	*	-	-
	PLACE1005453	7.65	9.23	18.96	3.09	5.38	3.63	2.3	4.42	3.43				
	PLACE1005467	10.75	11.01	23.28	4.33	7.93	7.46	6.29	7.36	5.29				
	PLACE1005471	7.1	9.43	5.6	3.8	6.04	3.15	3.31	6.18	12.95				
55	PLACE1005476	29.52	27.39	29.6	15.57	12.74	15.37	14.04	14.17	16.62	**	**	-	-
	PLACE1005477	9.37	7.91	13.74	3.68	6.31	4.63	5	3.74	6.24	*	*	-	-
	PLACE1005480	7.1	8	8.36	5.61	4.81	4.45	4.92	2.94	2.27	**	**	-	-
	PLACE1005481	10.21	6.44	10.18	3.66	4.76	4.41	5.76	4.63	3.43	*	*	-	-
	PLACE1005494	9.19	9.94	10.69	3.34	4.05	3.41	4.87	3.69	4.02	**	**	-	-

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	PLACE1005495	11.05	11.48	9.86	5.01	5.38	4.26	3.3	3.97	3.58	**	**	-	-
	PLACE1005497	9.89	9.26	8.02	3.87	6.07	3.47	3.99	3.58	2.73	**	**	-	-
	PLACE1005499	23.46	21.47	29.66	8.65	19.6	10.05	16	19.54	21.59	*	*	-	-
5	PLACE1005502	9.18	6.48	6.37	3.45	3.87	4.29	4.21	4.81	4.94	*	*	-	-
	PLACE1005513	33.31	27.28	25.19	10.65	9.46	7.45	5.15	5.68	9.33	**	**	-	-
	PLACE1005515	11.7	9.47	10.48	3.66	3.88	4.7	6	4.7	5.35	**	**	-	-
	PLACE1005519	8.43	6.62	7.72	4.49	2.77	2.81	3.1	2.36	5.05	**	*	-	-
	PLACE1005526	8.8	10.4	11.16	2.78	4.21	2.23	3.21	3.51	3.18	**	**	-	-
10	PLACE1005528	26.91	22.55	23.87	12.32	10.17	9.81	19.08	11.09	17.43	**	*	-	-
	PLACE1005530	20.34	15.73	21.3	12.14	14.27	9.82	8.49	8.49	4.49	*	**	-	-
	PLACE1005536	18.12	14.92	18.89	3.17	4.7	3.13	5.93	4.22	4.19	**	**	-	-
	PLACE1005539	42.25	35.31	35.69	15.02	20.49	15.33	32.11	27.06	37.95	**	*	-	-
	PLACE1005543	35.86	20.69	14.02	11.25	7.4	11.67	9.96	8.84	11.47	*	*	-	-
15	PLACE1005544	4.98	5.73	4.38	2.31	2.15	3.58	3.94	2.43	3.09	*	*	-	-
	PLACE1005550	26.58	26.63	19.78	16.15	16.36	16.32	11.17	10.41	11.67	*	*	-	-
	PLACE1005554	23.49	15.23	16.27	7.02	8.22	4.71	11.04	7.45	10.06	*	*	-	-
	PLACE1005557	10.41	9.97	10.58	3.15	3.37	2.55	4.57	1.9	2.76	**	**	-	-
	PLACE1005563	10.87	11.46	9.72	4.64	6.41	6.88	7.08	5.98	5.9	**	**	-	-
	PLACE1005569	27.85	17.24	16.24	8.47	8.97	6.39	9.6	5.75	9.27	*	*	-	-
20	PLACE1005574	29.21	21.31	10.09	12.87	15.06	14.88	14.12	11.93	13.7	*	*	-	-
	PLACE1005584	80.18	66.17	69.3	73.19	89.15	68.42	53.92	40.06	44.96	*	*	-	-
	PLACE1005590	14.81	9.97	11.59	6.51	9.72	8.47	7.14	6.35	7.74	*	*	-	-
	PLACE1005595	23.18	18.25	21.16	12.01	10.55	9.94	19.07	11.17	15.91	**	*	-	-
	PLACE1005601	11.31	7.51	15.39	5.61	6.28	8.37	7.21	9.02	6.01	*	*	-	-
25	PLACE1005603	18.98	21.86	14.52	8.39	9.87	6.77	12.21	11.52	14.3	*	*	-	-
	PLACE1005604	8.92	8.05	5.89	5	4.08	4.67	3.54	2.41	2.72	*	**	-	-
	PLACE1005611	33.68	22.2	29.76	11.8	16.07	9.26	20.54	21.42	26.07	*	*	-	-
	PLACE1005622	30.69	27.64	23.31	11.83	18.8	12.91	22.33	27.88	24.08	*	*	-	-
	PLACE1005623	9.95	5.8	5.03	2.69	3.21	2.46	4.37	5.18	4.94	*	*	-	-
	PLACE1005630	8.17	9.56	9.09	4.43	7.2	3.43	4.75	3.89	4.7	*	**	-	-
	PLACE1005639	60.6	66.64	49.38	29.59	36.73	29.78	61.43	55.47	68.03	**	*	-	-
30	PLACE1005646	17.8	13.84	15.64	9.47	9.48	7.41	6.37	4.37	5.79	**	**	-	-
	PLACE1005647	13.8	11.09	12.51	5.66	5.78	5.71	6.46	4.42	5.24	**	**	-	-
	PLACE1005648	28.95	31.24	20.78	11.15	9.99	10.48	23.48	13.79	10.43	**	*	-	-
	PLACE1005653	16.03	13.03	11.9	5.52	4.03	5.5	8.65	5.02	7.5	**	*	-	-
	PLACE1005656	15.9	11.93	10.98	7.3	8.49	5.09	13.9	11.98	12.97	*	*	-	-
35	PLACE1005659	10.5	8.34	6.31	5.3	4.01	3.82	4.61	3.03	4.74	*	*	-	-
	PLACE1005660	12.82	10.45	9.32	4.78	5.95	3.56	5.23	2.26	5.04	**	**	-	-
	PLACE1005664	23.43	27.28	25.73	6.86	20.98	19.65	21.23	13.1	15.7	*	*	-	-
	PLACE1005666	12.43	11.64	13.67	7.79	10.52	6.99	11.1	12.9	13.47	*	*	-	-
	PLACE1005669	14.08	13.16	10.98	6.36	8.32	3.2	8.01	5.64	11	*	*	-	-
	PLACE1005682	22.57	20.73	18.81	7.71	18.55	7.1	12.18	6.07	11.14	**	**	-	-
40	PLACE1005698	7.18	6.68	8.02	7.04	5.88	4.02	4.11	5.29	4.18	**	*	-	-
	PLACE1005708	17.69	17.02	22.05	11.44	15.51	9.8	12.59	9.54	8.25	*	*	-	-
	PLACE1005725	9.73	11.27	13.97	7.09	8.31	6.27	4.4	6.46	6.4	*	*	-	-
	PLACE1005727	10.04	8.34	11.08	6.79	10.76	10.55	4.59	6.83	6.56	*	*	-	-
	PLACE1005730	13.44	12.68	11.77	6.36	7.19	8.47	5.04	7.92	8.47	**	**	-	-
	PLACE1005736	5.83	5.5	7.74	3.15	14.38	1.73	4.63	3.09	3.33	*	*	-	-
45	PLACE1005739	7.01	13.06	9.75	7.43	7.8	5.14	2.96	4.16	3.47	*	*	-	-
	PLACE1005745	8.04	6.14	6.43	4.26	4.82	5.89	4.13	2.63	4.39	*	*	-	-
	PLACE1005752	128.36	102.07	139.38	89.6	72.86	89.83	103.85	94.56	103.55	*	*	-	-
	PLACE1005755	13.46	9.22	14.54	4.95	6.97	3.84	5.58	5.65	3.87	*	*	-	-
	PLACE1005758	10.54	16.55	18.56	10.11	10.69	10.1	6.71	10.57	12.53	*	*	-	-
50	PLACE1005760	5.35	5.71	8.64	9.33	6.58	7.47	2.74	8.03	2.74	*	*	-	-
	PLACE1005763	18.11	17.1	15.35	9.45	11.68	9.73	7.29	9.29	9.82	**	**	-	-
	PLACE1005768	19.31	21.05	13.08	10.64	11.47	13.73	6.13	9.41	9.52	*	*	-	-
	PLACE1005771	24.23	23.82	24.14	14.86	21.27	9.53	16.05	19.49	20.2	*	*	-	-
	PLACE1005783	6.96	4.13	7.26	3.95	3.94	3.49	3.16	3.04	5.15	*	*	-	-
	PLACE1005799	43.95	40.56	57.56	28.57	25.86	15.96	30.85	26.7	32.18	*	*	-	-
55	PLACE1005802	18.73	15.75	12.71	10.65	14.22	15.85	21.48	13.68	14.38	*	*	-	-
	PLACE1005803	14.16	12.88	18.69	6.94	7.06	7.31	4.95	5.48	3.9	**	**	-	-
	PLACE1005804	16.14	16.06	21.67	10.66	8.62	11.66	4.49	6.03	5.63	*	*	-	-
	PLACE1005813	7.59	9.87	17.86	7.9	9.25	7.77	3.93	4.99	5.43	*	*	-	-
	PLACE1005815	17.11	19.5	18.51	7.94	18	6.6	9.57	8.13	8.77	**	*	-	-

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	PLACE1005828	21.32	17.86	17.66	18.38	28.15	11	8.41	12.77	17.42				
	PLACE1005833	19.04	15.23	17.55	13.68	13.86	12.16	11.62	13.97	12.02	*	*	-	-
5	PLACE1005834	31.23	40.41	42.31	19.53	15.14	12.45	22.97	22.37	27.18	**	*	-	-
	PLACE1005835	8.38	4.15	8.95	3.69	3.05	3.25	2.72	13.93	4.26			-	-
	PLACE1005836	6.34	4.47	7.11	2.85	2.55	2.1	1.11	4.41	2.67	*		-	-
	PLACE1005845	7.96	5.73	10.94	3.26	4.7	1.75	3.2	4.47	3.62	*	*	-	-
	PLACE1005850	7.12	8.63	11.96	4.89	4.51	3.39	2.96	4.97	6.83	*		-	-
10	PLACE1005851	49.92	45.46	36.8	28.76	36.45	21.25	9.27	9.06	15.36	**		-	-
	PLACE1005856	9.13	9.45	9.68	4.42	6.52	4.26	5.66	4.96	7.88	**	*	-	-
	PLACE1005875	19.11	12.96	14.66	10.98	11.89	11.34	7.25	9.07	9.2	*		-	-
	PLACE1005876	6.84	5.72	8.26	3.52	3.77	3.26	2.47	4.32	3	*	*	-	-
	PLACE1005878	6.18	5.12	8.15	3.65	4.35	1.9	2.1	7.39	4.67			-	-
	PLACE1005880	10.13	10.1	15.44	15.29	7.51	5.59	11.17	12.56	8.92			-	-
15	PLACE1005884	15.13	11.77	15.14	4.99	6.58	3.8	5.03	3.76	7.31	**	**	-	-
	PLACE1005890	14.12	12.54	15.15	4.55	6.88	4.96	4.84	4.65	10.58	**	*	-	-
	PLACE1005898	22.47	43.11	28.59	9.23	15.21	13.1	10.14	6.45	7.84	*		-	-
	PLACE1005913	11.08	12.76	18.39	6.03	9.77	5.43	8.89	7.87	5.55	*		-	-
	PLACE1005921	38.7	26.83	45.11	14.95	20.53	13.93	14.46	15.3	19.69	*	*	-	-
	PLACE1005923	35.55	28.6	35.14	8.99	9.9	10.33	7.55	9.92	9.16	**	**	-	-
20	PLACE1005925	9.28	6.52	9.69	4.22	6.79	3.62	4.36	4.97	3.85	*		-	-
	PLACE1005927	8.32	7.66	16.91	2.68	3.86	2.87	2.78	4.08	4.5			-	-
	PLACE1005932	17.99	14.04	15.58	5.88	10.67	7.85	11.54	8.65	8.07	*	*	-	-
	PLACE1005934	7.56	7.52	8.85	2.45	3.18	2.78	2.65	3.47	4.68	**	**	-	-
	PLACE1005936	8.91	7.48	10.96	2.6	4	2.78	2.64	2.57	2.62	**	**	-	-
25	PLACE1005939	14.59	14.49	13.88	5.4	8.87	6.89	7.24	6.14	6.85	**	**	-	-
	PLACE1005951	184.11	138.22	202.24	63.95	124.2	100.53	163.66	124.76	76.11	*		-	-
	PLACE1005953	4.12	2.98	5.89	2.81	3.65	1.89	1.88	2.73	1.8			-	-
	PLACE1005955	147.21	90.51	163.74	157.35	162.66	147.78	83.65	73.22	67.87			-	-
	PLACE1005966	21.58	17.57	18.88	12.22	12.03	11.48	18.97	16.95	19.33	**		-	-
	PLACE1005968	7.85	6.96	6.59	3.18	3.12	3.27	2.21	3.25	2.08	**	**	-	-
	PLACE1005975	6.58	6.62	8.7	2.59	2.3	2.44	2.13	2.22	2.24	**	**	-	-
30	PLACE1005990	13.31	13.53	10.46	5.9	8.19	4.45	5.05	6.3	5.08	*	*	-	-
	PLACE1005997	11.27	8.34	8.61	3.34	7.86	4.32	3.83	4.17	2.65	**		-	-
	PLACE1006002	7.2	9.3	8.62	4.13	3.01	2.96	3.03	3.74	3.08	**	**	-	-
	PLACE1006003	19.13	15.27	13.68	6.84	9.41	7.04	14.37	14.53	15.21	*		-	-
	PLACE1006011	14.53	12.13	13.55	5.17	8.37	6.39	12.92	13.32	12.8	**		-	-
35	PLACE1006017	17.66	15.33	13.64	7.8	6.85	7.26	3.44	3.4	5.68	**	**	-	-
	PLACE1006037	19.54	15.54	16.94	5.06	9.69	7.93	15.52	15.45	11.65	**		-	-
	PLACE1006040	21.73	18.19	20.02	8.22	10.07	7.19	9.12	8.1	8.15	**	**	-	-
	PLACE1006063	18.04	22.51	29.29	15.12	25.84	15.72	12.74	9.35	9.64	*		-	-
	PLACE1006071	24.45	22.47	19.59	9.7	14.01	7.6	15.44	10.65	16.68	**	*	-	-
	PLACE1006073	38.01	25.19	30.05	16.58	19.75	14.04	20.88	12.98	14.52	*	*	-	-
40	PLACE1006074	21.69	19.68	21.99	13.65	9.89	8.37	10.34	8.49	11.16	**	**	-	-
	PLACE1006076	6.98	23.32	28.44	3.28	24.98	6.58	8.27	11.5	12.4			-	-
	PLACE1006079	5.36	7.59	6.02	3.43	3.4	2.8	2.82	1.59	5.77	*		-	-
	PLACE1006093	17.29	20.55	15.5	11.28	11.48	8.91	6.51	3.34	7.24	*	**	-	-
	PLACE1006116	5.66	4.88	6.43	2.05	2.48	1.97	3.15	0.18	1.1	**	*	-	-
	PLACE1006119	9.01	6.23	8.79	2.16	3.34	2.75	3.83	1.45	4.03	**	*	-	-
45	PLACE1006129	11.8	19.99	13.49	6.74	8.91	6.37	6.93	6.6	9.52	*	*	-	-
	PLACE1006139	11.03	9.2	11	5.5	4.05	3.54	5.37	5.2	8.18	**	*	-	-
	PLACE1006143	34.11	32.02	23.21	13.95	17.22	16.38	5.72	10.56	8.1	*	**	-	-
	PLACE1006157	20.08	16.11	21.21	6.21	8	10.58	9.26	6.55	9.67	**	**	-	-
	PLACE1006159	22.74	19.17	16.53	5.42	7.39	5.18	11.09	3.24	9.93	**	*	-	-
	PLACE1006164	10.4	12.06	12.25	3.81	6.89	2.98	4.98	2.08	3.84	**	**	-	-
50	PLACE1006167	150.43	130.54	128	105.79	82.45	55.54	118.18	93.17	93.5	*	*	-	-
	PLACE1006170	12.04	9.61	11.88	3.48	3.73	3.68	2.75	2.82	3.04	**	**	-	-
	PLACE1006181	14.32	10.9	10.36	5.74	6.23	4.42	6.29	2.91	4.76	**	*	-	-
	PLACE1006187	23.98	21.9	19.46	7.26	12.29	5.92	18.37	17.04	21.06	**		-	-
	PLACE1006195	27.43	19.87	20.2	13.18	6.92	6.66	10.17	6.16	5.89	*	**	-	-
55	PLACE1006196	14.88	10.51	8.01	6.22	7.31	2.89	4.66	4.93	4.37	*		-	-
	PLACE1006197	25.54	27.48	23.66	11.8	19.78	16.24	17.7	18.29	21.21	*	*	-	-
	PLACE1006198	12.15	16.37	13.46	4.05	5.5	3.12	5.11	3.17	4.8	**	**	-	-
	PLACE1006205	8.36	7.44	9.1	4.62	5.35	3.49	12.53	5	7.53	**	*	-	-
	PLACE1006208	10.95	10.22	9.53	5.04	9.25	5.28	4.47	4.13	4.33	**		-	-

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	PLACE1006211	18.15	19.46	15.85	7.8	6.56	8.15	10.56	8.16	8.98	**	**	-	-
	PLACE1006219	29.22	24.03	22.82	13.99	7.2	9.8	23.91	20.19	22.03	**	*	-	-
	PLACE1006223	33.12	26.98	22.85	14.69	11.86	8.81	23.65	22.74	28.77	**	*	-	-
5	PLACE1006225	9.38	7.86	6.1	4.18	4.91	3.81	6.34	5.77	7.67	*	*	-	-
	PLACE1006296	23.05	26.18	25.58	13.5	14.02	10.31	12.5	8.37	11.47	**	**	-	-
	PLACE1006239	7.77	5.03	5	2.21	3.14	2.06	2.98	3.13	3.81	*	*	-	-
	PLACE1006245	11.97	10.97	10.73	4.72	5.26	4.25	5.6	4.62	4.52	**	**	-	-
	PLACE1006246	14.07	10.52	9.12	4.17	12.12	4.44	10.44	8.15	11.84	*	*	-	-
10	PLACE1006248	10.3	9.17	8.56	6.54	7.06	2.85	7.67	4.65	5.48	*	*	-	-
	PLACE1006262	19.08	26.43	25.66	10.77	26.8	17.9	14.07	10.91	15.08	*	*	-	-
	PLACE1006269	6.36	4.8	5.62	2.78	2.48	2.42	4.23	3.67	2.13	**	*	-	-
	PLACE1006275	7.84	6.83	8.11	7.79	9.46	8.46	5.82	11.38	4.94	*	*	-	-
	PLACE1006277	18.16	15.2	14.15	12.95	19.65	15.77	6.69	13.62	7.81	*	*	-	-
	PLACE1006288	23.16	25	24.73	14.26	21	15.27	15.12	19.66	20.01	*	*	-	-
15	PLACE1006290	3.79	4.35	4.22	1.07	3.07	1.54	0.76	2.83	1.89	*	*	-	-
	PLACE1006298	31.99	33.57	40.35	21.62	22.17	18.83	30.18	26.42	31.31	**	*	-	-
	PLACE1006311	24.06	25.54	26.15	17.19	20.35	18.67	6.49	6.41	12.35	**	**	-	-
	PLACE1006318	23.92	22.31	22.74	9.17	11.04	10.73	16.57	17.39	15.35	**	**	-	-
	PLACE1006325	10.97	6.18	13.93	5.64	6.43	6.48	6.34	4.38	3.68	*	*	-	-
20	PLACE1006331	322.49	249.29	312.14	284.34	344.95	317.78	261.41	376.24	167.86	*	*	-	-
	PLACE1006335	6.01	6.97	9.42	6.43	10.77	6.27	4.79	4.63	3.75	*	*	-	-
	PLACE1006357	23.6	23.65	28.41	15.45	19.92	11.71	10.11	13.97	13.07	*	**	-	-
	PLACE1006360	39.03	55.89	60.83	32.56	29.33	36.42	18.81	22.42	24.3	*	*	-	-
	PLACE1006364	4.49	3.79	4.52	5.2	5.32	3.04	3.31	4.72	3.85	*	*	-	-
	PLACE1006365	8.87	13.33	7.94	4.35	7.31	4.11	4.93	6.19	6.08	*	*	-	-
25	PLACE1006368	7.6	5	7.22	4.35	3.51	2.72	3.12	4.28	3.68	*	*	-	-
	PLACE1006371	12.84	8.89	13.13	6.85	5.51	3.89	5.93	6.19	7.36	*	*	-	-
	PLACE1006373	31.88	31.57	27.89	11.44	15.9	12.05	24.23	17.9	24.85	**	*	-	-
	PLACE1006382	15.81	18.11	17.64	20.83	24.97	21.9	28.68	49.67	48.66	*	*	+	+
	PLACE1006385	23.74	24.67	19.54	18.57	28.47	23.59	6.72	12.92	8.24	**	*	-	-
	PLACE1006391	7.09	8.24	10.32	5.76	7.9	5.35	7.26	7.31	6.16	*	*	-	-
30	PLACE1006412	14.35	15.98	15.55	14.85	16.87	8.6	8.42	8.73	11.54	**	*	-	-
	PLACE1006414	30.64	63.89	32.69	29.17	49.53	18.72	7.89	13.37	10.44	*	*	-	-
	PLACE1006419	23.86	16.38	19.21	8.34	10.82	5.22	6.84	8.36	7.76	*	**	-	-
	PLACE1006438	16.88	12.75	13.77	5.93	7.83	5.98	6.47	9.15	5.41	**	*	-	-
	PLACE1006443	7.62	8.28	7.5	4.32	3.07	4.42	2.72	3.77	2.68	**	**	-	-
	PLACE1006445	53.01	52.47	65.34	48.09	51.7	50.7	24.1	26.92	30.98	**	**	-	-
35	PLACE1006447	16.45	17.73	17.35	9.64	12.61	9.03	5.67	7.16	5.82	**	**	-	-
	PLACE1006466	5.01	5.76	10.4	3.6	5.26	3.03	3.62	2.47	3.82	*	*	-	-
	PLACE1006469	8.97	6.93	12.7	4.45	5.94	2.99	6.14	5.96	3.89	*	*	-	-
	PLACE1006470	14.91	13.1	13.03	5.44	14.24	9.05	12.65	15.12	16.52	*	*	-	-
	PLACE1006472	32.56	24.9	52.53	14.86	22.47	15.58	27.13	60.66	18.13	*	*	-	-
40	PLACE1006476	75.24	88.04	95	49.93	69.66	43.58	73.04	95.42	77.62	*	*	-	-
	PLACE1006482	19.52	14.87	22.77	7.46	8.75	5.8	9.29	24.88	15.09	**	*	-	-
	PLACE1006488	13.42	9.61	14.11	5.93	5.56	7.22	5.43	7.77	6	*	*	-	-
	PLACE1006492	53.41	60.91	65.09	29.78	38.14	28.4	41.31	52.42	43.57	**	*	-	-
	PLACE1006506	8.93	8.04	10.96	3.97	6.16	3.99	2.77	5.01	4.34	*	**	-	-
	PLACE1006515	6.57	6.17	10.41	2.69	4.8	3.13	3.49	3.57	2.51	*	*	-	-
45	PLACE1006516	7.77	7.4	8.18	2.65	6.76	3.8	4.8	4.81	1.69	*	*	-	-
	PLACE1006520	85.74	60.72	84.5	67.76	73.09	68.07	40.48	30.38	37.31	**	*	-	-
	PLACE1006521	5.4	3.13	7.19	3.67	3.58	2.13	2.56	2.69	1.53	*	*	-	-
	PLACE1006529	21.37	16.93	24.45	11.55	12.23	11.32	13.1	15.15	16.91	*	*	-	-
	PLACE1006531	8.98	4.63	8.46	3.15	2.87	3.1	2.57	4.69	2.69	*	*	-	-
	PLACE1006534	11.34	12.38	19.26	6.83	8.12	7.2	8.08	5.98	8.82	*	*	-	-
50	PLACE1006540	17.3	13.48	19.89	6	9.01	6.33	5.04	4.77	5.56	**	**	-	-
	PLACE1006549	57.43	76.29	59.13	33.67	55.25	39.07	49.85	36.47	56.34	*	*	-	-
	PLACE1006550	27.31	23.34	17.69	10.6	24.86	11.76	7.55	11.98	6.46	*	*	-	-
	PLACE1006552	41.43	35.42	38.21	18.37	17.9	12.42	28.67	34.48	34.92	**	*	-	-
	PLACE1006557	58.91	37.26	57.05	36.71	38.26	34.22	31.47	33.21	28.65	*	*	-	-
	PLACE1006563	12.53	9.16	14.73	7.21	10.95	7.06	5.43	4.33	7.28	*	*	-	-
55	PLACE1006579	8.16	5.5	6.78	3.56	3.74	3.1	2.74	1.94	3.28	*	**	-	-
	PLACE1006594	8.47	4.75	7.36	2.29	3.19	1.42	2.51	1.45	1.95	*	*	-	-
	PLACE1006598	14.33	13.22	15.98	9.86	13.18	9.6	7.97	4.5	6.78	**	*	-	-
	PLACE1006607	18.95	13.98	15.61	10.13	11.36	9.36	8.88	8.34	9.06	*	**	-	-

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	PLACE1006610	9.23	9.13	6.93	3.56	3.78	2.24	3.21	1.79	1.8	**	**	-	-
	PLACE1006615	5.13	4.58	7.74	3.64	4.24	3.19	3.42	3.13	4.2			-	-
5	PLACE1006617	10.84	9.51	10.64	5.44	6.44	4.54	8.05	7.55	8.94	**	*	-	-
	PLACE1006618	16.8	17.21	17.66	12.4	9.99	12.65	9.96	9.85	12.85	**	**	-	-
	PLACE1006626	9.9	9.38	11.8	4.89	3.64	3.15	3.8	3.9	3.22	**	**	-	-
	PLACE1006629	97.87	77.5	62.9	75.16	89.13	71.45	50.39	46.85	45	*	*	-	-
	PLACE1006637	20.62	30.53	27.31	15.03	24.3	12.77	12.77	11.41	9.09	**	*	-	-
	PLACE1006640	146.09	116.55	121.62	98.73	144.79	100.95	65.85	61.12	81.72	**	*	-	-
10	PLACE1006644	10.36	13.76	11.01	6.08	7.62	8.85	6.47	3.27	4.59	*	*	-	-
	PLACE1006657	9.47	8.7	8.11	3.37	3.88	4.59	4.46	4.41	6.15	**	**	-	-
	PLACE1006673	128.37	101.12	117.47	60.38	47.28	69.57	78.35	78.65	91.83	**	*	-	-
	PLACE1006678	13.14	7.54	6.57	3.78	6.24	6.14	3.95	3.22	3.7			-	-
	PLACE1006682	5.12	3.88	4.9	2.21	2.14	1.84	2.5	1.43	2.09	**	**	-	-
	PLACE1006684	8.48	6.37	7.5	1.9	2.47	2.03	3.67	2.97	2.03	**	**	-	-
15	PLACE1006698	24.65	21.3	17.88	6.94	8.35	11.27	7.31	3.9	5.72	**	**	-	-
	PLACE1006704	10.75	10.1	9.67	7.04	6.45	4.58	4.88	2.24	3.52	**	**	-	-
	PLACE1006708	6.82	6.62	4.54	1.43	4.58	2.49	4.44	1.95	2.6	*	*	-	-
	PLACE1006711	7.97	5.26	8.07	5.12	5.44	5.92	5.18	4.48	3.42			-	-
	PLACE1006714	19.78	16.32	14.11	6.39	7.42	10.52	4.46	5.02	4.69	*	**	-	-
20	PLACE1006716	21.34	19.47	16.01	5.39	7.72	5.97	12.01	9.74	13.28	**	*	-	-
	PLACE1006731	8.76	6.59	9.88	4.19	4.28	3.45	3.4	4.54	3.95	*	*	-	-
	PLACE1006754	12.83	10.26	11.39	6.83	5.2	6.24	8.13	4.13	6.6	**	*	-	-
	PLACE1006760	17.66	24.39	15.04	22.5	23.46	11.75	21.46	9.03	14.39			-	-
	PLACE1006779	14.53	14.99	8.23	6.82	4.21	3.38	5.07	3.29	2.38	*	*	-	-
	PLACE1006782	13.34	14.85	8.6	8.19	13.03	7.71	10.87	6.95	6.98			-	-
25	PLACE1006783	26.1	20.43	20.94	18.8	23.33	15.04	25.48	18.52	26.77			-	-
	PLACE1006786	16.5	11.01	11.97	10.81	6.14	7.77	7.76	8.87	8.16	*	*	-	-
	PLACE1006792	43	29.6	28.89	12.14	32.07	8.88	14.31	11.42	11.6	*	*	-	-
	PLACE1006795	6.46	5.54	6.42	3.27	4.53	2.37	5.98	1.9	3.55	*	*	-	-
	PLACE1006800	14.69	12.26	14.82	7.42	7.86	5.36	11.02	8.63	12.6	**	*	-	-
30	PLACE1006805	297.4	379.55	330.72	251.58	242.8	138.41	164.1	78.29	121.42	*	**	-	-
	PLACE1006809	17.57	15.02	14.01	6.89	5.54	5.55	12.59	5.67	9	**	*	-	-
	PLACE1006815	36.78	37.15	24.97	22.04	27.53	19.08	12.45	10.62	14.81	**	*	-	-
	PLACE1006819	8.55	8.96	7.82	3.54	3.27	1.58	3.56	2.07	3.34	**	**	-	-
	PLACE1006820	11.34	11.23	10.69	7.26	7.6	3.88	6.72	6.8	7.48	*	**	-	-
	PLACE1006826	11.68	10.21	8.37	4.26	6.11	3.55	4	5.42	6.14	*	*	-	-
35	PLACE1006829	8.66	7.12	6.95	4.95	4.5	3.35	3.73	4.63	3.79	*	**	-	-
	PLACE1006853	7.76	9.04	10.06	4.43	5.8	3.94	5.55	3.81	3.65	**	**	-	-
	PLACE1006860	13.3	14.13	11.82	7.29	7.57	5.64	7.39	5.43	7.17	**	**	-	-
	PLACE1006867	20.52	19.65	17.03	7.58	12.2	4.52	8.89	4.5	9.57	*	**	-	-
	PLACE1006875	6.86	5.29	3.98	1.69	3.65	1.95	4.64	3.37	3.97	*	*	-	-
	PLACE1006878	5.96	7.5	9.4	3.45	4.02	4.56	4.29	5.32	7.08	*	*	-	-
40	PLACE1006883	17.58	24.05	25.14	11.43	14.88	9.68	8.41	13.21	13.16	*	*	-	-
	PLACE1006898	34.11	35.72	38.43	15.89	26.64	17.27	29.81	38.71	32.24	*	*	-	-
	PLACE1006901	35.59	25.34	29.52	17.57	24.59	23.14	7.06	14.35	10.26	**	*	-	-
	PLACE1006904	283.91	237.86	265.1	210.53	264.05	203.01	176.62	324.88	215.9			-	-
	PLACE1006917	8.87	8.87	10.42	4.77	9.67	4.27	2.96	3.43	5.44	**	*	-	-
	PLACE1006932	13.9	19.05	15.16	17.43	14.76	12.47	12.23	11.92	6.34			-	-
45	PLACE1006935	5.15	5.68	5.5	4.25	5.6	3.94	4.66	3.59	4.94			-	-
	PLACE1006956	73	65.43	79.54	37.1	42.04	37.7	45.33	35.06	47.75	**	**	-	-
	PLACE1006958	14.71	17.1	17.16	7.75	10.57	5.67	10.62	14.42	12.92	**	*	-	-
	PLACE1006959	6.43	6.88	7.06	3.86	5.4	3.09	3.53	7.7	6.81	*	*	-	-
	PLACE1006961	11.78	13.88	26.99	6.58	7.47	6.43	7.89	10.93	8.94			-	-
	PLACE1006962	8.5	7.71	10.43	6.5	8.54	6.61	4.94	6	6.79	*	*	-	-
50	PLACE1006966	30.69	63.35	44.81	30.7	31	25.61	17.51	20.36	25.7			-	-
	PLACE1006973	9.85	10.88	9.97	5.88	6.1	5.13	5.32	5.52	6.47	**	**	-	-
	PLACE1006989	21.14	43.35	32.93	27.05	47.4	17.28	23.49	21.59	16.62			-	-
	PLACE1007001	14.41	12.66	17.15	10.97	5.54	6.74	6.74	7.87	8.22	*	**	-	-
	PLACE1007014	9.24	9.35	10.83	6.4	6.04	5.94	4.96	6.16	5.52	**	**	-	-
55	PLACE1007021	56.53	38.34	63.46	20.03	40.71	38.97	20.72	29.77	27.88	*	*	-	-
	PLACE1007026	65.54	56.8	77.56	57.55	60.7	57.93	57.5	56.64	67.29			-	-
	PLACE1007028	8.5	10.76	17.58	7.89	7.62	6.26	3.31	5.38	3.91	*	*	-	-
	PLACE1007038	7.96	7.89	13.66	4.19	6.33	3.79	2.05	3.52	4.03	*	*	-	-
	PLACE1007040	8.13	9.51	15.11	4.74	7.09	4.87	8.84	8.35	6.98			-	-

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	PLACE1007045	15.78	21.85	22.19	13.09	30.39	13.83	9.78	12.74	10.75	*	*	-	-
	PLACE1007048	19.3	14.44	24.23	9.41	10.57	11.83	9.91	12.06	15.93	*	*	-	-
	PLACE1007053	9.31	5.29	12.35	5.07	3.06	4.56	5.35	25.19	5.41	*	*	-	-
	PLACE1007068	8.67	4.77	10.34	5.02	4.28	3.54	2.63	5.02	2.74	*	**	-	-
5	PLACE1007070	18.55	13.15	15.29	11.03	10.78	10.43	6.96	7.21	5.68	*	*	-	-
	PLACE1007076	17.03	17.73	24.8	24.48	28.32	20.68	16.51	16.83	13.48	*	*	-	-
	PLACE1007077	7.35	10.92	12.26	4.54	5.11	3.6	6.43	5.8	5.66	*	*	-	-
	PLACE1007081	41.36	35.79	51.18	37.04	46.87	29.31	28.18	20.46	26.31	*	*	-	-
	PLACE1007082	14.74	14.27	12.93	7.51	10.12	5.83	13.51	10.86	10.42	*	*	-	-
10	PLACE1007092	9.52	6.79	8.77	4.99	5.23	4.04	4.42	5.84	7.46	*	*	-	-
	PLACE1007096	8.7	7.04	11.33	3.9	6.35	2.61	4.31	10.62	7.33	*	*	-	-
	PLACE1007097	5.03	2.47	6.96	1.99	2.48	1.11	1.28	4.01	1.45	*	*	-	-
	PLACE1007099	14.43	9.17	8.68	4.57	6.07	4.14	4.7	5.17	7.04	*	*	-	-
	PLACE1007105	9.93	9.89	19.72	4.22	5.46	3.96	5.83	6.27	9.12	*	*	-	-
15	PLACE1007108	7.87	5.2	13.72	3	3.64	1.32	1.96	5.82	6.69	*	**	-	-
	PLACE1007111	24.26	33.98	33.96	8.75	19.56	14.7	10.61	6.46	7.98	*	*	-	-
	PLACE1007112	13.01	15.69	10.39	7.41	17.53	7.08	9.51	4.37	5.03	*	*	-	-
	PLACE1007130	7.28	5.04	7.51	3.97	3.76	4.18	4.15	3.12	4.45	*	*	-	-
	PLACE1007132	11.01	5.03	12.54	6.14	8.23	7.16	4.79	4.84	3.32	*	*	-	-
	PLACE1007140	8.1	6.86	9.39	5.74	3.15	5.4	5.1	3.71	4.08	*	*	-	-
20	PLACE1007143	7.85	4.78	7.3	2.76	4.42	3.52	3.05	2.29	1.7	*	*	-	-
	PLACE1007169	21.25	20.42	20.37	9.68	16.47	8.01	13.15	12.99	9.63	*	**	-	-
	PLACE1007178	5.69	6.23	10.18	2.7	4.22	2.51	2.33	2.04	2.65	*	*	-	-
	PLACE1007180	9.72	11.86	11.22	5.23	6.85	7.11	6.69	5.59	16.1	**	*	-	-
	PLACE1007201	11.31	9.93	8.97	4.82	6.82	3.46	5.63	4.72	7.11	*	*	-	-
	PLACE1007202	14.96	8.83	16.56	5.53	5.66	4.16	5.42	6.71	5.73	*	*	-	-
25	PLACE1007226	110.77	93.69	99.41	39.5	91.72	72.21	82.39	66.08	68.98	*	*	-	-
	PLACE1007238	53.4	44.43	54.82	32.05	30.06	27.04	24.59	23.68	27.03	**	**	-	-
	PLACE1007239	22.01	21.57	16.94	9.88	9.77	7.42	7.13	6.76	5.92	**	**	-	-
	PLACE1007242	8.39	6.41	6.58	2.97	3.53	2.45	2.76	1.3	1.2	**	**	-	-
	PLACE1007243	51.6	47.43	46.65	38.48	53.48	36.76	30.03	24.3	28.99	*	*	-	-
30	PLACE1007247	13.13	15.22	14.84	6.24	10.32	8.42	5.62	3.59	3.12	*	*	-	-
	PLACE1007257	10	9.05	8.75	2.44	7.1	2.96	4.72	2.48	2.64	*	**	-	-
	PLACE1007274	7.6	6.25	7.77	4.39	3.79	3.63	3.01	2.85	2.82	**	**	-	-
	PLACE1007276	4.51	6.36	6.4	3.01	2.72	2.17	2.35	3.34	6.03	**	*	-	-
	PLACE1007282	6.97	4.05	5.61	2.64	2.11	3.66	3.82	3.22	3.39	*	*	-	-
	PLACE1007286	11.57	9.64	10.32	4.04	6.1	5.17	5.17	3.51	3.72	**	**	-	-
35	PLACE1007296	16.68	11.68	9.05	4.46	6.87	6.7	3.08	3.72	1.93	*	*	-	-
	PLACE1007301	14.64	13.62	12.24	3.61	5.07	2.97	5.09	2.86	3.16	**	**	-	-
	PLACE1007314	9.78	10.14	10.9	5.59	4.99	2.5	3.88	2.16	3.2	**	*	-	-
	PLACE1007317	8.02	7.14	6.45	3.78	5.35	2.25	2.6	5.13	4.46	*	*	-	-
	PLACE1007329	6.93	6.45	9.13	3.46	3.47	2.66	3.68	2.3	2.77	**	**	-	-
	PLACE1007338	57.3	54.81	50.58	25.62	27.62	24.63	49.58	43.5	58.48	**	*	-	-
40	PLACE1007342	41.9	26.92	32.51	26.5	30.16	25.56	24.13	20.5	25.41	*	*	-	-
	PLACE1007345	5.67	4.07	4.44	3.74	2.2	1.81	1.89	2.39	3.75	*	*	-	-
	PLACE1007346	20.5	15.07	16.51	8.68	6.27	3.82	4.58	3.48	4.29	**	**	-	-
	PLACE1007359	41.26	41.58	38.73	21.16	26.14	23.96	27.05	27.12	33.74	**	**	-	-
	PLACE1007367	8.65	8.31	7.96	1.51	3.49	1.31	3.83	1.42	3.11	**	**	-	-
	PLACE1007375	12.55	10.83	9.7	1.39	5.63	1.68	2.54	2.85	2.14	**	**	-	-
45	PLACE1007377	6.98	4.2	6.44	4.26	4.62	2.93	3.59	4.11	3.58	*	*	-	-
	PLACE1007386	12.07	10.56	14.15	4.68	4.55	5.21	6.12	7.62	8.27	**	*	-	-
	PLACE1007392	24.21	18.68	19.13	13.92	12.02	7.51	28.83	13.55	12.42	*	*	-	-
	PLACE1007402	16.76	19.32	15.87	8.17	8.78	7.34	11.49	10.03	10.79	**	**	-	-
	PLACE1007409	9.51	9.82	11.04	5.11	5.51	7.23	4.08	2.01	3.77	*	*	-	-
50	PLACE1007416	22.54	28.88	22.62	18.84	13.11	6.16	9.22	5.36	7.49	*	*	-	-
	PLACE1007420	14.67	16.22	16.74	8.73	9.19	6.79	10.55	5.47	7.91	**	**	-	-
	PLACE1007431	28.03	25.88	21.18	15.73	16.55	11.3	26.89	15.55	26.27	*	*	-	-
	PLACE1007450	6.82	6.06	4.68	4.06	4.16	1.71	5.65	4.38	4.35	*	*	-	-
	PLACE1007452	14.4	7.71	4.99	5.04	6.12	1.89	4.23	8.8	6.06	*	*	-	-
	PLACE1007454	49.36	46.08	36.43	21.1	38.54	20.65	11.86	16.68	14.49	**	*	-	-
55	PLACE1007460	11.52	10.93	12.45	8.16	8.35	4.82	9.8	9.12	12.38	*	*	-	-
	PLACE1007478	12.6	13.38	10.86	4.17	8.16	7.05	7.4	4.59	6.97	*	*	-	-
	PLACE1007484	10.71	6.45	6.68	3.65	4	2.5	4.9	2.97	5.47	*	*	-	-
	PLACE1007488	14.59	14.99	17.16	7.24	4.48	5.55	6.08	3.67	8.77	**	**	-	-

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Table 484

	PLACE1007507	16.63	14.22	12.4	6.49	10.52	5.63	19.33	11.77	17.21	*	-	-
	PLACE1007511	13.25	11.24	10.12	3.93	3.98	2.6	3.01	2.43	4.23	**	**	-
	PLACE1007513	4.53	2.47	3.69	3.11	1.64	1.97	3.06	2.87	2.04	*	-	-
5	PLACE1007524	49.4	41.73	37.58	21.38	27.05	16.04	48.44	42.69	43.18	*	-	-
	PLACE1007525	7.48	5.19	4.73	2.29	4.06	1.12	3.74	3.09	4.25	*	*	-
	PLACE1007537	8.42	7.3	9.61	4.91	5.72	3.83	6.57	5.7	5.93	*	*	-
	PLACE1007544	5.67	4.7	5.81	1.28	3.36	2.37	4.39	1.96	2.74	*	*	-
	PLACE1007547	15.52	13.81	13.32	8.64	13.2	6.38	11.36	9.38	8.52	*	-	-
	PLACE1007557	22.7	26.33	16.93	8.14	13.6	7.63	24.98	15.24	20.74	*	-	-
10	PLACE1007560	25.9	29.34	29.57	9.23	13.41	19.28	21.02	29.63	20.17	*	-	-
	PLACE1007565	3.88	2.26	3.15	1.89	4.77	2.57	1.98	2.22	2.43	*	-	-
	PLACE1007580	4.59	3.09	5.83	2.2	6.97	1.42	1.87	5.45	1.54	*	-	-
	PLACE1007583	3.85	2.11	3.18	1.64	4.14	4.12	2.02	2.49	2.5	*	-	-
	PLACE1007591	5.53	6.61	10.65	2.9	4.26	2.95	4.34	4.96	5.37	*	-	-
15	PLACE1007598	9.38	9.28	9	2.96	15.1	3.88	2.92	7.29	5.52	*	-	-
	PLACE1007610	3.93	7.09	11.32	4.32	11.34	3.52	4.35	8.81	6.31	*	-	-
	PLACE1007618	4.85	4.13	5.18	3.66	4.39	5.01	3.62	3.16	4.04	*	-	-
	PLACE1007621	20.28	8.69	15.56	6.24	12.9	7.98	10.43	10.06	8.81	*	-	-
	PLACE1007626	35.43	28.05	45.42	25.74	50.46	26.54	38.37	49.51	35.74	*	-	-
20	PLACE1007632	8.18	6.61	8.24	5.02	13.18	12.74	5.22	7.37	5.53	*	-	-
	PLACE1007635	17.84	21.72	22.91	16.26	21.82	12.51	7.83	15.31	12.34	*	-	-
	PLACE1007645	29.46	44.32	50.79	23.79	28.69	29.97	18.24	19.23	26.32	*	-	-
	PLACE1007649	5.43	7.86	6.71	4.51	9.04	3.18	4.73	2.18	2.74	*	-	-
	PLACE1007659	23.48	33.01	29.15	18.02	23.66	14.9	25	27.47	23.31	*	-	-
	PLACE1007669	17.27	10.25	11.99	6.18	6.01	5.07	11.02	11.92	11.97	*	-	-
25	PLACE1007677	15.06	16.35	15.01	8.53	7.7	12.44	11.15	10.52	8.69	*	**	-
	PLACE1007688	30.37	21.3	31.84	9.3	9.6	6.97	5.43	7.59	4.3	**	**	-
	PLACE1007690	15.29	14.9	13.94	8.07	9.45	10.99	5.55	6.43	7.69	**	**	-
	PLACE1007697	7.22	8.07	8.65	7.42	10.69	12.34	4.08	7.67	5.36	*	-	-
	PLACE1007702	9.68	16.27	14.18	8.71	12.06	12.61	6.79	7.15	7.48	*	-	-
	PLACE1007706	14.91	16.84	14.3	10.72	14.81	6.93	5.13	7.31	8.61	**	-	-
30	PLACE1007725	15.22	10.08	11.32	8.01	8.72	6.5	4.92	7.04	8.09	*	-	-
	PLACE1007729	9.62	8.04	8.37	6.72	6.7	9.05	5.49	8.22	6.25	*	-	-
	PLACE1007730	14.54	9.51	13.82	11.08	11.03	10.92	7.95	12.03	8.17	*	-	-
	PLACE1007737	26.23	17.29	21.46	12.32	15.98	9.58	13.89	16.95	16.37	*	-	-
	PLACE1007743	15.62	16.04	17.86	8.71	10.59	7.11	6.26	11.61	4.77	**	*	-
35	PLACE1007746	42.92	48.93	37.39	28.78	37.1	35.26	16.78	10.7	15.4	**	-	-
	PLACE1007753	14.39	18.43	15.85	13.55	30.64	24.37	6.15	10.27	7.82	**	-	-
	PLACE1007769	10.21	11.59	12.77	11.76	15.29	7.33	6.11	7.79	6.57	**	-	-
	PLACE1007780	5.74	2.24	6.02	2.59	3.98	3.4	2.92	4.75	4.26	*	-	-
	PLACE1007791	7.33	7.57	11.32	6.64	9.26	5.56	5.87	21.8	5.42	*	-	-
	PLACE1007807	10.4	6.68	8.59	5.19	10.28	4.84	5.47	15.67	6.17	*	-	-
40	PLACE1007810	21.71	5.64	13.76	5.45	11.67	20.68	5.72	5.81	5.21	*	*	-
	PLACE1007814	23.92	18.73	27.74	15.47	17.03	13.06	6.08	14.46	7.51	*	-	-
	PLACE1007828	9.64	11.73	14.79	8.65	13.95	8.98	3.79	6.99	9.71	*	-	-
	PLACE1007829	21.85	26.65	22.58	10.61	17.88	12.23	16.05	20.8	14.7	*	-	-
	PLACE1007841	12.3	14.26	16.38	8.52	14.37	8.97	13.64	10.06	9.74	*	-	-
	PLACE1007842	7.29	10.66	10.16	4.04	8.15	4.63	12.33	6.69	8.73	*	-	-
45	PLACE1007843	8.16	7.8	8.23	4.71	8.29	4.31	4.49	6.71	2.94	*	-	-
	PLACE1007845	14.45	11.07	14.52	8.03	11	7.42	8.69	6.18	6.07	*	-	-
	PLACE1007846	9.52	9.87	9.08	6.82	5.35	6.86	5.9	8.42	7.28	**	*	-
	PLACE1007848	10.96	7.82	17.21	7.21	6.58	4.31	3.05	6.37	4.05	*	-	-
	PLACE1007852	38.45	42.72	20.94	14.02	16.83	14.13	8.86	9.78	9.37	*	*	-
	PLACE1007858	19.55	23.44	22.4	13.38	19.15	12.06	12.86	10.77	11.27	*	**	-
50	PLACE1007866	106.06	120.7	80.75	100.84	136.45	101.33	115.22	114.23	135.63	**	*	-
	PLACE1007871	46.64	38.13	36.79	13.91	18.93	11.35	19.19	30.79	21.75	*	-	-
	PLACE1007877	11.11	8.45	11.03	7.02	8.84	8.93	6.39	7.32	5.13	*	-	-
	PLACE1007878	37.18	35.47	41.1	20.44	30.52	24.13	17.29	22.96	22.69	*	**	-
	PLACE1007881	7.08	8.99	9.43	6.21	6.72	5.42	3.38	3.24	2.37	*	-	-
	PLACE1007885	13.54	9.97	15.34	8.52	12.53	23.99	7.37	7.86	5.04	*	-	-
55	PLACE1007897	9.52	10.47	10.76	6.15	8.22	8.75	3.33	3.79	2.67	*	**	-
	PLACE1007908	27.14	31.91	21.03	11.57	16.17	12.14	8.02	9.92	9.32	*	**	-
	PLACE1007922	13.27	17.29	11.92	8.56	15.72	12.01	8.76	6.61	6.69	*	-	-
	PLACE1007946	8.9	7.88	9.69	3.7	5.72	2.73	4.49	7.73	5.93	**	-	-

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Table 485

	PLACE1007950	123	99.57	90.18	75	73.07	58.93	91.95	114.45	65.58	*	-	-
	PLACE1007954	8.61	7.27	7.95	5.58	7.49	5.54	3.77	4.03	2.97	**	-	-
	PLACE1007955	17.64	15.71	13.66	11.51	9.3	9.77	6.99	7.04	4.12	*	**	-
5	PLACE1007956	11.86	9.09	7.66	6.57	9.25	6.9	4.06	4.11	3.44	*	-	-
	PLACE1007958	9.03	7.99	9.04	2.65	4.9	3.85	2.65	3.75	2.07	**	**	-
	PLACE1007965	15.3	16.37	14.75	7.93	11.66	10.38	7.23	6.65	5.87	*	**	-
	PLACE1007969	24.54	27.08	14.83	16.49	16.9	27.64	8.5	10.51	6.83	*	-	-
	PLACE1007971	14.86	11.23	10.56	4.6	5.77	4.48	5.47	4.42	6.63	**	**	-
10	PLACE1007990	13.72	7.91	11.82	6.44	6.58	7.05	6.02	6.86	7.23			
	PLACE1008000	8.41	4.96	5.71	4.66	6.7	5.87	3.52	3.67	3.05			
	PLACE1008002	8.38	10.22	5.77	6.22	6.73	3.91	3.28	5.34	3.3	*	-	-
	PLACE1008037	7.47	6.35	4.25	2.21	4.95	4.35	2.35	1.88	2.58	*	-	-
	PLACE1008044	23.79	15.95	12.5	7.05	19.86	9.73	6.75	10	6.08			
	PLACE1008045	19.99	21.06	9.24	5.88	14.67	9.04	6.52	7.55	2.12			
15	PLACE1008080	15.75	26.6	10.27	8.38	25.41	7.91	16.05	14.95	13.99			
	PLACE1008092	7.67	5.27	5.41	3.04	5.53	3.46	4.86	3.3	3.17			
	PLACE1008095	16.14	13.84	10.97	4.61	15.55	7.49	3.99	9.83	5.13	*	-	-
	PLACE1008105	10.75	13.42	9.63	5.46	13.95	7.7	10.03	7.96	6.35			
	PLACE1008107	6.1	7.51	5.49	4.1	6.68	4.81	2.94	3.48	3.2	**	-	-
20	PLACE1008111	12.94	8.4	7.21	4.85	8.37	6.82	4.56	1.47	2.41	*	-	-
	PLACE1008113	48.12	32.36	36.95	30.18	28.53	18.75	11.39	9.55	15.2	**	-	-
	PLACE1008122	12.52	11.61	10.25	6.59	8.27	7	4.17	3.46	4.27	**	**	-
	PLACE1008129	12.19	11.22	9.29	6.85	14.96	11.14	8.9	8.46	6.51			
	PLACE1008132	21.17	14.41	14.91	9.14	12.76	11.94	8.42	8.33	8.23	*	-	-
	PLACE1008137	10.44	6.69	4.43	4.58	5.26	3.39	2.11	5.99	2.53			
25	PLACE1008174	12.98	8.11	5.85	5.98	7.01	8.19	6.41	5.88	5.58			
	PLACE1008177	5.92	6.91	4.83	3.39	4.55	3.28	3.39	1.53	3.61	*	*	-
	PLACE1008181	12.18	13.31	12.04	4.81	8.68	5.04	4.65	2.16	4.62	**	**	-
	PLACE1008195	13.39	9.3	9.62	7.44	7.76	6.35	5.1	3.44	5.91	*	-	-
	PLACE1008198	12.57	11.23	9.83	6.75	6.36	4.49	7.75	4.45	5.55	**	*	-
	PLACE1008201	10.88	12.64	8.33	6.13	9.66	7.65	6.3	5.05	9.18			
30	PLACE1008209	10.96	9.72	8.1	4.34	4.16	5.71	10.15	7.4	9.7	**	-	-
	PLACE1008226	27.87	17.88	18.73	12.29	14.5	8.3	21.53	17.31	27.74			
	PLACE1008227	19.93	14.99	13.17	9.05	11.55	7.15	13.25	11.51	13.73	*	-	-
	PLACE1008231	7.21	4.7	4.12	4.59	4.49	3.26	5.49	4.08	3.39			
	PLACE1008238	12.79	18.51	15.04	5.47	8.57	11.49	6.6	7.97	4.88	*	**	-
	PLACE1008244	10.53	9.75	8.28	4.31	8.05	4.21	4.37	5.37	5.5	*	**	-
35	PLACE1008249	15.98	17.02	8.54	6.34	10.36	6.43	17.75	4.65	8.03			
	PLACE1008266	102.69	124.96	102.56	88.83	113.4	78.29	73.83	64.62	80.68	*	-	-
	PLACE1008273	14.29	12.39	14.99	6.95	10.06	11.71	9.42	8.24	5.42	*	-	-
	PLACE1008275	5.26	4.99	6.79	3.64	10.8	3.9	3.08	3.54	1.54	*	-	-
	PLACE1008280	6.85	6.62	6.82	4.72	8.46	4.99	3.58	6.79	2.88			
	PLACE1008282	12.89	9.41	16.7	11.11	18.66	13.55	5.47	11.9	7.88			
40	PLACE1008297	12.14	13.11	10.26	7.3	9.97	7.71	3.51	6.91	7.44	*	*	-
	PLACE1008303	11.47	15.79	13.39	11.12	14.28	7.92	5.84	6.87	4.96	**	-	-
	PLACE1008309	4.41	7.26	5.38	6.98	9.29	6.05	3.56	4.2	4.65			
	PLACE1008315	19.59	15.1	15.12	9.86	9.1	7.96	7.41	8.94	11.54	**	*	-
	PLACE1008329	9.22	7.92	9.32	5.09	12.42	9.18	10.32	5.48	5.2			
45	PLACE1008330	11.04	9.94	11.21	6.66	7.9	5.74	7.19	13.56	9.01	**	-	-
	PLACE1008331	9	15.63	14.68	4.1	11.97	13.67	4.88	7.64	5.55	*	-	-
	PLACE1008351	12.84	22	18.28	7.61	13.2	12.68	4.26	8.16	3.26	*	-	-
	PLACE1008356	13.82	13.87	16.44	11.31	18.42	14.21	4.74	8.97	9.76	*	-	-
	PLACE1008359	10.61	8.67	5.76	4.5	6.41	4.58	3.38	3.42	3.83	*	-	-
	PLACE1008368	15.16	18.55	18.33	11.79	13.53	6.82	4.87	5.65	5.64	**	-	-
50	PLACE1008369	3.81	2.08	4.52	1.83	1.71	1.5	2.12	2.77	3.86			
	PLACE1008392	11.15	8.41	9.64	4.52	7.73	5.42	7.63	11.47	6.48	*	-	-
	PLACE1008394	11.83	9.98	11.91	7.27	9.44	5.81	12.55	9.98	4.42	*	-	-
	PLACE1008398	23.83	19.35	38.34	11.94	10.53	17.6	18.05	34.01	14.62			
	PLACE1008401	9.05	11.72	16.92	8.36	9.24	6.49	5.59	6.98	7.72			
55	PLACE1008402	8.61	13.91	16.2	7.29	15.86	9.77	4.08	3.77	5.17	*	-	-
	PLACE1008409	93.35	102.54	109	58.1	65.02	51.5	64.76	63.76	63.34	**	**	-
	PLACE1008409	9.15	10.93	10.45	7.65	10.56	6.32	5.13	6.5	6.16	**	-	-
	PLACE1008420	4.6	3.84	4.48	2.08	3.3	3.48	3.03	3.37	1.89	*	-	-
	PLACE1008424	8.77	7.89	8.59	4.05	4.03	4.43	4.27	11.48	5.37	**	-	-

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Table 486

	PLACE1008426	9.02	4.49	7.91	3	6.94	4.35	2.2	4.69	5.02				
	PLACE1008429	6.72	4.48	8.18	2.61	5.16	2.94	4.14	3.81	3.51				
	PLACE1008430	14.21	10.67	13.56	6.18	13.27	13.78	7.02	13.13	6.7				
5	PLACE1008437	10.05	12.15	13.23	7.3	7.15	7.37	5.37	12.87	6.84	**	-	-	
	PLACE1008453	9.93	7.46	12.22	2.24	6.5	5.48	4.46	4.26	3.11	*	*	-	
	PLACE1008454	21.6	22.78	23.98	10.1	17.4	10.34	15.68	15.08	11.82	*	**	-	
	PLACE1008455	34.62	30.32	25.55	12.02	19.33	14.29	16.61	22	23.57	*	*	-	
	PLACE1008457	11.67	8.98	10.52	6.51	8.83	5.84	9.41	9.29	9.88	*	*	-	
10	PLACE1008465	7.78	1.83	9.65	2.4	6.54	3.49	3.66	7.05	5.33				
	PLACE1008469	9.74	7.14	10.33	5.36	5.23	4.43	4.05	9.23	7.36	*	-	-	
	PLACE1008488	7.69	9.06	16.27	2.87	27.47	11.79	3.3	10.09	3.95				
	PLACE1008519	13.67	13.58	16.65	12.54	13.83	10.17	7.48	12.69	9.26				
	PLACE1008524	16.01	17.28	16.34	7.24	7.92	7.96	6.91	6.21	5.65	**	**	-	
	PLACE1008531	10.83	9.9	10.84	3.6	7.89	4.88	5.5	5.84	4.3	*	**	-	
15	PLACE1008532	31.22	27.65	29.16	13.43	17.17	10.64	20	23.65	23.08	**	**	-	
	PLACE1008533	16.83	14.02	15.02	5.15	9.56	6.45	8.04	10.1	5.87	**	**	-	
	PLACE1008542	11.05	6.89	12.38	7.62	8.01	5.5	3.52	4.43	4.89	*	-	-	
	PLACE1008549	8.08	8.32	6.56	2.76	4.31	2.64	3.19	4.98	1.09	**	*	-	
	PLACE1008560	9.22	6.82	8.11	4.41	4.7	3.86	2.93	3	1.98	**	**	-	
20	PLACE1008567	12.46	12.8	11.19	3	4.87	3.75	6.88	4.77	3.6	**	**	-	
	PLACE1008568	11.23	14.36	12.98	7.02	10.07	9.2	4.7	4.88	4.71	*	**	-	
	PLACE1008569	26.76	24.83	18.12	14.19	21.2	18.33	7.27	6.81	8.32	**	-	-	
	PLACE1008584	12.08	11.9	8.94	4.22	7.86	8.69	3.89	8.17	12.55				
	PLACE1008585	31.41	26.84	21.37	12.16	16.5	14.29	13.28	12.03	8.95	*	**	-	
	PLACE1008603	88.44	58.86	85.85	77.22	107.17	81.02	46.69	50.43	38.76	*	-	-	
25	PLACE1008621	8.51	5.24	9.31	3.02	5.85	4.1	5.45	4.49	4.31				
	PLACE1008625	5.93	4.92	6	3.54	3.65	3.16	1.59	3.39	1.97	**	**	-	
	PLACE1008626	7.17	7.14	8.41	4.47	6	4.22	1.34	2.51	2.04	*	**	-	
	PLACE1008627	16.63	17.04	15.47	5.85	10.41	6.49	6.26	6.1	3.78	**	**	-	
	PLACE1008629	17.85	11.92	13.81	7.55	20.73	20.07	19.18	21.96	10.11				
	PLACE1008630	10.34	9.61	9.25	3.39	5.31	3.93	4.34	4.76	3.98	**	**	-	
30	PLACE1008643	13.74	8.06	11.06	4.37	9.48	6.43	6.52	10.46	6.53				
	PLACE1008650	8.08	8.41	6.76	5.59	6.65	6.55	3.49	3.07	2.46	**	-	-	
	PLACE1008657	20.07	16.69	13.65	10.15	11.39	11.63	13.41	12.65	11.83	*	-	-	
	PLACE1008664	16.27	13.14	9.24	7.33	8.26	11.12	3.83	4.48	3.67	*	-	-	
	PLACE1008693	19.24	12.55	11.48	5.9	7.48	8.22	10.23	10.76	7.26	*	-	-	
35	PLACE1008696	15.27	18.92	13.52	8.56	14.35	6	9.09	6.63	6.3	**	-	-	
	PLACE1008715	12.07	13.35	10.97	4.79	8.42	4.36	3.79	3.86	5.13	*	**	-	
	PLACE1008716	9.95	8.16	6.63	2.27	4.4	4.51	4.19	6.11	4.54	*	*	-	
	PLACE1008722	23.06	17.9	16.82	6.63	6.45	7.4	2.92	4.69	5.05	**	**	-	
	PLACE1008738	22.32	18.29	21.17	13.47	19.87	5.51	15.63	19.57	23.28				
	PLACE1008742	84.96	67.74	75.79	53.3	53.65	55.26	60.09	57.16	55.95	*	*	-	
40	PLACE1008744	16.51	21.18	12.37	7.32	20.16	7.33	4.32	8.49	4.3	*	-	-	
	PLACE1008748	11.7	8.68	7.89	3.6	3.19	1.95	5.93	2.92	4.46	**	*	-	
	PLACE1008757	11.86	10.89	13.3	7.9	13.9	4.82	5.45	7.52	5.79	**	-	-	
	PLACE1008766	12.58	9.83	17.07	7.19	5.62	5.22	3.78	3.59	4.47	*	*	-	
	PLACE1008785	10.19	7.64	9.9	4.61	6.56	4.55	5.8	6.94	7.6	*	-	-	
	PLACE1008790	13.83	10.34	7.69	5.61	9.25	7.49	3.5	9.44	5.2				
45	PLACE1008798	38.55	17.87	28.15	8.39	18.4	13.81	20.54	7.92	18.2				
	PLACE1008807	7.39	8.08	6.82	3.5	7.58	4.57	3.41	3.26	4.62	**	-	-	
	PLACE1008808	14.69	14.79	11.52	7.99	7.57	5.08	6.28	4.51	3.87	**	**	-	
	PLACE1008813	11.75	10.29	9.69	7.89	7.9	5.45	5.57	3.03	5.81	*	**	-	
	PLACE1008836	10.67	11.89	10.55	6.13	6.4	5.79	6.93	5.51	7.49	**	**	-	
50	PLACE1008851	17.38	11.13	11	56.43	9.1	6.6	16.91	8.29	14.77				
	PLACE1008854	6.2	6.11	5.28	5.3	4.42	2.5	6.46	5.33	5.1				
	PLACE1008864	19.27	13.51	11	10.42	10.96	6.46	14.43	10.21	14.23				
	PLACE1008867	23.06	15	11.22	6.2	9.84	4.86	5.54	7.61	6.44	*	-	-	
	PLACE1008876	175.15	214.21	204.76	126.27	307.85	120.09	159.59	163.82	275.73				
	PLACE1008887	10.24	8.9	12.49	4.83	6.78	7.78	5.17	4.7	6.53	*	*	-	
55	PLACE1008902	13.44	7.31	7.6	4.55	6.21	3.19	5.49	3.64	7.36				
	PLACE1008911	20.57	23.29	15.12	14.15	10.76	7.02	9.39	4.72	9.35	*	*	-	
	PLACE1008917	7.8	5.68	7.21	2.11	3.42	3.23	3.5	4.03	3.26	**	**	-	
	PLACE1008920	3.68	3.98	2.25	1.85	2.38	2.78	2.45	2.52	1.03				
	PLACE1008925	6.03	2.49	3.19	2.51	4.89	2.3	3.22	3.16	2.76				

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	PLACE1008930	19.58	15.04	12.13	4.18	13.75	5.17	6.22	5.55	4.1	*	-
	PLACE1008934	16.24	5.52	7.38	4.49	6.52	4.37	6.49	7.37	5.19		
5	PLACE1008941	7.73	6.12	5.84	2.96	5.21	1.59	3.04	3.68	3.45	**	-
	PLACE1008947	14.65	13.48	10.43	5.14	6.75	4.89	11.51	10.32	9.84	**	-
	PLACE1008984	13.25	12.98	9.34	5.45	4.62	4.47	6.01	1.98	3.15	**	-
	PLACE1008985	7.07	4.44	3.91	3.08	5.06	1.59	3.53	4.2	7.06	*	-
	PLACE1008994	3.13	3.32	2.46	1.43	1.88	1.44	1.4	0.58	1.95	**	-
10	PLACE1009020	10.8	10.64	11.79	9.97	10.93	10.07	6.16	7.97	6.48	**	-
	PLACE1009027	3.76	1.41	3.27	1.39	2.64	1.03	1.54	3.8	0.71		-
	PLACE1009039	4.77	3.08	3.94	1.85	3.67	1.57	1.09	2.8	1.86	*	-
	PLACE1009045	8.82	6.04	9.52	3.29	4.82	2.76	2.8	7.24	2.61	*	-
	PLACE1009048	2.06	2.51	4.63	1.04	3.38	1.38	0.62	1.42	2.18		-
	PLACE1009050	3.79	3.3	4.62	1.78	8.12	1.71	2.85	3.16	1.84		-
15	PLACE1009060	19.41	22.53	16.93	15.31	14.46	12.87	9.32	9.93	14.15	*	-
	PLACE1009067	9.68	7.46	10.13	4.56	10.58	6.42	9.09	6.46	12.36		-
	PLACE1009071	20.58	20.38	20.82	12.02	12.73	10.86	11.69	13.76	13.78	**	-
	PLACE1009090	9.2	7.98	10.33	4.26	8.7	11	5.63	8.05	9.63		-
	PLACE1009091	83.22	75.58	81.93	64.69	72.29	69.99	50.11	57.74	52.35	*	-
	PLACE1009094	10.97	9.99	9.32	7.26	14.47	8.52	5.42	12.88	9.03		-
20	PLACE1009099	8.3	10.72	9.62	5.36	7.81	7.04	3.55	4.21	4.97	*	-
	PLACE1009110	7.1	4.33	5.05	4.77	6.82	3.04	3.19	5.04	4.48		-
	PLACE1009111	4.96	7.16	3.67	5.5	7.31	3.03	4.35	3.44	4.4		-
	PLACE1009113	16.47	13.6	10.85	8.16	11.25	17.03	7.41	8	12.76		-
	PLACE1009130	13.26	8.46	18.05	9.61	8.47	7.77	7.71	8.47	5.51	*	-
	PLACE1009150	9.24	9.08	10.56	5.69	8.31	5.53	5.87	7.76	4.55	*	-
25	PLACE1009155	15.03	18.94	19.94	9.19	13.17	10.27	14.29	28.01	20.9	*	-
	PLACE1009158	11.31	7.28	10.08	9.16	8.65	7.93	4.47	5.84	5.53	*	-
	PLACE1009166	6.72	5.63	9.02	5.97	6.75	3.86	4.53	5.03	5.29		-
	PLACE1009172	12.12	10.58	13.44	7.25	11.43	5.16	4.32	7.13	6.22	**	-
	PLACE1009174	15.11	18.12	12.65	13.74	20.86	11.26	7.87	11.41	11.21		-
30	PLACE1009183	26.21	21.05	18.45	14.71	13.12	9.63	13.01	10.13	17.14	*	-
	PLACE1009186	16.33	12.69	14.24	9.34	9.66	8.31	3.27	14.09	4.74	**	-
	PLACE1009190	10.56	9.79	11.19	7.65	14.06	8.19	4	6.56	7.14	*	-
	PLACE1009196	13.22	10.75	11.8	7.38	9.71	7.53	10.55	12.57	8.91	*	-
	PLACE1009200	19.33	23.87	22.95	10.45	11.73	10.18	10.96	16.99	17.03	**	-
	PLACE1009217	14.13	24.09	16.64	11.71	10.57	10.58	3.82	4.64	6.12	*	-
35	PLACE1009230	27.31	26.63	32.64	10.81	26.12	18.34	16.83	20.7	24.31	*	-
	PLACE1009236	9.03	10.62	12.67	7.18	9.87	8.71	6.77	9.24	7.63		-
	PLACE1009246	21.48	34.44	20.99	9.29	20.22	19.2	9.84	35.09	13.46		-
	PLACE1009265	18.86	26.11	25.51	7.08	18.04	9.4	9.34	41.89	9.73	*	-
	PLACE1009279	13.38	8.53	11.2	5.1	7.71	6.09	11.6	8.18	8.91	*	-
	PLACE1009298	49.41	26.44	34.52	26.24	34.87	27.55	30.84	25.04	29.21		-
40	PLACE1009308	9.89	13.34	12.22	3.57	6.53	4.13	6.2	4.88	5.8	**	-
	PLACE1009319	11.98	14.82	14.36	7.73	14.05	5.85	5.29	9.69	4.23	*	-
	PLACE1009328	12.86	13.58	15.59	6.43	10.45	5.86	7.1	8.23	11.41	*	-
	PLACE1009335	8.34	6.5	7.11	3.99	9.88	4.55	4.35	7.62	2.32		-
	PLACE1009338	14.56	12.99	17.79	6.9	13.74	10.92	6.69	5.83	8.27	**	-
	PLACE1009344	6.92	5.13	5.98	3.02	11.98	4.73	3.18	3.89	2.88	*	-
45	PLACE1009355	23.17	22.99	26.45	20.27	18.4	17.42	10.13	10.79	9.83	*	-
	PLACE1009368	8.63	5.09	6.32	3.35	3.66	2.95	3.35	6.92	2.66	*	-
	PLACE1009375	8.35	5.94	11.71	3.65	4.61	3.52	3.31	4.45	3.97	*	-
	PLACE1009388	18.28	22.47	42.99	8.1	17.38	17.02	11.33	10.99	17.5		-
	PLACE1009398	16.02	15.66	15.45	5.65	12.56	7.13	6.81	5.4	4.18	*	-
50	PLACE1009404	17.98	10.01	28.67	4.73	28.94	16.4	9.28	9.88	5.15		-
	PLACE1009410	13.78	15.39	9.6	5.62	6.24	5.55	5.28	4.64	5.63	*	-
	PLACE1009417	16.73	9.41	10.65	12.79	9.15	6.2	6.71	6.82	7.05		-
	PLACE1009424	9.71	6.5	9.08	4.75	4.94	4.28	3.44	4.18	4.16	*	-
	PLACE1009434	21.73	12.22	10.01	6.12	7.87	5.95	3.69	5.83	2.87	*	-
	PLACE1009443	7.33	14.79	8.94	2.98	3.24	2.54	4.85	2.06	4.82	*	-
	PLACE1009444	13.13	14.77	17.33	7.6	10.32	8.01	6.52	5.24	6.76	*	-
55	PLACE1009459	8.33	7.91	9.2	3.33	5.72	4.79	3.49	3.56	3.33	**	-
	PLACE1009460	9.94	14.6	11.32	7.7	8.3	7.62	5.02	3.61	2.95	*	-
	PLACE1009468	12.43	12.85	9.11	5.4	5.98	4.76	4.66	5.65	8.17	**	-
	PLACE1009476	7.02	4.9	5.38	3	3.07	3.32	3.74	3.76	3.61	*	-

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	PLACE1009477	13.59	11.11	12.81	10.3	9.83	6.89	8.75	11.15	10.89				
	PLACE1009493	5.63	4.68	4.85	3.04	3.33	2.25	3.06	2.29	1.49	**	**	-	-
	PLACE1009502	11.43	9.62	8.39	5.92	5.81	5.8	4.63	7.61	3.19	*	*	-	-
5	PLACE1009524	7.56	7.26	7.63	1.87	3.86	2.97	2.66	3.37	2.46	**	**	-	-
	PLACE1009527	18.34	12.36	9.71	6.88	11.49	9.95	6.88	5.14	3.52	*	*	-	-
	PLACE1009531	25.38	45.76	31.03	26.02	25.63	22.82	19.07	17.64	15.03				
	PLACE1009535	12.3	11.08	8.3	3.83	6.2	5.84	3.36	3.71	4.06	*	**	-	-
	PLACE1009539	8.83	10.23	7.02	4.34	7.56	5.81	5.39	6.61	6.43				
10	PLACE1009540	37.43	26.63	27.99	14.5	25.74	28.63	21	11.9	8.26	*	*	-	-
	PLACE1009542	12	5.45	5.7	3.62	4.51	6	3.18	3.69	2.67				
	PLACE1009546	12.67	10.42	6.26	3.72	5.36	5.98	4.35	10.8	3.66				
	PLACE1009556	7.91	6.37	6.72	5.1	4.62	3.16	3.16	2.46	2.95	*	**	-	-
	PLACE1009569	11.99	15.44	10.67	4.76	13.77	8.59	5.94	5.33	6.24	**	**	-	-
	PLACE1009571	7.82	9.37	5.59	3.8	7.13	3.69	5.84	2.83	4.48				
15	PLACE1009573	22.09	15.96	12.31	9.76	17.27	9.7	8.26	8.91	7.87	*	*	-	-
	PLACE1009576	13.53	9.49	9.65	4.21	6.31	4.13	5.49	5.78	4.15	*	*	-	-
	PLACE1009580	9.86	9.33	7.56	5.13	7.69	4.5	8.75	3.59	4.85				
	PLACE1009581	12.95	12.1	8.15	7.19	5.84	4.99	3.45	2.48	3.53	*	**	-	-
	PLACE1009587	13.3	7.18	8.26	7.06	6.26	5.41	3.85	4.9	4.28				
20	PLACE1009593	18.08	14.97	12.54	14.73	10.76	9.75	5.8	5.66	6.75	**	**	-	-
	PLACE1009595	24.28	22.3	15.19	12.22	14.76	12.77	19.19	14	13.81				
	PLACE1009596	8.31	5.39	3.71	3.49	5.52	2.24	4.95	2.48	3.3				
	PLACE1009600	19.52	17.07	12.01	6.59	8.79	3.99	8.49	7.24	8.2	*	*	-	-
	PLACE1009604	19.98	10.38	8.96	4.18	6.3	6.58	3.83	5.54	4.55				
	PLACE1009607	17.2	18	14.19	8.35	9.63	7.56	19.54	17.62	14.33	**	**	-	-
25	PLACE1009613	8.31	8.44	6.06	5.1	6.18	4.22	4.39	2.55	3.96	*	*	-	-
	PLACE1009621	18.02	17.88	15.95	7.12	14.76	8.85	8.46	6.45	12.83	*	*	-	-
	PLACE1009622	16.93	9.51	8.44	5	5.84	4.46	4.96	3.18	4.98				
	PLACE1009624	23.04	19.02	15.23	8.31	9.71	5.05	7.94	5.67	7.85	*	**	-	-
	PLACE1009637	8.56	7.93	7.76	3.81	7.55	4.55	3.93	3.27	4.29	**	**	-	-
	PLACE1009639	14.9	6.92	3.57	7.62	5.31	8.34	6.06	5.69	7.84				
30	PLACE1009654	23.03	16.88	13.87	7.6	11.88	8.66	7.4	8.09	10.22	*	*	-	-
	PLACE1009659	17.62	16.71	15.38	8.59	15.54	12.83	6.78	8.01	7.95	**	**	-	-
	PLACE1009665	13.55	12.11	8.08	5.71	10.66	10.87	8.53	10.59	6.01				
	PLACE1009669	10.91	11.58	11.44	5.71	8.38	5.23	8.32	8.02	8.98	**	**	-	-
	PLACE1009670	10	4.03	5.32	3.93	4.76	8.45	5.57	4.18	5.29				
35	PLACE1009708	13.41	10.39	7.63	11.97	12.63	3.57	6.84	3.75	9.58	*	*	-	-
	PLACE1009721	15.79	10.82	9.31	5.16	6.52	4.42	9.11	3.24	6.91	*	*	-	-
	PLACE1009731	5.6	6.57	11.06	5.5	8.58	5.78	5.45	4.8	9.13				
	PLACE1009735	9.43	10.36	12.52	8.67	8.77	6.91	8.15	10.58	12.7				
	PLACE1009737	8.36	8.02	10.98	5.74	17.02	9.89	4.98	11.47	4.66				
	PLACE1009741	8.67	7.59	11.34	6.59	7.8	4.16	2.63	4.89	4.5	*	*	-	-
40	PLACE1009752	9.51	12.78	18.39	7.46	12.57	11.15	4.36	9.17	6.85				
	PLACE1009763	16.81	19.39	15.73	12.5	15.24	13.69	4.1	8.02	6.41	**	**	-	-
	PLACE1009766	7.54	8.76	7.16	6.98	11.81	6.16	9.17	7.21	6.61				
	PLACE1009772	12.62	18.28	13.46	16.58	26.84	15.97	7.94	11.57	13.51				
	PLACE1009782	7.96	6.95	7.99	4.24	6.2	9.33	6.26	4.41	4.35	*	*	-	-
	PLACE1009794	8.71	9.98	15.31	6.91	7.94	5.64	5.81	8.68	9.35				
45	PLACE1009798	15.7	11.58	19.23	8.55	9.28	7.81	5.76	14.83	6.68	*	*	-	-
	PLACE1009845	5.69	8.07	10.29	5.79	6.81	9.4	3.27	3.21	4.35	*	*	-	-
	PLACE1009849	4.29	6.11	7.54	5.25	6.21	5.82	3.81	4.56	5.57				
	PLACE1009857	5.97	7.92	9.09	4.47	4.42	3.68	4.36	2.37	3.86	*	*	-	-
	PLACE1009861	21.52	19.65	20.31	10.08	12.87	8.67	13.97	16.84	16.62	**	*	-	-
	PLACE1009872	225.97	496.72	352.07	405.22	548.08	335.22	583.26	839.73	801.36	*	*	-	-
50	PLACE1009877	93.23	95.23	121.84	37.51	29.99	31.46	33.83	34.28	50.76	**	**	-	-
	PLACE1009879	8.31	6.4	8.23	4.6	3.94	4.45	5.4	6.04	6.14	**	**	-	-
	PLACE1009886	8.21	5.71	6.04	3.1	4.43	3.64	3.76	3.74	3.91	**	**	-	-
	PLACE1009888	16.61	15.12	18.96	7.12	11.3	10.4	7.67	15.82	6.68	*	*	-	-
	PLACE1009908	10.69	13.22	16.94	7.9	15.1	13.2	5.89	21.59	11.16				
	PLACE1009919	18.85	20.8	15.18	25.14	44.25	16.53	6.38	10.08	17.42				
55	PLACE1009921	12.5	11.43	13.89	6.9	11.45	10.84	6.74	7.53	6.61	**	**	-	-
	PLACE1009923	37.38	53.14	35.03	28.71	69.72	45.4	23.4	36.13	28.69				
	PLACE1009924	26.03	16.67	21.48	6.94	14.99	12.69	29.73	40.32	10.81				
	PLACE1009925	10.23	25.64	14.3	6.85	14.35	14.82	6.32	35.83	7.94				

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	PLACE1009931	29.02	24.07	26.54	12.24	15.5	14.51	9.57	9.79	10.08	**	**	-	-
	PLACE1009935	8.86	7.44	9.7	2.78	11.02	5.42	14.95	3.43	6.35			-	-
	PLACE1009947	6.29	6.77	9.33	4.25	4.43	3.14	2.04	2.93	4.01	*	*	-	-
5	PLACE1009961	7.86	10.21	16.93	5.24	6.64	4.49	4.58	6.45	5			-	-
	PLACE1009971	7.79	7.18	10.26	3.38	7.18	3.34	3.67	4.69	3.08	*	*	-	-
	PLACE1009982	20.35	18.31	15.25	6.6	11.54	11.1	7.87	5.59	13.47	*	*	-	-
	PLACE1009992	12.32	8.01	11.62	6.39	8	6.72	5.24	5.76	6.38	*	*	-	-
	PLACE1009995	21.27	22.11	27.33	13.99	19.4	11.61	8.12	16.7	12.66	*	*	-	-
10	PLACE1009997	23.76	8.03	15.66	6.79	12.9	5.63	10.63	9.44	8.19			-	-
	PLACE1010002	14.56	6.35	12.19	4.66	8.08	5.35	5.32	14.28	7.75			-	-
	PLACE1010011	15.51	14.11	17.86	6.19	7.34	6.29	9.9	6.46	10.43	**	*	-	-
	PLACE1010013	6.16	5.13	12.68	2.37	2.99	1.56	3.53	4.24	2.98			-	-
	PLACE1010021	15.95	20.29	19.12	7.11	14.51	9.31	5.22	8.04	6.15	*	**	-	-
	PLACE1010023	27.49	31.11	21.32	17.41	29.7	20.44	16.49	7.28	6.33	*		-	-
15	PLACE1010031	20.87	15.58	32.54	10.16	16.34	7.15	9.85	8.36	10.28			-	-
	PLACE1010039	20.5	6.62	10.22	3.99	6.51	3.25	2.91	6.23	3.6			-	-
	PLACE1010045	11.17	9.8	13.16	5.75	8.43	6.1	5.11	5.8	5.51	*	**	-	-
	PLACE1010053	7.04	5.22	9.04	6.47	4.19	2.39	2.32	2.12	1.16	*		-	-
	PLACE1010060	18.9	18.89	15.21	7.4	8.59	8.37	12.03	13.21	10.77	**	*	-	-
	PLACE1010069	10.06	6.9	13.66	5.33	6.93	4.79	2.86	4.42	3.79	*		-	-
20	PLACE1010070	8.15	7.09	9.72	2.34	9.93	4.09	3.65	3.87	2.87	**		-	-
	PLACE1010074	63.56	56.74	39.11	24.21	42.72	26.72	25.32	15.29	17.22	*		-	-
	PLACE1010076	60.58	44.35	55.45	21.22	23.2	19.4	13.41	12.75	17.59	**	**	-	-
	PLACE1010078	13.76	11.23	14.35	6.69	10.2	8.63	4.38	4.87	4.45	*	**	-	-
	PLACE1010081	27.34	19.16	21.57	12.55	15.05	11.39	11.73	7.47	11.77	*	*	-	-
25	PLACE1010083	7.1	7.48	5.64	1.97	2.64	2.62	1.69	2.61	1.96	**	**	-	-
	PLACE1010089	11.95	9.65	9.57	5.5	5.81	4.38	4.84	2.48	4.43	**	**	-	-
	PLACE1010095	14.85	29.75	16.35	5.81	14.35	9.63	7.28	8.67	5.49			-	-
	PLACE1010102	22.29	34.08	23.15	9.26	16.03	13.51	7.63	9.06	7.61	*	**	-	-
	PLACE1010105	18.16	20.35	15.99	6.52	12.73	7.6	4.02	4.82	4.1	*	**	-	-
	PLACE1010106	19.44	22.57	15.73	8.29	8.94	12.84	10.96	10.43	10.44	*	*	-	-
30	PLACE1010130	6.82	6.56	4.7	3.25	3.39	2.18	3.26	3.47	3.87	*	*	-	-
	PLACE1010132	20.18	25.39	20.56	20.18	19.1	12.29	12.71	11.47	12.5	**		-	-
	PLACE1010134	10.35	11.42	9.66	6.05	6.05	5.55	6.72	4.12	2.88	**	*	-	-
	PLACE1010139	74.68	88.11	79.85	37.26	51.16	43.94	15.68	26.17	18.6	**	**	-	-
	PLACE1010148	10.48	7.43	9.71	13.14	7.54	4.86	3.27	4.13	7.63			-	-
35	PLACE1010155	9.79	7.58	7.63	3.3	5.89	2.96	2.11	2.26	2.53	*	**	-	-
	PLACE1010156	32.59	25.06	24.61	14.7	18.09	11.09	7.29	10.58	14.48	*	**	-	-
	PLACE1010161	8.48	13.16	10.69	5.15	8.21	6.03	4.47	3.31	5.46	*		-	-
	PLACE1010181	8.66	8.08	6.51	2.62	6.54	5.02	3.74	4.12	2.93	**		-	-
	PLACE1010194	8.57	7.46	6.67	3.93	4.98	3.84	2.86	2.08	2.37	**	**	-	-
	PLACE1010202	8.39	6.76	12.45	8.31	10.9	5.79	3.56	3.42	2.04	*		-	-
40	PLACE1010231	12.97	10.31	14.49	7.96	15.61	7.14	8.93	9.42	8.37	*		-	-
	PLACE1010235	12.62	15	11.24	4.59	11.54	4.53	6.11	5.14	4.76	**		-	-
	PLACE1010237	5.04	3.77	4.4	2.18	2.37	2.25	2.72	0.64	1.32	**	*	-	-
	PLACE1010251	9.46	4.47	6.29	5.09	4.79	10.14	3.78	5.92	3.88			-	-
	PLACE1010261	8.26	6.41	4.7	3.42	2.86	2.61	4.52	5.73	4.64	*		-	-
	PLACE1010270	7.53	8.07	6.36	3.29	6.44	3.19	3.88	4.95	3.8	**		-	-
45	PLACE1010273	8.97	10.55	5.7	2.72	5.68	3.04	2.78	2.04	3.83	*		-	-
	PLACE1010274	20.97	18.72	29.56	10.88	16.29	14.38	6.73	5.73	6.16	**		-	-
	PLACE1010277	15.29	14.99	14.3	8.87	13.93	8.53	11.24	4.25	6.68	*		-	-
	PLACE1010293	16.94	20.61	17.07	9.41	11.63	8.24	17.5	8.1	13.23	**		-	-
	PLACE1010297	38.08	33.94	34.95	17.91	31.69	15.63	31.8	20.1	25.32			-	-
50	PLACE1010300	21.55	15.58	11.87	9.15	8.78	7.88	3.82	5.36	5.08	*		-	-
	PLACE1010310	323.02	293.14	231.29	170.36	221.96	136.69	214.56	235.35	207.22	*		-	-
	PLACE1010321	10.7	10.58	7.81	4.96	7.93	6.91	5.6	6.6	6.56	*		-	-
	PLACE1010324	6.25	5.69	6.54	2.88	4.51	2.6	4.43	3.34	2.72	*	**	-	-
	PLACE1010329	14.25	11.37	11.93	5.93	10.64	4.89	9.64	9.84	9.32	*		-	-
	PLACE1010330	12.28	14.21	10.49	11.84	10.18	7.63	12	7.94	17.86			-	-
55	PLACE1010335	27.7	52.66	38.23	18.39	9.7	13.5	16.61	15.38	28.61	*		-	-
	PLACE1010341	6.44	4.91	4.72	2	3.7	1.35	4.14	2.93	4.21	*		-	-
	PLACE1010342	2.35	2.93	2.85	2.16	1.61	1.84	1.14	1.19	0.83	*	**	-	-
	PLACE1010346	10.42	6.88	7.23	4.08	5.74	2.77	5.84	6.92	5.88	*		-	-
	PLACE1010362	13.25	8.57	9.24	6.56	7.06	3.38	11.5	13.76	14.05			-	-

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	PLACE1010364	11.29	7.43	7.22	2.26	3.51	2.16	4.95	3.65	4.16	*	*	-	-
	PLACE1010368	10.78	8.61	7.03	3.98	6.56	5.19	7.58	7.15	5.73	*	*	-	-
5	PLACE1010373	30.2	28.61	24.17	14.82	22.58	10.46	24.63	20.09	20.87	*	*	-	-
	PLACE1010383	18.56	18.15	16.04	10	15.54	3.52	27.13	12.41	12.03	*	*	-	-
	PLACE1010385	2.48	1.73	1.18	0.83	2.33	0.49	2.65	1.19	2.06	*	*	-	-
	PLACE1010389	8.48	7.51	8.42	3.76	4.47	5.47	3.96	4.51	2.91	**	**	-	-
	PLACE1010401	3.24	0.96	4.6	2.29	2.49	1.63	2.81	2.31	1.6	*	*	-	-
	PLACE1010410	22.91	15.39	21.28	8.31	20.95	12.79	12.79	10.9	11.3	*	*	-	-
10	PLACE1010418	18.78	19.01	17.17	5.75	13.45	6.67	11.25	18.37	11.11	*	*	-	-
	PLACE1010425	10.58	10.75	18.36	4.2	4.88	3.19	8.87	11.17	8.75	*	*	-	-
	PLACE1010443	12.48	14.66	16.77	5.6	14.99	6.09	8.79	8.23	11.76	*	*	-	-
	PLACE1010445	36.17	45.7	37.43	17.56	20.28	18.29	39.23	32.46	41.56	**	**	-	-
	PLACE1010481	60.4	46.95	65.37	22.92	26.42	21.44	27.71	30.53	27.4	**	**	-	-
	PLACE1010482	127.4	82.31	84.53	104.64	120.51	109.85	62.48	50.87	49.97	*	*	-	-
15	PLACE1010491	71.28	72.3	73.41	43.51	47.95	35.09	68.63	86.51	74.84	**	**	-	-
	PLACE1010492	20.32	20.74	19.72	20.62	27.04	23.27	9.07	12.55	10.15	**	**	-	-
	PLACE1010509	11.2	13.07	17.83	8.18	12.58	8.24	5.79	8.34	7.68	*	*	-	-
	PLACE1010518	9.76	12.31	18.67	8.17	8.57	7.5	8.04	6.33	6.73	*	*	-	-
	PLACE1010522	8.32	9.35	9.63	6.71	11.42	6.63	6.37	5.88	7.65	*	*	-	-
20	PLACE1010529	13.09	22.15	14.64	11.31	17.05	8.58	7.61	9.45	9.29	*	*	-	-
	PLACE1010547	36.79	34.33	38.34	12.39	16.81	11.19	21.21	24.3	23.05	**	**	-	-
	PLACE1010560	10.15	9.34	9.56	6.09	4.54	5.89	6.02	5.35	6.13	**	**	-	-
	PLACE1010562	4.79	4.39	12.01	8.8	8.65	6.38	6.41	7.48	4.4	*	*	-	-
	PLACE1010579	74.54	67.98	59.08	46.33	48.92	48.24	56.27	84.49	60.31	*	*	-	-
	PLACE1010580	38.79	45.7	46.75	22.24	30	17.17	31.95	38.27	36.2	*	*	-	-
25	PLACE1010599	29.35	25.54	32.71	12.61	15.12	14.18	19.83	24.34	23.16	**	**	-	-
	PLACE1010606	31.76	30.37	40.62	15.46	19.15	14.23	22.77	25.83	28.81	**	**	-	-
	PLACE1010616	16.39	26.11	18.04	12.86	17.78	7.33	3.49	3.67	4.92	**	**	-	-
	PLACE1010622	9.08	4.75	12.08	2.52	4.26	2.63	11.54	11.12	6.28	*	*	-	-
	PLACE1010624	292.79	228.16	204.46	212.8	278.86	210.51	166.11	171.99	155.01	*	*	-	-
	PLACE1010628	48.66	44.83	51.05	27.25	26.82	37.41	15.79	19.04	21	*	**	-	-
30	PLACE1010629	19.03	17.43	20.71	12.12	16.38	15.36	14.93	10.66	11.67	*	*	-	-
	PLACE1010630	15.62	16.61	29.46	8.82	19.7	10.88	11.96	14.1	11.42	*	*	-	-
	PLACE1010631	22.99	34.46	25.54	20.07	21.82	17.69	19.23	10.89	16.98	*	*	-	-
	PLACE1010651	8	10.03	11.34	5.4	9.54	5.75	4.35	5.43	5.06	**	**	-	-
	PLACE1010661	13.76	16.34	32.78	7.67	13.64	27.31	6.28	10.55	7.26	*	*	-	-
	PLACE1010662	28.68	22.75	30.53	8.67	12.27	9.85	25.45	28.04	24.56	*	*	-	-
35	PLACE1010668	37.33	37.7	40.55	22.62	25.66	20.72	36.78	44.21	37.46	**	**	-	-
	PLACE1010702	12.3	6.26	13.51	6.5	7.73	5.88	8.16	17.08	6.46	*	*	-	-
	PLACE1010709	70.65	75.49	68.95	55.09	47.9	57.04	50.07	52.69	55.39	**	**	-	-
	PLACE1010713	80.41	68.48	77.71	36.46	48.82	48.26	28.63	32.14	23.64	**	**	-	-
	PLACE1010714	14.85	12.78	15.24	4.19	7.98	4.28	3.33	8.97	5.69	**	**	-	-
40	PLACE1010716	10.07	15.73	17.8	4.88	22.94	9.1	5.99	13.73	3.7	*	*	-	-
	PLACE1010717	16.27	25.02	15.64	13.63	18.64	10.49	10.76	15.16	3.55	*	*	-	-
	PLACE1010720	27.48	32.65	34.2	14.65	18.34	8.25	20.45	22.85	22.74	**	*	-	-
	PLACE1010739	32.05	33.62	24.71	15.33	21.42	15.16	17.5	28.68	18.95	*	*	-	-
	PLACE1010743	44.76	28.81	34.77	15.52	24.11	19.41	14.02	9.67	5.8	*	**	-	-
	PLACE1010752	26.13	19.45	22.02	11.29	9.49	11.37	16.27	24.35	13.97	**	**	-	-
45	PLACE1010761	15.13	12.05	32.55	15.98	9.45	8.78	11.14	13.99	12.89	*	*	-	-
	PLACE1010771	28.91	75.96	37.99	25.83	90.51	39.2	31.02	18.86	25.47	*	*	-	-
	PLACE1010784	98.45	116.91	93.11	48.56	63.14	52.26	30.32	31.37	33.38	**	**	-	-
	PLACE1010786	16.19	15.53	16.87	8.23	15.52	9.85	7	6.49	9.87	**	**	-	-
	PLACE1010789	46.25	33.26	40.6	14.8	19.17	10.09	44.64	47.22	35.88	**	**	-	-
50	PLACE1010800	13.97	9.78	14.67	8.91	6.6	5.82	4.05	5.43	4.76	*	**	-	-
	PLACE1010802	13.35	16.74	27.18	16.21	23.96	4.91	12.32	5.78	37.85	*	*	-	-
	PLACE1010811	26.9	21.58	31.28	13.09	18.01	12.69	11.33	11.86	10.25	*	**	-	-
	PLACE1010813	10.21	6.96	9.67	4.84	4.38	4.87	3.92	2.83	2.64	*	**	-	-
	PLACE1010827	10.79	10.81	12.05	5.43	7.46	5.87	6.65	5.02	3.76	**	**	-	-
	PLACE1010833	9.18	9.98	8.82	3.14	6.94	3.42	1.97	2.07	1.97	*	**	-	-
55	PLACE1010839	24.14	30.08	20.18	11.7	20	12.82	16.21	11.13	15.42	*	*	-	-
	PLACE1010856	15.47	10.08	17.88	6.16	6.58	4.26	11.23	8.32	12.26	*	*	-	-
	PLACE1010857	32.67	31.48	18.71	21.99	18.34	15.41	16.23	15.82	15.61	*	*	-	-
	PLACE1010870	5.83	4.92	4.28	3.87	3.55	2.92	2.91	2.04	1.94	*	**	-	-
	PLACE1010877	26.87	20.6	20.89	14.13	8.42	9.71	13.42	12.71	7.25	**	*	-	-

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	PLACE1010882	17.06	13.54	8.42	6.17	5.69	5.82	7.13	5.03	5.37	*	-
	PLACE1010891	27.43	30.32	21.15	13.46	14.41	7.46	15.38	15.07	24.71	*	-
5	PLACE1010896	13.62	18.23	16.16	6.92	8.03	5.78	3.54	4.62	4.06	**	**
	PLACE1010900	66.6	75.65	67.62	55.68	59.03	45.47	67.12	53.92	39.14	*	-
	PLACE1010916	104.52	71.53	76.5	35.13	35.16	33.1	29.84	23.73	27.17	**	**
	PLACE1010917	14.21	14.67	11.27	7.82	5.59	7.41	7.69	7.06	8.76	**	**
	PLACE1010924	5.86	2.7	4.5	2.89	4.47	3.08	2.47	3.1	1.31	*	-
	PLACE1010925	4.94	4.55	4.99	1.88	2.53	1.67	3.09	1.69	1.78	**	**
10	PLACE1010926	13.94	11.16	11.63	5.87	7.64	6.22	5.6	4.23	4.29	**	**
	PLACE1010942	207.77	196.21	175.46	147.15	130.24	102.36	197.42	120.16	123.73	*	-
	PLACE1010943	31.5	26.2	22.98	12.49	22.16	9	15.12	16.22	13.62	*	-
	PLACE1010944	83.2	92.75	68.43	51.82	78.63	47.87	87	58.47	73.16	*	-
	PLACE1010947	33.76	22.26	22.3	12.84	13.89	8.22	22.66	11.99	13.89	*	-
15	PLACE1010954	10.33	11.3	11.05	5.3	5.81	5.51	5.34	5.12	4.22	**	**
	PLACE1010960	15.62	30.44	20.31	7.94	8.28	7.04	11.37	9.05	8.5	*	-
	PLACE1010965	13.17	14.34	9.79	7.54	4.78	3.78	4.15	4.73	5.18	*	-
	PLACE1010968	18.41	14.95	14.27	6.84	9.6	5.59	12.62	6.34	9.37	**	*
	PLACE1010978	57.65	54.74	36.05	40.68	34.09	13.7	16.85	10.36	20.32	*	-
	PLACE1010982	21.44	26.06	15.9	7.42	6.54	11.09	10.66	7.85	9.32	*	-
20	PLACE1010990	327.98	344.55	256.15	258.07	367.78	240.66	208.45	171.08	173.44	*	-
	PLACE1011017	100.16	59.4	54.99	23.72	27.4	15.8	91.94	75.46	99.74	*	-
	PLACE1011019	13.37	8.64	6.46	8.37	6.37	4.79	6.61	7.41	7.81	*	-
	PLACE1011026	17.67	16.91	13.69	8.74	11.48	8.93	15.71	13.37	15.94	*	-
	PLACE1011032	5.5	8.88	7.51	2.84	5.75	2.99	4.5	3.38	3.21	*	-
25	PLACE1011041	11.32	11.72	11.41	4.79	6.17	4.9	2.74	0	1.85	**	**
	PLACE1011045	30.68	27.07	24.09	20.73	22.77	14.24	25.88	22.96	30.06	*	-
	PLACE1011046	10.75	10.03	9.15	3.68	6.42	4.38	4.21	3.5	2.56	**	**
	PLACE1011054	23.11	26.67	18.54	13.24	17.45	11.68	27.3	21.77	27.93	*	-
	PLACE1011056	5.67	3.31	3.16	3.73	4.11	8.46	6.33	3.05	6.91	*	-
	PLACE1011057	10.04	10.53	7.99	8.15	6.14	3.72	11.95	6.55	7.6	*	-
30	PLACE1011059	19.4	17.96	11.33	7.08	9.45	9.52	6.53	6.86	9.19	*	-
	PLACE1011066	9.28	7.31	5.97	5.75	7.03	4.1	2.13	5.18	0.49	*	-
	PLACE1011087	26.84	40.15	33.04	57.32	27.46	16.29	127.9	19.42	37.4	*	-
	PLACE1011090	10.52	7.52	6.48	3.01	5.18	3.1	6.04	4.61	6.16	*	-
	PLACE1011109	43.09	16.58	13.76	6.5	19.94	4.84	12.2	7.21	13.97	*	-
35	PLACE1011114	17.98	24.04	19.89	13.12	19.15	8.13	12.09	13.25	14.96	*	-
	PLACE1011116	30.03	28.53	37.37	10.98	8.87	7	8.26	10.18	5.99	**	**
	PLACE1011122	5.9	6.6	5.93	4.16	4.82	3.11	3.97	4.69	2.89	*	-
	PLACE1011133	6.47	4.35	6.51	3.81	3.93	3.81	2.72	5.8	2.91	*	-
	PLACE1011134	5.48	5.99	6.34	4.28	4.27	3.84	3.72	3.86	3.76	**	**
	PLACE1011143	4.76	9.67	5.59	2.21	5.45	3.27	2.93	3.83	4.13	*	-
40	PLACE1011146	10.48	13.56	12.48	9.3	11.11	4.11	4.38	6.69	4.48	**	-
	PLACE1011160	7.71	9.99	6.71	4.98	7.77	3.25	6.45	4.47	3.78	*	-
	PLACE1011165	21.99	27.95	32.58	8.87	19.75	11.93	12.6	15.59	9.42	*	-
	PLACE1011181	5.25	3.37	6	2.06	4.49	2.29	2.61	4.09	3.85	*	-
	PLACE1011185	60.3	36.78	36.17	37.68	34.15	24.31	17.32	33.87	29.05	*	-
	PLACE1011186	25.07	30.45	27.42	12.69	20.01	15.83	19.93	27.9	21.4	*	-
45	PLACE1011203	10.27	18.2	13.8	9.36	12.5	6.63	8.02	13.49	10.02	*	-
	PLACE1011214	7.39	9.12	10.92	5.57	5.78	3.95	1.49	2.02	3.84	*	-
	PLACE1011219	7.03	5.86	7.27	8.39	4.52	4.58	9.07	4.64	3.23	*	-
	PLACE1011221	10.63	11.42	9.42	5.44	10.51	4.92	4.92	5.52	6.28	**	-
	PLACE1011229	13.76	13.72	12.78	9.23	7.48	4.86	6.43	7.1	4.99	**	**
	PLACE1011231	34.58	28.7	50.02	23.03	24.8	13.83	19.12	24.97	26.97	*	-
50	PLACE1011236	13.02	10.94	13.98	5.99	7.59	5.06	4.42	6.98	4.82	**	**
	PLACE1011247	571.8	409.73	639.71	528.63	738.01	566.23	553.23	542.58	267.58	*	-
	PLACE1011263	4.49	7.26	9.65	4.09	5.29	4.39	2.77	4.83	3.37	*	-
	PLACE1011273	9.77	15.11	15.29	8	7.81	4.87	6.04	5.28	3.97	*	-
	PLACE1011278	21.08	26.71	20.88	9.67	19.17	11.18	9.31	5.1	7.74	**	-
	PLACE1011289	8.76	9.56	9.49	5.47	7.47	4.38	4.05	4.14	4.61	*	-
55	PLACE1011291	3.27	1.73	2.37	1.38	1.37	0.09	2.52	4.22	1.75	*	-
	PLACE1011296	15.1	14.79	20.48	7.86	6.09	7.28	12.72	18.07	15.96	**	-
	PLACE1011310	49.57	40.91	47.27	26.08	24.65	29.49	26.25	31.46	34.3	**	-
	PLACE1011311	12.85	11.18	13.64	5.84	6.4	7.88	4.02	7.29	3.99	**	**
	PLACE1011321	316.11	225.18	251.29	230.23	241.81	208.08	340.56	284.43	231.07	*	-

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	PLACE1011325	67.49	68.67	34.36	32.79	55.55	25.52	26.06	16.66	23.25	*	-
	PLACE1011332	37.6	32.99	20.69	24.89	22.84	17.06	26.8	25.99	39.36		
	PLACE1011340	6.86	4.22	8.9	7.42	3.33	10.93	4.69	3.22	3.76		
5	PLACE1011353	13.06	9.45	9.31	4.05	5.07	3.21	9.83	8.83	10.17	**	-
	PLACE1011360	7.09	6.29	7.09	5.01	4.64	2.08	4.25	9.92	6.13	*	-
	PLACE1011364	36.2	48	46.69	18.82	32.17	16.48	29.76	23.08	23.29	*	-
	PLACE1011365	56.47	40.06	43.45	30.4	25.78	22.53	35.29	36.44	44.51	*	-
	PLACE1011371	8.03	11.85	15.3	3.37	4.12	3.15	3.67	7.88	4.18	*	-
	PLACE1011375	7.04	6.27	10.93	2.06	3.1	2.3	1.72	3.77	5.21	*	-
10	PLACE1011386	164.83	196.07	182.53	143.65	164.65	123.82	185.62	179.87	160.52		
	PLACE1011399	13.53	14.93	12.77	5.31	8.23	5.03	14.49	12.53	13.08	**	-
	PLACE1011406	24.35	18.36	25.14	17.24	17.93	13.01	14.05	16.63	13.24	*	-
	PLACE1011407	11.96	8.15	11.8	4.39	4.52	4.88	4.7	7.06	4.99	**	-
	PLACE1011419	45.6	33.74	47.01	28.72	27.55	25.25	33.12	24.14	29.66	*	-
15	PLACE1011433	12.4	6.05	13.11	5.89	9.23	4.52	4.03	6.39	4.28		
	PLACE1011440	22.91	21.43	16.68	17.18	6.65	6.34	4.22	2.79	3.13	**	-
	PLACE1011452	21.99	27.18	21.9	7.47	5.58	8.33	1.98	2.55	3.76	**	-
	PLACE1011465	8.59	10.4	8.63	4.43	3.74	3.61	3.27	3.42	2.9	**	-
	PLACE1011472	12.35	11.03	8.39	5.76	5.63	4.74	4.12	4.06	4.53	*	-
20	PLACE1011477	6.89	4.15	8.42	3.82	3.1	2.49	5.68	5.36	7.03		
	PLACE1011478	147.8	127.45	151.17	98.43	129.14	92.91	97.94	88.28	67.65	**	-
	PLACE1011492	8.86	4.94	8.71	5.63	3.6	3.44	4.78	2.62	3.91		
	PLACE1011498	11.86	13.27	11.87	6.42	7.11	5.44	7.49	6.76	6.34	**	-
	PLACE1011501	5.51	5	4.76	1.97	2.88	1.92	1.53	1.09	0.63	**	-
	PLACE1011503	8.36	7.18	8.72	3.16	3.42	2.41	3.54	1.96	1.63	**	-
25	PLACE1011509	6.79	8.76	6.6	2.67	3.22	3.57	3.54	1.66	2.46	**	-
	PLACE1011514	19.36	42.6	35.59	29.05	24.04	21.59	28.05	21.32	28.44	**	-
	PLACE1011516	2.25	2.2	3.02	1.65	1.39	0.92	2.22	1.19	1.28	*	-
	PLACE1011520	56.28	54.22	44.97	60.14	59.13	46.66	37.37	33.63	31.08	*	-
	PLACE1011538	3.92	2.67	3.99	1.41	2.25	0.89	1.63	0.52	1.52	*	-
	PLACE1011555	5.04	5.36	4.18	1.71	1.41	2.12	2.42	1.56	2.13	**	-
30	PLACE1011561	40.83	32.97	31.05	28.42	20.97	80.97	15.06	18.06	18.45	**	-
	PLACE1011563	10.59	8.43	6.69	4.39	3.31	1.28	2.74	2.46	2.05	*	-
	PLACE1011567	8.99	5.72	8.85	4.85	2.48	0.94	3.39	1.71	1.08	*	-
	PLACE1011569	17.38	15.57	12.39	8.98	14.17	5.41	4.61	3.24	6.59	**	-
	PLACE1011576	9.4	4.88	4.15	2.79	3.81	3.52	4.89	6.65	7.51		
	PLACE1011586	11.29	10.02	9.62	6.88	3.58	5.49	4.18	5.75	5.57	**	-
35	PLACE1011635	30.93	17.84	23.55	13.98	14.55	6.78	13.1	10.06	12.62	*	-
	PLACE1011641	17.21	13.31	15.5	11.83	10.3	8.13	12.16	8.31	8.02	*	-
	PLACE1011642	14.04	9.07	8.81	4.73	3.8	2.98	2.08	3.09	1.68	*	-
	PLACE1011643	21.88	15.91	14.82	9.69	7.73	4.5	12.37	9.92	7.66	*	-
	PLACE1011646	50.88	55.98	42.92	29.54	24.58	20.05	12.83	13.88	9.31	**	-
40	PLACE1011649	101.51	209.33	140.08	111.98	127.38	61.19	33.86	36.5	31.67	*	-
	PLACE1011650	21.23	16.3	17.27	6.34	7.58	5.35	13.14	9.77	13.14	**	-
	PLACE1011661	36.54	29.6	21.98	17.54	11.85	16.02	29.9	27.07	30.09	*	-
	PLACE1011664	4693.7	3704.8	3103.3	1925.9	2495.7	2690.1	3091.7	3779.5	2474.5	*	-
	PLACE1011672	14.58	19.19	17.05	4.82	11.54	6.52	8.71	6.37	8.66	*	-
	PLACE1011675	27.27	28.5	23.64	11.76	7.61	13.02	10.47	6.83	11.83	**	-
	PLACE1011682	31.95	30.83	21.79	24.47	12.69	9.16	19.26	16.69	17.56	*	-
45	PLACE1011708	240.54	265.47	223.19	186.79	250.35	199.96	147.11	130.97	144.28	**	-
	PLACE1011719	2115.1	1324.5	1826.8	1953.8	1265.9	1000.2	1428.6	860.26	1269.9		
	PLACE1011725	14.63	11.44	8.67	4.74	6.3	2.04	9.22	9.94	8.53	*	-
	PLACE1011729	17.92	12.45	10.92	5.48	6.85	3.57	9.59	6.92	10.12	*	-
	PLACE1011741	19.11	16.45	8.97	6.48	6.39	4.13	6.03	4.62	6.01	*	-
50	PLACE1011749	198.63	245.38	186.1	98.37	139.73	93.5	146.64	106.95	169.56	*	-
	PLACE1011757	55.97	64.31	51.13	22.6	27.43	20.99	59.9	47.96	65.48	**	-
	PLACE1011762	112.55	118.61	84.99	68.65	83.7	57.21	113.37	92.71	109.2	*	-
	PLACE1011778	14.17	14.57	14.58	9.09	8.23	7.54	9.58	8.34	17.29	**	-
	PLACE1011783	34.3	38.67	23.05	14.78	12.16	17.09	15.47	21.92	20.45	*	-
	PLACE1011795	26.86	17.86	14.49	8.41	7.89	4.41	13.16	9.37	14.56	*	-
55	PLACE1011810	6.46	2.52	3.35	2.53	2.07	0.8	3.19	3.06	3.38		
	PLACE1011824	86.62	55.93	50.79	29.92	21.66	12.01	21.62	24.56	19.64	*	-
	PLACE1011825	47.11	53.31	45.03	28.52	34.47	24.16	61.42	44.87	47	**	-
	PLACE1011835	12.82	11.42	11.32	5.55	7.84	4.84	7.39	9.98	8.67	**	-

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	PLACE1011836	18.92	14.13	10.67	5.56	9.72	5.44	13.34	9.9	14.01				
	PLACE1011847	18.99	15.08	12.62	9.39	11.06	5.84	18.15	10.26	13.1	*	-		
	PLACE1011855	44.57	41.99	25.3	17.11	33.33	14.76	55.6	42.68	40.57				
5	PLACE1011858	17.26	15.38	17.11	5.33	7.08	6.53	6.22	8.74	5.1	**	**	-	-
	PLACE1011874	23.12	12.72	25.74	16.84	19.22	7.85	10.17	8.71	12.51				
	PLACE1011875	10.58	9.98	11.17	5.18	10.63	6.87	7.18	6.04	4.93	**	**	-	-
	PLACE1011877	4.39	5.14	4.95	3.7	5.52	3.78	2.59	4.05	4.24				
	PLACE1011891	21.71	17.57	18.99	7.39	14.47	8.67	8.21	9.15	7.86	*	**	-	-
10	PLACE1011896	15.35	16.64	24.3	10.41	10.14	12.14	5.01	8.13	7.98	*	*	-	-
	PLACE1011920	16.12	14.42	15.9	7.68	8.85	7.76	6.46	2.46	3.24	**	**	-	-
	PLACE1011922	9.14	7.55	8.03	4.49	8.39	4.08	7.97	6.15	5.33				
	PLACE1011923	166.86	139.43	146.9	104.2	117.42	86.95	136.93	140	124.61	*	-		
	PLACE1011937	11.45	9.18	10.8	8.58	6.75	5.1	5.71	6.29	5.46	*	**	-	-
	PLACE1011939	20.33	21.55	26.93	12.79	15.19	13.44	14.58	11.31	12.67	*	*	-	-
15	PLACE1011940	46.38	48.76	46.73	35.11	34.53	31.67	43.31	41.44	39.86	**	**	-	-
	PLACE1011962	58.59	70.73	80.18	30.15	38.09	28.84	47.96	47.68	42.57	**	*	-	-
	PLACE1011964	53.78	49.36	46.95	41.43	47.33	36.34	22.23	20.62	20.74	**	*	-	-
	PLACE1011978	50.21	52.86	64.71	38.6	31.39	22.36	22.46	20.19	18.12	*	**	-	-
	PLACE1011980	13.57	18.54	10.96	9.65	15.28	6.53	4.68	9.99	8.31				
20	PLACE1011981	46.23	28.89	45.44	16.98	15.61	9.98	14.66	11.01	11.18	*	**	-	-
	PLACE1011982	116.69	99.4	123.56	57.42	68.6	45.01	97.45	90.55	115.07	**	*	-	-
	PLACE1011995	8.31	11.27	12.33	5	7.29	7.22	6.27	8.29	4.87	*	-		
	PLACE1012023	36.36	36.13	39.16	21.46	26.03	23.3	20.6	21.06	24.79	**	**	-	-
	PLACE1012026	72.96	80.46	66.75	52.71	40.29	50.42	21.72	33.87	25.71	**	**	-	-
	PLACE1012031	6.69	7.34	9.86	2.73	6.11	3.89	3.41	3.11	3.97	*	-		
25	PLACE2000003	144.75	222.75	62.64	74.47	133.88	40.79	39.01	32.21	30.64				
	PLACE2000005	20.72	25.78	18.16	9.79	22.43	11.52	5.79	8.65	14.3	*	-		
	PLACE2000006	74.92	51.78	61.3	27.4	24.75	21.12	50.02	43.94	72.77	**	-		
	PLACE2000007	11.31	11.29	12.53	6.68	7.02	5.2	5.63	10.02	7	**	*	-	-
	PLACE2000011	20.07	19.36	23.84	14.92	4.58	15.77	9.39	11.52	19.43				
	PLACE2000014	10.47	6.72	12.3	4.76	6.02	3.48	3.63	6.9	4.73	*	-		
30	PLACE2000015	63.77	83.22	43.62	34.06	43.14	43.39	19.29	26.64	36.8	*	-		
	PLACE2000017	64.44	66.07	78.07	40.68	48.09	29.95	59.7	61.53	44.91	*	-		
	PLACE2000021	131	136.36	142.32	116.28	142.66	101.82	89.75	68.71	86.35	**	-		
	PLACE2000022	6.52	6.75	7.52	3.85	5.14	3.55	4.53	1.84	5.72	**	-		
	PLACE2000030	277.16	275.48	252.39	182.81	167.16	156.31	125.23	96.07	135.65	**	**	-	-
35	PLACE2000032	8.03	6.4	8.8	4.38	5.33	2.81	4.32	15.18	4.01	*	-		
	PLACE2000033	19.24	16.61	20.22	9.43	14.03	10.83	8.93	12.91	10.87	*	**	-	-
	PLACE2000034	212.75	182.06	146.24	219.9	195.88	170.13	146.86	112.34	125.26				
	PLACE2000039	8.9	10.84	13.51	4.94	3.89	4.8	3.72	4.38	6.52	**	*	-	-
	PLACE2000043	13.64	20.44	15.11	6.28	13.12	6.04	6.05	7.64	6.22	*	-		
	PLACE2000044	7.28	9.48	9.44	3.48	5.71	4.79	4.48	4.25	4.59	*	**	-	-
40	PLACE2000047	17.41	19.39	12.83	6.83	12.83	7.05	7.81	8.54	5.78	*	-		
	PLACE2000050	18.34	17.87	22.05	7.34	8.98	7.31	7.51	8.31	7.94	**	**	-	-
	PLACE2000061	53.75	61.97	78.23	34.92	41.03	37.86	22.68	14.04	20.77	*	**	-	-
	PLACE2000062	44.19	44.8	62.08	41.54	45.17	33.58	38.88	38.06	40.24				
	PLACE2000072	216.69	181.79	181.98	200.73	185.27	186.23	111.76	113.44	105.53	**	-		
	PLACE2000073	8.16	10.75	9.27	3.77	4.89	3.62	4.56	4.79	3.59	**	**	-	-
45	PLACE2000097	120.94	128.07	120.9	148.48	131.74	105.73	90.14	87.25	86.79	**	-		
	PLACE2000100	13.48	14.19	15.99	6.02	8.77	5.56	4.8	3.51	6.24	**	**	-	-
	PLACE2000103	355.83	328.95	197.42	251.22	436.52	235.01	231.23	336.03	237.95				
	PLACE2000106	32.23	23.41	23.14	14.46	6.17	13.03	9.13	10.5	5.27	*	**	-	-
	PLACE2000111	152.37	157.38	125.3	88.6	105.91	83.66	90.52	44.23	69.19	*	**	-	-
	PLACE2000115	27.01	16.97	16.32	19.6	21.67	16.26	13.74	11.32	11.63				
50	PLACE2000118	229.23	214.41	143.27	124.01	152.19	92.15	153.7	62.85	67.07				
	PLACE2000124	7.33	5.71	5.57	2.12	1.78	1.55	2.01	1.56	1.09	**	**	-	-
	PLACE2000132	18.07	19.01	19.11	15.64	11.16	12.49	9.7	6.52	8.48	*	**	-	-
	PLACE2000136	33.6	40.68	26.33	13.95	42.68	22.54	9.98	17.8	18.28	*	-		
	PLACE2000137	6.87	5.34	6.91	1.61	2.95	2.09	1.24	1.8	2.36	**	**	-	-
55	PLACE2000140	11.37	11.51	12.2	8.07	9.45	9.49	11.48	11.25	10.8	**	-		
	PLACE2000147	10.22	7.24	9.46	6.01	5.85	4.51	7.52	7.6	9.27	*	-		
	PLACE2000153	17.95	21.42	13.85	5.51	9.57	6.43	4.84	5.27	2.27	*	**	-	-
	PLACE2000164	8.53	12.11	9.44	3.18	4.26	4.12	4.98	3.97	2.13	**	**	-	-
	PLACE2000170	38.84	46.93	33	28	28.56	22.27	30.03	23.36	30.82	*	-		

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	PLACE2000172	9.55	12.02	10.86	4.88	5.87	3.32	4.01	4.8	6.2	**	**	-	-
	PLACE2000173	16.63	20.86	19.04	9.66	11.13	9.7	6.74	6.23	3.14	**	**	-	-
	PLACE2000174	6.73	7.76	6.4	3.37	4.73	2.4	3.08	3.26	1.62	*	**	-	-
5	PLACE2000176	47.07	39.92	36.01	26.8	32.78	24.97	24.68	26.79	25.41	*	**	-	-
	PLACE2000187	11.49	9.44	7.22	4.28	4.58	4.45	2.47	4.64	3.94	*	*	-	-
	PLACE2000216	15.24	13.28	16.1	7.83	10.53	7.67	11.12	11.23	10.67	**	*	-	-
	PLACE2000219	43.32	28.21	37.3	18.17	6.67	13.94	7.68	7.79	6.4	*	**	-	-
	PLACE2000221	9.58	7.64	7.46	2.22	3.99	1.24	4.08	2.43	3.07	**	**	-	-
10	PLACE2000223	16.67	12.34	12.95	4.95	6.75	4.32	4.43	2.01	2.87	**	**	-	-
	PLACE2000231	8.48	8.65	7.01	3.78	5.92	4.27	4.19	2.32	3.59	*	**	-	-
	PLACE2000235	7.02	5.03	3.66	1.54	5.33	1.9	4.43	3.57	3.78			-	-
	PLACE2000246	21.31	17.8	13.21	7.9	13.4	6.47	11.52	9.6	10.91	*		-	-
	PLACE2000264	41.11	43.3	30.68	20.28	22.27	18.14	15.54	15.85	15.69	*	**	-	-
	PLACE2000274	6.8	7.42	7.36	4.35	3.04	1.89	3.84	3.12	4.31	**	**	-	-
15	PLACE2000287	32.11	30.76	24.99	20.39	25.61	21.53	17.96	15.3	19.45	**		-	-
	PLACE2000296	42.94	34.88	35.63	23.36	22.17	20.37	32.02	14.36	29.35	**		-	-
	PLACE2000302	252.74	304.77	237.45	265.35	267.99	217.29	124.09	112.58	108.48	**		-	-
	PLACE2000305	21.47	23.58	17.69	16.14	17.23	16.65	22.14	18.21	22.01			-	-
	PLACE2000317	37.2	38.12	23.24	20.01	28.38	14.37	31.05	33.16	31.64			-	-
20	PLACE2000324	18.44	17.84	10.35	6.13	8.75	4.98	3.24	8.74	3.2	*	*	-	-
	PLACE2000334	21.38	17.6	11.43	10.36	9.7	9.37	7.54	6.15	9.1	*		-	-
	PLACE2000335	71.59	66.59	54.82	51.15	35.99	40.86	33.77	36.69	29.67	*	**	-	-
	PLACE2000340	20.62	28.95	19	17.88	23.88	12.85	16.23	14.73	16.82			-	-
	PLACE2000341	14.8	11.92	10.45	5.66	5.34	5.33	5.38	5.46	7.66	**	*	-	-
	PLACE2000342	23.53	21.95	21.97	16.28	11.86	11.51	22.81	14.69	23.12	**		-	-
25	PLACE2000347	9.57	9.26	10.05	4.16	2.94	3.3	5.78	3.54	5.48	**	**	-	-
	PLACE2000357	112.17	70.59	69.73	83.45	100.62	78.25	23	68.79	48.54			-	-
	PLACE2000358	57.37	32.59	34.74	25.22	20.69	15.46	44.93	47.18	42.01			-	-
	PLACE2000359	66.39	48.68	57.2	40.91	54.54	32.45	1.96	27.1	55			-	-
	PLACE2000366	24.09	23.36	19.56	12.65	12.71	9.05	11.75	9.72	10.83	**	**	-	-
	PLACE2000371	12.17	9.37	8.13	5.98	7.76	4.49	7.64	10.97	6.2			-	-
30	PLACE2000373	8.3	7.58	8.83	4.52	6.25	4.81	3.89	1.17	2.44	**	**	-	-
	PLACE2000374	20.82	21.57	18.21	16.3	16.71	14.02	11.71	11.44	14.19	*	**	-	-
	PLACE2000379	109.97	110.55	125.02	99.68	141.5	89.14	84.64	65.75	71.64	**		-	-
	PLACE2000386	27.43	27.19	20.99	10.83	12.4	11.22	15.3	17.99	10.26	**	*	-	-
	PLACE2000388	250.97	170.84	203.4	172.85	236.63	173.11	130.31	109.84	93.57	*		-	-
35	PLACE2000392	241.74	206.31	271.34	159.33	199.67	145.83	119.57	115.9	95.8	*	**	-	-
	PLACE2000394	10.9	10.42	13.61	8.59	15.25	7.68	5.68	9.12	6.51	*	*	-	-
	PLACE2000398	16.83	19.82	17.04	9.21	12.98	10.99	7.5	15.14	8.57	**	*	-	-
	PLACE2000399	30.6	27.17	17.03	25.83	27.41	28.06	9.08	19.74	20.17			-	-
	PLACE2000402	5.25	8.04	8.31	4.2	9.81	3.39	4.84	3.89	6.41			-	-
	PLACE2000404	24.79	49.52	29.14	49.74	21.66	25.22	16.23	19.06	8.51			-	-
40	PLACE2000411	5.67	8.96	6.76	7.21	11.84	6.13	5.19	4.54	7.08			-	-
	PLACE2000418	10.3	8.94	9.67	6.1	3.09	4.67	4.68	5.3	4.11	**	**	-	-
	PLACE2000419	96.71	94.48	148.23	58.48	57.97	27.06	44.37	46.85	45.47	*	*	-	-
	PLACE2000425	9.83	11.3	13.49	7.49	11.26	6.24	5.84	7.49	5.62	*		-	-
	PLACE2000427	15.21	22.92	21.67	15.7	21.56	15.92	5.61	6.9	4.76	**	**	-	-
45	PLACE2000433	25.58	27.32	28.12	13.97	18.4	14.15	21.62	27.64	18.08	**		-	-
	PLACE2000435	16.36	18.11	21.19	9.69	13.76	7.6	8.43	10.79	12.73	*	*	-	-
	PLACE2000438	35.17	36.25	36.72	24.14	34.38	15.98	38.19	37.23	25.32			-	-
	PLACE2000450	24.38	41.59	23.11	16.35	37.33	18.21	23.47	16.65	30.25			-	-
	PLACE2000455	51.05	47.04	53.6	30.31	36.57	21.71	39.12	34.02	35.42	*	**	-	-
	PLACE2000458	13.07	11.58	13.21	6.82	7.75	7.03	6.6	8.78	5.76	**	**	-	-
50	PLACE2000464	9.95	10.55	11.94	7.59	6.37	5.51	7.66	8.47	7.16	**	*	-	-
	PLACE2000466	182.2	189.36	208.18	166.02	148.04	156.91	139.29	234.97	151.61	*		-	-
	PLACE2000473	23.66	24.51	24.43	18.65	18.15	16.44	24.18	30.07	29.1	**		-	-
	PLACE2000477	14.25	12.47	18.55	9.69	12.47	6.23	10.6	9.09	9.9	*		-	-
	PLACE3000004	49.49	41.47	56.9	42.63	53.35	39.93	39.48	28.43	32.45	*		-	-
	PLACE3000009	30.13	36.74	28.18	19.79	35.05	20.31	13.54	15.44	20.29	**	**	-	-
55	PLACE3000020	27.99	24.44	23.74	13.45	15.64	8.65	14.29	14.44	13.63	**	**	-	-
	PLACE3000029	13.95	12.7	16.35	6.3	9.27	7.3	4.68	16.59	5.52	**		-	-
	PLACE3000038	6.52	4.32	7.69	5.63	3.97	4.12	2.68	6.95	6.18			-	-
	PLACE3000052	8.21	5.21	10.48	3.53	4.29	4.15	2.75	5.07	2.29			-	-
	PLACE3000059	7.39	6.1	10.8	4	5.08	2.55	2.83	4.28	4.31	*	*	-	-

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	PLACE3000067	49.68	45.52	57.37	38.78	41.13	26.16	39.8	46.08	41.69			
	PLACE3000069	22.6	20.15	23	9.32	14.75	10.81	1.9	9.3	14.16	**	*	-
	PLACE3000070	28.36	29.24	22.17	14.93	25.34	18.73	8.92	18.55	16.21	*	*	-
5	PLACE3000103	7.35	7.9	9.44	5.25	4.6	6.13	2.42	4.32	5.29	*	*	-
	PLACE3000119	35.89	28.1	30.76	15.16	14.79	15.09	26.05	30.71	30.91	**		-
	PLACE3000121	42.11	31.92	37.82	38.13	38.16	27.02	30.65	23.15	27.55			-
	PLACE3000124	419.8	380.05	314.65	379.74	412.05	282.09	411.56	374.59	344.25			-
	PLACE3000135	20.62	25.87	28.77	15.03	9.64	8.12	18.24	11.89	14.6	**	*	-
10	PLACE3000136	7.68	8.11	13.16	2.72	3.39	4.18	4.52	3.19	1.88	*	*	-
	PLACE3000142	24.15	28.81	26.5	11.04	24.59	15.08	9.37	6.94	11.56	**		-
	PLACE3000145	16.45	12.13	16.32	7.23	16.52	6.93	8.46	9.12	6.76	*	*	-
	PLACE3000147	109.42	62.46	138.9	40.47	87.42	32.89	57.71	63.5	68.14			-
	PLACE3000148	66.44	59.97	67.42	62.74	65.96	38.34	37.63	26.14	36.79	**		-
	PLACE3000154	10.3	11.14	12.88	7.95	8.64	6.56	7.31	6.3	7.57	*	**	-
15	PLACE3000155	54.28	50.77	22.77	23.49	28.34	24.7	10.12	11.93	8.34	*	*	-
	PLACE3000156	9.77	6.45	8.44	2.67	5.36	4.07	2.62	2.16	2.62	*	**	-
	PLACE3000157	38.44	50.52	36.49	23.64	29.36	25.04	21.36	24.91	20.01	*	*	-
	PLACE3000158	10.22	9.34	10.13	4.45	4.83	3.36	2.93	2.25	3.02	**	**	-
	PLACE3000160	19.92	29.65	15.93	8.71	11.7	10.32	5.77	7.29	4.57	*	*	-
	PLACE3000169	4.65	6.89	7.95	4.88	4.57	2.21	2.88	2.72	3.49	*	*	-
20	PLACE3000181	12.63	9.87	13.46	6.15	6.69	4.33	5.58	7.04	5.47	**	**	-
	PLACE3000194	1627	2636.2	1913.4	1710.4	2606.8	2399	3320.1	2826.5	2357.1			-
	PLACE3000197	7.18	4.55	8.38	2.14	1.71	1.66	2.79	2.24	2.57	*	*	-
	PLACE3000199	19.46	15.17	17.17	4.98	8.73	7.24	6.33	5.56	6.07	**	**	-
	PLACE3000205	12.53	16.93	16.84	6.91	6.83	4.67	7.28	5.87	4.15	**	**	-
25	PLACE3000207	7.97	6.69	7.83	2.48	4.45	2.85	2.71	2.19	2.08	**	**	-
	PLACE3000208	5.49	5.5	6.02	1.68	6.49	2.8	2.64	3.52	2.46	**		-
	PLACE3000213	40.02	27.48	31.62	27.29	30.91	23.89	26.59	30.58	23.2			-
	PLACE3000215	20.76	15.1	17.45	10.19	8.64	8.25	15.48	14.18	17.02	**		-
	PLACE3000218	13.39	10.52	10.44	6.03	3.81	4.29	4.65	4.57	4.68	**	**	-
	PLACE3000220	61.41	56.02	42.84	39.7	37	28.53	36.15	41.5	44.54	*	*	-
30	PLACE3000221	12.37	9.42	8.54	5.7	3.63	2.33	5.09	3.54	2.87	*	**	-
	PLACE3000225	180.89	144.07	131.66	176.14	175.29	127.3	77.77	64.65	86.2	**		-
	PLACE3000226	20.28	21.59	18.74	7.11	11.09	6.3	3.48	2.23	3.79	**	**	-
	PLACE3000230	17.46	18.98	14.94	6.27	14.11	10.52	4.65	3.25	5.88	**		-
	PLACE3000231	17.8	13.66	8.65	9.08	2.29	4.95	6.33	9.35	7.91			-
35	PLACE3000235	9.61	7.55	8.28	4.48	5.65	4.02	5.72	2.93	4.77	**	*	-
	PLACE3000242	58.11	27.4	48.85	17.82	13.76	17.4	11.61	10.29	11.25	*	*	-
	PLACE3000244	18.63	13.16	20	8.5	7.54	7.64	10.16	10.96	16.61	*	*	-
	PLACE3000253	56.99	47.97	42.85	32.37	25.93	24.8	32.98	24.76	32.96	*	*	-
	PLACE3000254	27.82	25.4	19.01	15.47	10.42	14.64	15.57	11.42	13.74	*	*	-
	PLACE3000271	14.58	20.8	13.28	5.71	8.52	5.71	8.32	6.43	8.38	*	*	-
	PLACE3000276	13.09	13.68	8.83	2.78	7.9	3.42	3.8	5.28	3.1	*	**	-
40	PLACE3000304	37.31	49.14	39.5	28.72	17.9	18.26	33.17	28.5	40.23	*	*	-
	PLACE3000309	12.29	9.64	9.42	6.2	5.6	4.27	5.42	4.79	6.47	**	**	-
	PLACE3000310	51.34	49.06	45.31	11.5	35.47	14.78	19.66	9.79	16.36	*	**	-
	PLACE3000320	24.3	28.51	23.33	14.31	20.51	12.27	15.7	15.03	15.45	*	**	-
	PLACE3000322	43.24	35.12	33.62	31.55	31.68	23.75	27.52	20.55	23.56	*	*	-
45	PLACE3000330	28.37	27.71	24.49	12.33	15.5	11.35	20.66	17.37	21.33	**	*	-
	PLACE3000331	6.68	8.07	7.67	6.55	5.13	3.84	2.57	2.99	0.04	**		-
	PLACE3000336	393.24	473.08	270.29	359.87	515.03	306.41	470.46	662.39	717.67			-
	PLACE3000339	11.78	5.98	6.82	3.79	5.41	2.48	9.74	10.29	11.53			-
	PLACE3000341	12.2	6.88	6.99	4.2	5.65	4.02	4.35	5.75	4.94			-
50	PLACE3000350	13.71	12.66	10.21	4.86	8.13	4.84	5.77	4.37	7.49	*	*	-
	PLACE3000352	17.23	29.11	20.8	9.42	15.27	8.16	11.43	7.14	13.58	*	*	-
	PLACE3000353	14.74	14.96	16.82	8.78	8.26	6.98	10.37	5.48	6.79	**	**	-
	PLACE3000362	57.42	93.8	72.53	67.02	59.59	35.38	59.68	38.27	60.6			-
	PLACE3000363	9.44	8.61	10.55	4.39	5.19	4.3	7.06	4.68	6.56	**	*	-
	PLACE3000365	5.59	7.45	4.94	1.48	2.65	3.2	4.78	2.37	2.95	*	*	-
55	PLACE3000373	38.45	30.27	25.57	4.05	7.88	3.63	14.16	11.37	15.74	**	*	-
	PLACE3000374	48.65	44.25	34.93	16.2	26.01	11.78	24.23	27.25	23.51	*	*	-
	PLACE3000387	5.55	3.77	3.38	1.58	3.57	0.43	3.58	2.95	3.21			-
	PLACE3000388	26.03	22.21	15.9	9.86	12.79	6.37	21.94	26.7	24.22	*	*	-
	PLACE3000399	15.37	13.07	9.83	5.64	4.9	3.93	10.68	11.05	9.52	**		-

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	PLACE3000400	42.78	33.52	30.29	11.43	26.51	8.47	52.76	33.47	38.46	*	-	-
	PLACE3000401	137.51	137.03	95.06	91.28	111.28	51.38	81.66	72.2	62.65	*	-	-
	PLACE3000402	8.43	7.72	4.24	2.44	6.58	2.29	8.31	7.96	5.44			
5	PLACE3000405	7.33	4.67	7.44	2.73	3.5	5.1	3.7	5.44	3.66			
	PLACE3000406	4.67	3.39	6.42	4.46	6.89	4.16	3.34	4.69	2.59			
	PLACE3000413	12.33	14.38	16.34	10.31	15.31	7.77	6.83	11.34	9.07	*	-	-
	PLACE3000416	84.6	58.17	41.71	94.16	126.08	86.52	51.61	89.65	63.01			
	PLACE3000425	2.87	4.19	4.03	2.67	4.11	2.12	2.08	0.77	1.54	*	-	-
10	PLACE3000437	6.08	4.62	9.74	3.57	11.5	3	3.57	3.67	4.77			
	PLACE3000455	6.66	7.45	7.23	5.48	5.38	4.19	5.5	5.74	3.82	*	*	-
	PLACE3000475	4.99	6.71	5.08	4.69	5.48	5.91	3.2	5.35	2.87			
	PLACE3000477	12.61	9.21	10.6	8.81	9.19	10.36	8.13	7.94	5.96	*	-	-
	PLACE4000003	30	20.47	39.94	8.43	18.43	9.82	12.11	10.52	8.23	*	*	-
	PLACE4000008	8.19	8.19	9.59	5.97	7.85	6.93	4.18	5.57	3.47	**	-	-
15	PLACE4000009	46.86	36	37.99	37.22	51.39	35.97	11.09	18.85	7.53	**	-	-
	PLACE4000014	18.34	18.57	19.39	16.62	19.49	16.59	6.08	13.2	15.87			
	PLACE4000029	5.3	5.07	5.95	2.91	4.87	2.62	3.69	3.02	2.87	**	-	-
	PLACE4000034	10.02	8.01	6.28	5.12	7.93	4.55	5.88	5.27	5.14			
	PLACE4000049	21.86	18.28	18.64	14.38	19.7	19.05	12.54	13.96	11.06	**	-	-
20	PLACE4000052	47.63	33.03	40.39	17.99	15.08	20.28	24.01	22.07	24.29	**	*	-
	PLACE4000062	53.46	46.6	50.02	32.69	40.48	28.08	39.71	36.99	45	*	*	-
	PLACE4000063	56.25	68.62	67.5	55.27	69.37	73.66	45.78	60.53	44.9			
	PLACE4000088	10.35	13.86	13.41	10.66	10.48	9.25	5.68	5.4	5.66	**	-	-
	PLACE4000093	15.33	18.02	19.57	10.49	13.84	10.33	17.17	14.6	14.04	*	-	-
	PLACE4000100	8.21	7.32	11.21	7.61	6.2	7.32	5.19	5.2	4.71	*	-	-
25	PLACE4000103	13.85	15.73	12.84	8.67	14.38	6.43	4.02	8.73	6.65	**	-	-
	PLACE4000106	32	18.81	23.23	18.35	21.38	15.86	17.78	20.58	18.06			
	PLACE4000128	22.05	18.53	23.14	8.88	10.24	9.57	11.18	17.49	11.76	**	*	-
	PLACE4000129	266.34	156.01	188.25	120.37	95.41	112.42	146.64	98.31	136.33	*	-	-
	PLACE4000131	59.1	45.51	65.57	41.68	34.82	39.78	18.29	19.7	30.83	*	**	-
	PLACE4000147	7.89	7.51	11.76	3.51	5.07	3.96	2.77	6.32	2.52	*	*	-
30	PLACE4000156	15.48	18.75	19.37	9.1	12.85	10.65	15.8	15.48	10.02	*	-	-
	PLACE4000175	12.45	10.41	18.08	11.94	9.67	2.46	6.38	6.69	6.89	*	-	-
	PLACE4000190	40.84	40.93	32.85	23.06	35.22	26.66	12.42	10.73	11	**	-	-
	PLACE4000192	35.69	24.13	23.88	16.77	21.59	17.55	17.75	19.51	19.4			
	PLACE4000206	33.82	29.03	26.48	11.73	17.97	14.5	17.45	20.16	20.02	**	*	-
35	PLACE4000211	12.98	13.88	13.86	7.96	9.94	9.19	6.64	31.04	6.54	**	-	-
	PLACE4000214	13.12	6.23	9.29	3.45	7.5	4.16	4.96	7.25	13.71			
	PLACE4000222	35.35	30.73	34.54	24.03	24.44	20.1	20.58	28.37	25.46	**	*	-
	PLACE4000223	14.88	14.83	15.03	7.36	10.28	5.52	4.16	7.67	5.85	**	**	-
	PLACE4000229	12.38	12.15	12.52	4.51	6.31	4.98	4.32	4.28	3.98	**	**	-
	PLACE4000230	9.56	8.77	9.56	4.68	7.06	5.7	4.97	9.82	3.71	**	-	-
	PLACE4000233	22.71	24.01	29.85	11.57	13.98	13.77	8.53	11.22	9.26	**	**	-
40	PLACE4000239	10.07	7.4	9.42	6.8	7.34	6.09	4.49	4.54	3.54	**	-	-
	PLACE4000247	15	11.82	15.56	9.41	13.91	8.87	8.67	6.24	7.39	**	-	-
	PLACE4000250	16.14	18.27	20.25	16.54	17.86	12.73	10.47	8.04	11.21	**	-	-
	PLACE4000252	10.01	5.15	12.75	1.39	3.96	3.1	2.21	3.92	2.7	*	-	-
	PLACE4000259	25.72	27.31	16.16	12.78	19.39	8.44	8.29	19.39	9.08			
45	PLACE4000261	23.52	25.16	22.9	11.05	14.2	9.22	13.61	14.62	13.29	**	**	-
	PLACE4000264	176.03	156.54	119.76	135.7	191.67	147.27	105.16	95.1	89.72	*	-	-
	PLACE4000269	71.18	49.07	62.08	23.03	41.63	24.74	71.71	82.6	52.18	*	-	-
	PLACE4000270	7.6	6.37	8.9	4.69	5.92	4.81	3.06	3.68	3.44	*	**	-
	PLACE4000281	15.26	16.07	18.29	6.09	10.92	7.61	6.44	6.66	5.1	**	**	-
50	PLACE4000300	8.43	9.82	8.78	6.3	8.5	7.03	3.68	2.93	2.96			
	PLACE4000320	12.37	11.22	11.92	6.27	10.09	6.43	4.47	4.26	2.85	*	**	-
	PLACE4000323	15.16	16.25	19.16	9.12	14.06	10.9	6.05	4.54	4.03	*	**	-
	PLACE4000326	11.15	8.97	10.53	4.35	4.69	4.13	4.28	3.68	4.65	**	**	-
	PLACE4000344	27.71	32.93	24.51	14.27	30.44	19.64	5.14	9.78	8.98	**	-	-
	PLACE4000347	156.82	129.54	154.28	89.79	129.04	79.82	138.06	137.09	135.75			
55	PLACE4000354	15.47	9.46	11.43	7.01	8.32	6.55	3.28	5.96	4.83	*	-	-
	PLACE4000367	8.63	5.47	7.82	5.38	5.39	6.72	3.84	3.95	3.64	*	-	-
	PLACE4000369	11.27	6.37	9.31	5.27	4.5	4.05	4.11	4.32	3	*	*	-
	PLACE4000379	6.35	6	4.77	3.22	2.93	2.33	3.1	3.32	2.21	**	**	-
	PLACE4000387	25.99	34.88	32.06	17.28	20.68	16.67	6.75	8.86	3.97	*	**	-

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	PLACE4000392	8.31	9.76	11.01	3.63	5.95	3.64	5.73	2.01	2.93	**	*	-	-
	PLACE4000399	53.9	51.54	53.26	20.64	28.55	18.63	37.94	35.1	44.54	**	**	-	-
	PLACE4000401	4.22	3.76	3.44	3.96	3.49	2.6	3.5	3.9	1.61			-	-
5	PLACE4000403	8.42	5.82	6.5	4.19	7.67	4.85	3.96	3.29	3.53	*		-	-
	PLACE4000411	20.23	15.5	15.73	8.23	11.19	9.81	14.98	10.1	11.34	*		-	-
	PLACE4000415	8.15	4.8	4.61	4.06	6.07	4.23	2.98	3.98	4.5			-	-
	PLACE4000416	35.43	25.11	24.69	17.72	17.34	16.23	24.55	17.6	25.73	*		-	-
	PLACE4000424	43.93	33.38	31.83	13.69	19.37	13.98	27.93	23.64	33	**		-	-
10	PLACE4000431	10.44	8.78	8.78	5.88	4.85	3.5	4.69	2.33	4.08	**	**	-	-
	PLACE4000443	50.64	44.47	41.43	26.49	37.08	21.33	51.22	33.11	43.74	*		-	-
	PLACE4000445	5.42	4.17	3.6	3.57	7.43	5.38	2.23	3.95	2.66			-	-
	PLACE4000450	9.85	6.68	6.23	4.72	6.64	4.07	3.56	7.58	3.73			-	-
	PLACE4000455	187.91	132.51	128.81	98.87	124.22	95.79	172.16	139.08	172.24			-	-
	PLACE4000465	31.84	25.74	18.83	10.79	23.42	11.27	11.29	10.8	17.69	*		-	-
15	PLACE4000466	13.01	11.54	9.57	6.56	6.92	4.59	5.76	4.65	5.6	*	**	-	-
	PLACE4000472	165.28	158.69	152.44	150.34	164.09	112.33	151.06	116.56	147.01			-	-
	PLACE4000487	10.38	6.99	9.12	4.68	4.63	2.93	3.52	2.06	3.49	*	**	-	-
	PLACE4000489	6.8	7.97	5.85	3.99	5.8	4.43	4.22	4.11	4.53	*		-	-
	PLACE4000494	70.51	55.91	43.58	29.17	31.84	24.64	72.67	73.79	78.08	*		-	-
20	PLACE4000502	204.58	180.8	176.1	156.92	166.08	118.92	216.32	165.78	200.53			-	-
	PLACE4000521	28.26	22.58	17.07	7.12	15.76	9	21.36	20.06	19.61	*		-	-
	PLACE4000522	18.46	20.38	16.27	10.46	14.51	9.51	16.91	13.88	17.23	*		-	-
	PLACE4000537	9.79	11.19	9.86	4.99	8.2	4.43	2.5	3.6	0.68	*	**	-	-
	PLACE4000548	12.35	10.52	9.27	3.9	4.07	4.41	4.08	3.04	3.64	**	**	-	-
	PLACE4000558	56.63	61.59	46.82	23.74	32.06	21.71	66.44	39.24	52.93	**	**	-	-
25	PLACE4000581	9.34	8.43	8.7	5.21	3.71	3.17	5.23	4.69	4.75	**	**	-	-
	PLACE4000590	4.28	4.39	2.54	2.29	1.9	1.58	2.69	1.47	1.72	*		-	-
	PLACE4000593	9.43	8.29	6.55	6.59	7.86	5.28	9.13	5.16	4.1			-	-
	PLACE4000612	50.54	44.64	46.86	32.73	32.12	18.75	8.58	0	9.68	*	**	-	-
	PLACE4000638	8.47	6.12	6.11	6.07	5.18	3.4	1.44	4.91	1.37	*		-	-
30	PLACE4000650	11.71	6	6.58	1.78	5.39	2.69	5.01	3.89	2.3			-	-
	PLACE4000651	10.02	10.01	7.86	4.63	8.67	3.43	7.21	6.04	5.23	*		-	-
	PLACE4000654	40.79	37.09	28.74	21.7	29.39	18.93	39.41	24.87	38.02			-	-
	PLACE4000670	7.33	7.03	6.77	5.23	9.34	3.97	6.41	3.63	6.87			-	-
	PLACE4000685	27.36	21.25	28.71	7.25	13.45	14.89	8.25	13.79	8.57	*	**	-	-
	PLACE4000687	5.87	2.72	5.94	3.75	3.52	3.04	2.8	3.66	2.1			-	-
35	PLACE5000003	13.69	15.66	16.08	8.92	15.85	13.17	6.36	9.93	8.84	**		-	-
	PLACE5000005	17.05	13.36	13.46	14.47	17.35	13.76	5.61	8.29	7.64	**		-	-
	PLACE5000019	9.12	11.38	11.73	6.9	5.65	5.55	3.51	3.39	6.14	**	**	-	-
	PLACE5000021	28.4	29.38	31.96	18.99	19.21	16.52	23.2	21.13	21.28	**	**	-	-
	PLACE5000022	44.41	69.47	62.06	68.78	41.05	40.85	49.9	41.64	44.86			-	-
	PLACE5000024	5.49	3.54	5.62	3.22	3.37	3.62	2.52	4.61	6.39			-	-
40	PLACE5000036	104.88	78.2	100.83	80.5	90.12	87.43	80.46	55.18	59.66			-	-
	PLACE5000059	13.88	12.58	10.61	5.28	9.26	6.17	6.41	11.67	8.16	*		-	-
	PLACE5000076	102.38	115.06	146.87	71.48	155.46	121.21	73.46	149.18	129.94			-	-
	PLACE5000117	10.83	17.74	16.15	14.79	20.06	15.63	5.73	9.53	5.57	*		-	-
	PLACE5000143	12.98	9.49	15.16	8.13	9.83	8.06	5.81	8.66	8.8			-	-
	PLACE5000152	183.88	202.8	96.28	147.85	104.4	116.95	74.92	70.73	75.92			-	-
45	PLACE5000154	90.81	106.58	44.13	75.4	77.68	45.59	40.84	23.33	50.85			-	-
	PLACE5000155	33.2	24.58	26.07	16.94	31.52	23.72	16.67	17.93	27.02			-	-
	PLACE5000165	113.75	76.52	82.55	90.32	103.03	88.36	32.72	55.94	39.36	*		-	-
	SKHNC1000004	1323.5	940.91	1083.3	665.71	1250.5	673.39	1094.9	1184.2	1060.5			-	-
	SKHNC1000011	8.28	9.06	11.81	4.48	12.47	5.45	4.79	5.44	8.03			-	-
	SKHNC1000013	14.72	15.01	20.62	10.84	11.72	12.41	4.74	6.54	6.23	**		-	-
50	SKHNC1000014	20.79	23.92	26.42	20.23	26.13	18.1	14.76	15.14	11.78	**		-	-
	SKHNC1000018	9.56	8.87	12.44	5.32	9.73	4.54	3.81	4.41	5.25	**		-	-
	SKHNC1000020	25.49	27.02	25.39	13.63	25.33	12.68	18.7	20.72	21.65	**		-	-
	SKHNC1000046	24.6	15.36	17.74	13.48	22.27	16.07	12.53	14.97	15.86			-	-
	SKHNC1000050	8.51	7.09	7.49	5.47	4.73	4.3	4.47	21.02	3.74	**		-	-
	SKHNC1000062	26.94	17.98	24.61	14.13	15.7	9.74	23.61	36.47	28.61	*		-	-
55	SKHNC1000075	11.6	7.44	13.24	7.34	10.78	7.51	4.21	5.3	7.09			-	-
	SKHNC1000082	22.01	16.02	26.11	8.38	13.04	9.62	12.8	21.17	16.8	*		-	-
	SKHNC1000091	36.26	39.39	43.7	12.98	23.22	18.68	24.3	27.26	22.42	**	**	-	-
	SKHNC1000099	11.34	8.86	15.64	6.38	7.5	4.4	5.83	7.15	6.38			-	-

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	SKNMC1000104	16.76	17.55	17.05	8.52	14.24	10.52	9.72	10.59	13.24	*	**	-	-
	SKNMC1000113	45.53	34.91	35.51	20.7	25.14	23.85	18.86	24.14	23.6	*	*	-	-
	SKNMC1000119	17.58	14.67	21.54	10.33	12.31	8.53	8.83	13.02	8.17	*	*	-	-
5	SKNMC1000142	16.52	20.57	23.49	7.26	16.72	11.75	8.01	11.68	14.09	*	*	-	-
	SKNMC1000170	242.49	183.41	211.38	201.28	226.18	182.82	247.45	216.7	250.73				
	SKNMC1000178	15.01	12.68	14.32	6.9	9.12	6.49	4.97	7.82	9.01	**	**	-	-
	SKNMC1000194	7.33	8.61	11.61	2.23	3.73	3.19	2.64	4.74	3.45	*	*	-	-
	SKNMC1000198	18.76	29.87	24.52	7.87	13.1	9.06	5.41	5.23	5.02	*	**	-	-
10	SKNMC1000225	100.44	119.68	87.32	52.94	84.28	50.45	35.91	33.78	44.06				
	SKNMC1000249	23.35	22.68	30.9	13.07	19.76	17.19	12.83	14.11	14.19	*	*	-	-
	SPLN1000007	10.7	10.7	16.74	6.92	9.27	7.23	6.86	7.37	5.89	*	*	-	-
	SPLN1000012	15.31	13.75	18.53	8.26	13.65	10.56	13.22	11.71	11.02				
	SPLN1000014	74.22	59.99	63.53	32.33	49.13	32.58	29.87	29.67	37.64	*	**	-	-
	SPLN1000036	14.69	11.54	10.05	7.95	8.19	6.93	3.18	3.76	2.42	*	**	-	-
15	SPLN1000059	39.71	33.5	32.87	12.1	19.81	12.24	19.97	18.35	17.18	**	**	-	-
	SPLN1000068	20.63	22.57	21.07	11.6	16.29	10.46	9.19	11.69	8.79	*	**	-	-
	SPLN1000072	19.88	16.83	14.96	6.06	9.86	7.47	5.18	4.49	6.78	**	**	-	-
	SPLN1000101	71.97	43.16	57.46	18.69	27.56	26.8	32.73	40.27	19.97	*	*	-	-
	SPLN1000108	7.69	6.28	7.07	3.65	4.35	2.67	3.12	2.84	2.04	**	**	-	-
20	SPLN1000113	11.47	6.64	12.13	7.54	8.23	7.26	5.5	6.27	7.59				
	SPLN1000114	16.01	14.75	14.36	7.29	9.65	6.3	8.14	8.22	8.73	**	**	-	-
	SPLN1000132	5.96	4.51	7.38	2.74	4.42	2.34	1.47	2.25	2.21	*	*	-	-
	SPLN1000135	10.57	8.18	9.39	3.86	4.71	4.73	4.9	2.38	2.97	**	**	-	-
	SPLN1000136	23.91	23.93	20.23	10.77	11.86	10.15	16.69	14.04	13.77	**	**	-	-
	SPLN1000141	42.88	39.73	42.83	27.16	32.91	23.4	23.31	18.41	20.57	**	**	-	-
25	SPLN1000164	15.72	13.33	13.69	7.76	12.46	6.69	9.59	8.11	9.12	**	*	-	-
	SPLN1000166	12.98	9.08	11.45	4.56	6.01	5.04	6.49	5.17	6.32	**	*	-	-
	SPLN1000175	19.26	16.94	15.5	7.48	9.23	6.92	11.34	13.49	13.41	**	*	-	-
	SPLN1000182	67.34	58.35	68.22	30.69	30.43	27.88	28.16	29.1	23.7	**	**	-	-
	SPLN1000185	6.38	8.35	5.56	4.69	4.56	3.06	2.86	2.31	1.51	**	*	-	-
30	THYMU1000004	48.79	34.96	41.97	30.97	32.65	27.64	26.98	17.5	13.12	*	*	-	-
	THYMU1000009	14.59	13.55	14.88	8.47	10.1	5	7.34	4.91	5.62	*	**	-	-
	THYMU1000015	19.34	18.55	12.08	8.34	11.37	5.93	10.39	10.96	13.03	*	*	-	-
	THYMU1000016	6.78	4.3	5.54	2.79	2.51	1.91	5.14	3.5	4.34	*	*	-	-
	THYMU1000023	6.35	6.23	6.53	4.39	3.65	4.2	3.1	5.69	3.98	**	*	-	-
	THYMU1000034	390.65	392.5	375.97	306.71	379.09	270.69	454.49	361.08	369.56				
35	THYMU1000035	8.93	7.8	9.14	5.88	4.95	4.81	5.06	3.93	4.36	**	**	-	-
	THYMU1000037	9.69	6.41	7.36	4.28	3.96	3.33	4.24	3.59	3.83	*	*	-	-
	THYMU1000042	6.85	3.93	5.82	2.75	3.24	2.02	2.08	1.63	1.09	*	*	-	-
	THYMU1000047	25.64	25.03	24.74	13.43	16.94	11.38	26.77	21.68	23.81	**	*	-	-
	THYMU1000080	20.17	51.54	27.22	17.42	19.98	26.99	13.06	15.8	14.07				
	THYMU1000094	11.12	6.99	9.51	6.45	6.49	4.35	11.14	9.41	9.31				
40	THYMU1000109	228.62	201.78	195.22	195.65	173.29	154.39	235.81	205.84	221.79				
	THYMU1000127	44.2	30.97	37.5	12.05	18.11	17.75	24.49	15.04	18.2	**	*	-	-
	THYMU1000130	21.64	17.3	15.84	7.65	12.45	8	10.24	3.41	8.22	*	*	-	-
	THYMU1000137	6.81	10.03	8.23	3.35	5.2	3.34	4.41	2.7	3.47	*	*	-	-
	THYMU1000146	11.97	7.39	7.48	8.11	7.24	6.17	5.13	3.03	6.19				
	THYMU1000159	10.45	10.21	8.17	6.28	6.42	3.77	4.54	3.62	4.78	*	**	-	-
45	THYMU1000163	8.08	8.93	9.7	5.33	5.95	3.66	7.57	4.17	4.21	**	*	-	-
	THYMU1000167	67.79	51.53	54.02	27.07	31.06	17.27	75.27	48.55	70.31	**	*	-	-
	THYMU1000186	8.38	8.15	3.89	3.94	4.49	2.65	3.36	2.91	3.02				
	THYRO1000017	24	17.58	11.71	8.21	11.63	5.25	6.04	5.8	4.42	*	*	-	-
	THYRO1000026	10.24	8.59	6.72	5.28	7.77	4.55	4.15	3.45	6.46	*	*	-	-
50	THYRO1000034	39.83	32.92	35.9	29.82	39.02	28.83	26.88	25.91	22.08	*	*	-	-
	THYRO1000035	34.67	27.15	24.29	22.39	30.44	22.35	22.09	19.28	23.65				
	THYRO1000036	16.2	14.28	11.79	9.92	10.8	4.36	7.94	4.75	8.23	*	*	-	-
	THYRO1000040	9.47	7.71	9.48	4.32	5.83	3	5.07	3.54	5.01	*	**	-	-
	THYRO1000061	18.28	19.76	15.63	8.28	5.85	4.81	6.42	5.28	9.19	**	**	-	-
	THYRO1000067	16.85	13.02	12.06	8.02	8.96	4.34	7.22	6.1	5.44	*	**	-	-
	THYRO1000070	9.96	13.03	10.58	5.63	9.48	4.69	20.02	18.33	15.63	*	*	-	-
55	THYRO1000072	21.57	19.92	18.73	19.89	17.94	12.39	9.77	9.74	9.5	**	*	-	-
	THYRO1000084	9.91	5.58	5.31	3.9	6.43	2.97	10.41	8.45	10.27				
	THYRO1000085	29.04	36.56	22.76	13.84	17.05	13.37	10.59	14.52	10.12	*	*	-	-
	THYRO1000086	13.56	10.42	8.08	7.5	9.36	4.87	6.64	6.5	4.47				

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	THYRO1000087	51.14	69.3	41.47	29.99	58.4	26.89	61.05	53.08	61.77				
	THYRO1000092	26.07	28.19	30.84	13.75	13.51	9.94	17.56	21.51	22.34	**	*	-	-
5	THYRO1000093	4.26	2.01	4.16	1.77	3.46	3.25	2.69	3.3	2.41				
	THYRO1000099	9.62	5.87	9.26	3.68	8.63	4.69	5.9	7.16	4.32				
	THYRO1000107	70.48	59.74	59.68	39.34	64.57	40.78	35.76	61.82	50.34				
	THYRO1000111	13.95	11.92	12.38	7.04	9.78	5.89	9.55	11.53	9.66	*	*	-	-
	THYRO1000121	31.45	32.43	38.13	15.06	18.17	17.71	26.05	28.32	34.79	**		-	-
	THYRO1000124	54.83	35.35	48.22	37.6	35.37	31.52	34.87	27.99	31.75				
10	THYRO1000129	8.59	9.01	8.49	5.14	9.82	6.06	8.93	8.73	10.55				
	THYRO1000130	12.23	8.25	10.08	6.62	6.95	6.32	6.99	9.76	9.68	*		-	-
	THYRO1000132	7.93	8.79	12	5.35	7.15	7.04	4.12	4.66	3.86		*	-	-
	THYRO1000134	17.2	6.06	9.3	6.24	6.27	12.5	5.33	7.31	5.41				
	THYRO1000144	23.66	30.56	32.27	27.55	32.97	28.83	18.04	19.4	19.02		*	-	-
	THYRO1000155	35.26	37.35	35.3	18.99	24.31	20.42	31.31	40.6	29.86	**		-	-
15	THYRO1000156	37.13	43.79	38.99	24.77	34.58	23.66	18.78	36.39	21.81	*		-	-
	THYRO1000163	56.18	53.4	58.15	23.96	28.08	23.46	11.7	14.01	16.02	**	**	-	-
	THYRO1000173	8.52	8.35	8.58	5.25	10.18	4.15	3.25	4.22	4.73	**		-	-
	THYRO1000186	35.39	31.09	36.48	14.41	13.8	14.41	7.62	12.05	15.91	**	**	-	-
	THYRO1000187	17.39	15.95	24.02	6.63	8.73	8.87	5.49	7.02	6.9	*	**	-	-
20	THYRO1000190	7.06	7.97	10.31	6.43	5.1	6.9	4.78	5.24	5.17		*	-	-
	THYRO1000196	8.72	14.15	13.33	14.25	10.93	7.74	3.75	6.65	9.84				
	THYRO1000197	13.75	17.13	15.02	14.96	17.34	16.5	8.34	11.47	6.36	*		-	-
	THYRO1000199	6.8	9.71	11.38	6.6	11.32	10.32	5.5	6.51	7.17				
	THYRO1000206	20.09	21.74	25.04	13.14	17.5	12.03	7.45	6.8	7.63	*	**	-	-
	THYRO1000221	6.96	7.15	5.44	4.48	8.31	3.94	3.81	4.45	3.66				
25	THYRO1000222	56.33	56.17	63.27	37.58	40.7	31.29	35.13	33.5	43.65	**	**	-	-
	THYRO1000228	148.64	127.09	184.25	73.36	64.55	57.59	55.06	55.21	55.09	**	**	-	-
	THYRO1000241	7.79	5.72	9.15	4.42	5	4.49	2.68	4.65	4.26	*	*	-	-
	THYRO1000242	18.16	23.99	29.76	25.09	51.85	27.45	12.5	20.02	16.61				
	THYRO1000246	21.57	18.12	24.56	19.46	20.13	15.33	9.29	10.17	9.72	**		-	-
	THYRO1000253	10.77	13.3	16.4	9.6	16.01	8.45	6.71	8.04	5.73	*		-	-
30	THYRO1000270	12.58	12.99	17.24	8.11	13.02	8.87	9.06	8.16	7.99	*		-	-
	THYRO1000279	15.04	13.53	16	8.28	14.2	7.73	7.71	7.11	4.92	**		-	-
	THYRO1000285	1215.2	1221.3	1148.5	961.64	1121.8	816.57	1261.8	1135.7	1518.7				
	THYRO1000288	24.11	22.65	22.01	13.89	25.53	14.41	22.83	21.93	20.34				
	THYRO1000296	40.86	36.2	38.51	33.51	37.84	29.24	32.78	49.02	40.29				
35	THYRO1000320	12.29	9.4	14.15	6.59	7.17	6.08	5.28	11.64	9.29	*		-	-
	THYRO1000322	37.49	34.76	35.08	17.69	26.05	19.02	19.43	23.34	20.74	**	**	-	-
	THYRO1000327	29.25	26.35	19.48	16.99	27.29	15.75	10.07	12.24	13.52	*		-	-
	THYRO1000343	16.65	12.58	17.82	8.18	11.42	7.21	10.1	9.05	8.44	*	*	-	-
	THYRO1000345	6.25	7.77	6.06	4.74	8.59	3.02	4.68	4.72	4.12	*	*	-	-
	THYRO1000358	13.06	10.33	11.35	6.24	8.76	7.32	8.15	6.51	9.21	*	*	-	-
40	THYRO1000368	5.38	5.26	6.26	3.15	3.94	2.68	6.19	3.06	2.43	**		-	-
	THYRO1000375	14.1	11.6	18.84	8.56	5.99	5.1	3.89	3.2	3.55	*	**	-	-
	THYRO1000381	10.31	8.3	9.78	4.37	5.3	5.96	4.17	5.35	3.59	**	**	-	-
	THYRO1000387	11.39	10.61	13.54	4.54	5.97	3.46	10.59	5.84	3.07	**		-	-
	THYRO1000394	61.78	50.97	22.02	14.67	26.91	8.08	6.98	9.73	11.33	*		-	-
	THYRO1000395	29.06	37.87	27.54	18.13	24.45	14.15	25.79	23.19	25.7	*		-	-
45	THYRO1000400	10.51	10.51	9.69	3.23	12.01	5.83	3.72	3.73	3.08	**		-	-
	THYRO1000401	10.42	9.53	10.77	6.74	5.06	4.73	3.24	5.18	5.6	**	**	-	-
	THYRO1000407	111.95	92.99	98.17	63.29	75.05	58.17	51.33	55.33	55.02	**	**	-	-
	THYRO1000420	15.01	13.25	17.92	11.1	11.62	8.56	12.79	12.37	14.41	*		-	-
	THYRO1000438	8.38	5.22	8.85	5.12	4.11	4.31	4.22	4.7	3.13	*		-	-
	THYRO1000452	15.04	12.59	12.97	5.92	10.6	6.13	2.16	3.93	4.57	*	**	-	-
50	THYRO1000455	7.17	8.57	9.52	2.62	3.31	3.44	2.83	2.18	2.11	**	**	-	-
	THYRO1000471	78.16	81.99	62.01	65.6	82.48	70.86	81.77	51.28	74.06				
	THYRO1000481	8.9	7.89	8.46	4.91	7.54	4.12	2.78	3.16	5.02	**		-	-
	THYRO1000484	19.83	12.76	16.87	10.37	11.59	9.38	11.21	9.7	11.91	*		-	-
	THYRO1000488	28.64	20.75	23.35	20.89	21.13	19.59	15.6	20.62	19.42				
55	THYRO1000501	11.59	12.72	13.28	7.74	9.03	6.79	8.05	7.95	10.26	**	*	-	-
	THYRO1000502	55.86	52.65	49.31	44.07	46.78	38.57	44.58	40.93	38.11	*	*	-	-
	THYRO1000505	9.64	7.65	7.27	5.56	5.82	3.06	3.98	5.47	2.02	*	*	-	-
	THYRO1000535	37.32	41.34	38.41	38.72	38.24	31.02	23.49	20.01	18.32	**		-	-
	THYRO1000556	102.92	92.57	85.3	76.31	104.96	62.73	51.56	50.77	49.93	**		-	-

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	THYRO1000558	8.54	7.17	6.38	4.15	8.61	3.01	4.26	2.04	3.45	*	-
	THYRO1000569	6.63	4.92	4.79	4.77	4	3.41	3.56	3.02	3.94	*	-
	THYRO1000570	9.09	6.95	8.33	5.27	6.38	6.54	5.25	4.89	7.09		
5	THYRO1000572	52.16	31.52	39.78	12.92	33.15	30.73	30.68	23.84	11.23		
	THYRO1000573	8.96	8.49	6.82	4.33	8.49	6.35	13.45	11.85	8.38		
	THYRO1000577	9.73	7.83	7.69	3.93	6.26	2.6	2.58	3.82	2.74	*	**
	THYRO1000580	40.56	32.54	29.95	22.22	19.86	19.81	24.19	17.34	25.52	*	*
	THYRO1000584	39.96	36.8	31.93	19.25	25.5	16.24	26.15	21.02	19.13	*	*
10	THYRO1000585	8.99	7.37	6.65	4.19	6.67	4.86	5.4	3.58	2.99	*	-
	THYRO1000596	43.85	33.14	32.61	22.94	31.65	11.59	15.52	10.88	14.47	**	-
	THYRO1000602	19.04	15.25	10.78	7.23	11.51	11.78	8.87	7.72	10.81		
	THYRO1000605	10.06	9.44	5.91	6.29	6.99	4.61	4.9	5.21	5.08		
	THYRO1000615	134.15	117.37	85.97	86.81	98.31	67.18	77.31	67	84.37		
	THYRO1000625	33.27	24.69	16.68	12.6	10.75	20.13	8.38	6.86	11.76	*	-
15	THYRO1000636	17.91	16.49	14.48	12.48	11.49	6.7	8.72	6.17	8.59	*	**
	THYRO1000637	18.22	22.2	13.43	10.39	14.05	9.78	9.07	5.2	7.26	*	-
	THYRO1000641	7.23	5.87	6.32	4.82	10.06	3.87	8.42	4.55	2.07		
	THYRO1000657	10.91	9.86	8.65	6.93	7.74	7.68	9.53	8.35	10.94	*	-
	THYRO1000658	14.37	9.48	5.1	6.28	6.83	5.43	4.59	4.62	4.77		
20	THYRO1000662	10.63	9.43	8.46	6.7	6.85	6.96	7.92	7.09	10.89	*	-
	THYRO1000666	30.51	33.5	45.43	12.9	20.33	13.81	14.6	13.53	16.48	*	**
	THYRO1000676	11.56	11.35	8.48	6.32	9.3	8.37	4.16	5.02	6.44	*	-
	THYRO1000678	23.44	18.73	20.73	10.13	15.99	8.49	9	7.38	9.87	*	**
	THYRO1000684	27.78	27.85	20.27	12.26	16.45	11.06	26.97	17.92	24.98	*	-
	THYRO1000694	16.87	11.78	10.72	5.47	10.25	5.99	12.29	9.36	8.6		
25	THYRO1000699	9.11	6.36	4.55	5.62	6.31	3.48	7.37	3.08	5.06		
	THYRO1000712	17.55	14.87	12.31	9.08	11.99	7.67	12.79	9.26	13		
	THYRO1000715	29.82	23.25	21.02	20.98	27.37	20.44	15.76	18.98	18.68		
	THYRO1000716	13.12	15.14	11.94	8.87	12	7.65	7.48	6.69	6.98	**	-
	THYRO1000717	11.89	15.21	12.45	6.9	9.22	5.08	30.93	6.96	7.18	*	-
	THYRO1000723	30.36	26.4	21.78	10.82	20.63	14.48	30.94	22.3	30.26	*	-
30	THYRO1000734	16.61	19.91	16.12	11.94	17.61	9.39	9.31	6.61	13.3	*	-
	THYRO1000748	17.46	14.06	15.87	5	7.52	5.42	7.82	5.84	7.09	**	**
	THYRO1000755	20.17	21.24	19.88	13.28	17.61	14.04	14.7	23.04	21.01	*	-
	THYRO1000756	369.81	334.57	369.63	298.51	345.41	273.28	259.37	366.07	273.4		
	THYRO1000776	4.97	4.99	7.55	4.25	6.18	4.82	2.58	5.02	3.55		
	THYRO1000777	5.42	5.63	6.34	5.34	6.01	4.03	3.82	3.75	3.21	**	-
35	THYRO1000779	483.37	458.9	483.51	453.87	549.42	449.1	368.6	510.93	458.47		
	THYRO1000782	17.27	20.25	23.35	14.58	17.12	13.37	15.61	16.4	16.35		
	THYRO1000783	5.74	5.45	6.68	5.43	9.62	4.88	3.62	5.19	3.8	*	-
	THYRO1000786	25.62	30.48	26.26	16.78	13.18	14.48	32.89	30.78	26.94	**	-
	THYRO1000787	50.52	37.21	54.05	28.71	18.06	26.25	20.11	24.5	22.66	*	**
40	THYRO1000792	14.11	12.1	15.65	4.55	6.72	7.1	8.13	7.14	8.33	**	**
	THYRO1000793	36.92	35.83	42.61	19.08	27.16	19.55	34.91	38.74	32.64	**	-
	THYRO1000795	37.33	45.29	88.32	42.19	57.36	40.15	12.57	21.17	13.38		
	THYRO1000796	10.25	11.83	14.01	6.19	10.21	5.98	7	11.89	11.1		
	THYRO1000798	9.87	14.22	12.83	9.06	8.1	7.49	5.04	7.33	5.2	*	*
	THYRO1000800	37.69	54.75	19.73	33.2	22.36	23.21	13.79	16.89	13.75		
45	THYRO1000805	8.27	6.21	6.02	5.33	8.39	4.44	3.81	4.14	3.82	*	-
	THYRO1000815	109.41	92.13	90.62	43.51	38.14	25.61	31.76	21.16	31.98	**	**
	THYRO1000829	33.86	25.13	34.71	19.68	21.68	18.45	16.87	14.34	12.65	*	**
	THYRO1000835	9.51	9.82	10.3	6.71	6.28	4.65	5.41	5.24	6.07	**	**
	THYRO1000843	27.06	16.5	24.96	16.28	19.34	15.73	6.22	7.81	8.06	**	-
	THYRO1000846	7.86	5.91	13.48	4.53	6.28	7.74	3.89	7.02	5.26		
50	THYRO1000852	24.69	25.37	23.66	12.87	20.2	12.5	9.33	10.39	11.62	*	**
	THYRO1000855	7.12	7.47	10.43	2.52	5.79	2.98	4.3	6.1	5.2	*	-
	THYRO1000865	9.21	5.67	8.64	3.4	6.56	3.18	5.99	8.76	7.67		
	THYRO1000866	57.27	46.1	51.69	32.85	43.74	27.97	46.24	39.05	41.55	*	-
	THYRO1000881	13.67	12.21	13.18	9.6	10.62	12.24	10.21	16.82	10.91		
	THYRO1000894	9.33	7.11	11.4	5.66	6.12	4.31	4.14	4.68	4.75	*	*
55	THYRO1000895	8.9	5.89	10.11	3.35	4.07	4.72	4.32	4.09	3.45	*	*
	THYRO1000916	9.19	7.72	16.87	5.02	6.67	5.27	4.16	6.12	3.42		
	THYRO1000917	6.89	10.63	12.32	4.97	9.51	5.39	6.77	7.94	6.2		
	THYRO1000926	14.99	10.81	12.37	6.79	9.95	6.06	7.42	7.03	11.27	*	-

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Table S01

	THYRO1000934	9.21	6.94	9.67	4.17	7.52	4.26	6.41	5.73	4.96	*	*	-	-
	THYRO1000951	21.19	13.82	17.24	10.15	10.71	6.54	7.11	11.34	11.56	*	*	-	-
5	THYRO1000952	38.82	45.17	51.97	24.88	24.37	18.77	17.55	26.97	13.34	**	**	-	-
	THYRO1000955	11.42	8.41	13.85	5.27	6.34	6.15	5.07	6.61	6.85	*	*	-	-
	THYRO1000960	9.97	3.83	8.63	2.78	4.13	2.34	2.46	2.03	6.43	*	*	-	-
	THYRO1000961	33.04	35.26	36.48	15.01	15.48	15.21	21.6	24.41	21.14	**	**	-	-
	THYRO1000964	14.43	12.46	17.93	3.92	6.7	5.62	5.43	7.53	4.58	**	**	-	-
	THYRO1000971	15.18	16.5	16.14	8.34	13.54	9	9.38	8.59	10.52	*	**	-	-
10	THYRO1000974	7.51	5.29	9.43	2.24	6.94	1.8	3.55	5.59	3.45				
	THYRO1000975	7.71	4.75	6.93	3.36	5.71	4.79	3.77	4.87	3				
	THYRO1000983	8.4	4.14	7.44	3.86	5.03	3.36	3.1	3.21	4.03	*	**	-	-
	THYRO1000984	9.35	8.4	11.52	6.49	7.32	5.22	5.08	2.55	2.65	*	**	-	-
	THYRO1000988	10.2	6.57	7.62	4.27	4.23	4.6	2.94	2.66	2.92	*	**	-	-
	THYRO1000991	12.33	10.95	12.47	5.27	7.49	7.34	5.57	6.15	6.01	**	**	-	-
15	THYRO1000999	9.77	12.84	10.64	5.68	8.33	5.92	5.68	3.11	2.9	*	**	-	-
	THYRO1001003	324.55	443.5	324.63	353.93	491.59	377.12	509.02	394.65	380.17				
	THYRO1001015	16.58	13.37	11.66	7.36	13.81	8.4	12.04	9.04	10.47				
	THYRO1001016	34.7	29.76	32.31	14.48	17.7	10.51	27.97	31.88	30.58	**		-	-
	THYRO1001022	27.6	17.2	20.61	6.98	9.39	10.85	5.35	6.58	6.8	*	**	-	-
20	THYRO1001031	15.75	9.57	11.29	5.12	7.05	5.99	8.13	6.39	9.34	*	*	-	-
	THYRO1001033	11.34	7.57	8.58	7.55	5.52	6.01	4.3	4.01	4.9	*	*	-	-
	THYRO1001062	12.86	12.45	12.49	4.68	5.59	4.88	3.54	3.68	2.79	**	**	-	-
	THYRO1001063	10.18	8.38	10.08	5.14	7.17	4.58	3.55	4.32	2.35	*	**	-	-
	THYRO1001071	18.49	15.5	18.23	9.12	10.91	7.86	5.73	5.41	5.84	**	**	-	-
	THYRO1001080	11.77	12.06	11.47	3.65	12.27	3.17	3.08	4.59	4.41	**	**	-	-
25	THYRO1001093	12.17	9.63	9.75	5.98	4.91	5	8.58	8.31	7.24	**	*	-	-
	THYRO1001100	33.06	27.59	26.02	30.29	27.98	30.28	66.02	40.22	70.38	*		+	
	THYRO1001102	10.18	6.7	5.95	5.04	6.9	4.52	4.36	4.71	4.45	*	*	-	-
	THYRO1001104	5.1	2.75	2.78	0.69	0.92	1.62	1.32	0.94	0.7	*	*	-	-
	THYRO1001109	19.62	18.07	14.26	10.98	10.98	9.76	8.55	11.06	8.68	*	*	-	-
	THYRO1001113	10.89	6.97	7.59	2.84	3.69	2.77	2.56	1.4	2.3	*	**	-	-
30	THYRO1001120	9.27	9	8.82	3.46	4.66	2.98	4.02	3.07	2	**	**	-	-
	THYRO1001121	20.41	16.36	16.91	9.1	13.05	6.93	13.22	15.3	13.97	*		-	-
	THYRO1001128	25.09	18.24	17.74	8.53	9.61	6.74	3.45	4.7	7.82	**	**	-	-
	THYRO1001133	7.42	6.4	5.88	4	5.05	4.23	3.88	4.14	3.81	*	**	-	-
	THYRO1001134	29.23	23.66	23.28	16.51	20.53	18.49	22.14	16.92	20.47	*		-	-
	THYRO1001142	5.04	4.99	5.1	2.78	3.05	3.47	2.44	2.26	1.6	**	**	-	-
35	THYRO1001173	31.85	26.04	28.94	20.36	18.72	13.59	18.5	15.33	18.17	*	**	-	-
	THYRO1001175	95.55	98.04	80.56	104.29	114.18	77.1	51.33	46.56	49.17	**		-	-
	THYRO1001177	10.9	11.18	11.71	5.13	7.17	5.9	4.63	5.82	5.02	**	**	-	-
	THYRO1001189	16.52	14.55	11.63	5.76	11.24	3.42	11.07	10.9	8.86			-	-
	THYRO1001194	11.83	6.2	11.19	5.29	7.22	4.28	5.84	7.01	6.86	*		-	-
40	THYRO1001204	52.04	33.32	32.8	18.53	22.19	18.27	39.75	37.94	46.59	*		-	-
	THYRO1001205	8.98	12.23	9.39	5.39	8.08	5.04	6.55	6.04	4.85	*	*	-	-
	THYRO1001213	41.54	37.73	35.86	23.36	25.7	20.79	37.67	32.41	38.62	**		-	-
	THYRO1001224	10.86	11.43	10.75	5.38	8.69	6.7	7.21	4.53	6.36	*	**	-	-
	THYRO1001237	16.76	20.25	15.97	16.59	13.69	5.38	9.78	5.69	6.27	**		-	-
	THYRO1001242	13.1	19.03	16.06	12.27	8.61	6.73	9.21	5.85	9.02	*	*	-	-
	THYRO1001258	27.32	21.68	20.65	9.74	18.76	12.77	10.51	6.86	13.04	*	**	-	-
45	THYRO1001262	8.57	4.74	4.06	3.76	5.65	4.02	4.79	3.93	5.05			-	-
	THYRO1001266	25.45	17.38	17.48	9.96	11.28	8.76	13.97	15.24	18.55	*		-	-
	THYRO1001271	27.85	25.6	17.14	13.77	18.43	9.74	22.54	18.92	23.05			-	-
	THYRO1001287	126.74	172.63	126.71	56.76	169.06	71.99	103.16	93.81	120.13			-	-
	THYRO1001290	11.3	8.82	9.68	4.97	7.48	6.55	3.86	5.84	8.41	*		-	-
50	THYRO1001291	13.9	16.44	13.22	8.85	8.33	3.9	6.83	3.64	6.66	*	**	-	-
	THYRO1001297	13.17	12.27	11.41	6.73	6.89	4.23	7.87	5.3	8.04	**	**	-	-
	THYRO1001302	28.98	24.47	17.01	9.99	19.11	8.25	41.39	28.42	36.98			-	-
	THYRO1001313	3.4	2.28	2.86	1.62	1.97	1.71	3.09	2.85	2.3	*		-	-
	THYRO1001320	4.85	2.3	4.45	3.81	2.95	2.21	2.67	2.22	1.94			-	-
	THYRO1001321	84.54	108.43	89.51	45.59	48.9	36.67	60.61	56.13	42.33	**	*	-	-
55	THYRO1001322	15.07	13.59	11.8	5.6	6.9	4.45	5.91	6.73	6.71	**	**	-	-
	THYRO1001327	61.14	62.79	47.56	27.21	36.08	29.25	40.32	44.89	30.36	**	*	-	-
	THYRO1001336	21.04	18.95	13.64	17.33	15.44	11.88	17.21	14.24	12.35			-	-
	THYRO1001347	42.47	35.49	29.56	20.44	37.43	12.7	20.26	16.34	15.93	**		-	-

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	THYRO1001358	6.96	7.77	6.52	4.41	8.39	3.78	5.37	5.5	4.22	*	*	-
	THYRO1001363	36.77	35.26	36.97	12.86	20.63	14.65	24.19	31.52	25.12	**	*	-
5	THYRO1001365	2.39	1.31	4.42	2.3	2.69	1.43	1.82	2.18	1.5			
	THYRO1001374	10.11	11.14	11.66	5.19	7.75	3.64	2.84	5.3	4.44	*	**	-
	THYRO1001401	11.45	8.59	8.77	5.02	5.3	5.96	5.5	8.56	6.31	*		-
	THYRO1001403	3.12	3.62	7.98	1.61	2.43	2.61	3.73	1.98	3.91			
	THYRO1001405	84.82	60.76	92.35	68.75	78.6	50.19	53.53	29.6	47.94	*		-
	THYRO1001406	13.59	7.57	12.02	4.76	6.87	3.76	11.69	13.59	9.54	*		-
10	THYRO1001411	4.72	4.15	5.65	3.88	2.4	3.38	2.52	2.5	3.6	*		-
	THYRO1001420	9.34	4.82	8.71	4.7	4.71	5.55	3.24	4.39	8.81			
	THYRO1001426	9.26	4.52	12.27	5.65	6.22	4.37	4.27	8.59	6.13			
	THYRO1001430	10.74	13.91	18.18	13.99	18.28	13.49	6.82	9.48	10.77			
	THYRO1001434	7.66	6.66	12.91	8.64	10.68	8.13	5.38	8.91	2.99			
	THYRO1001456	26.49	36.99	36.96	17.02	23.99	16.92	30.71	34.81	38.85	*		-
15	THYRO1001457	14.33	10.91	13.26	5.72	4.54	3.33	4.05	3.22	4.83	**	**	-
	THYRO1001458	15.32	13.83	12.78	10.99	10.13	5.72	4.4	7.29	6.97	*	**	-
	THYRO1001459	5.78	4.92	7.36	2.81	3.46	4.24	3.11	4.43	5.51	*		-
	THYRO1001471	13.48	10.81	13.3	5.13	9.62	6.19	6.36	8.85	9.45	*	*	-
	THYRO1001478	8.04	3.79	8.01	2.94	3.62	2.21	4.12	4.22	3.59			
20	THYRO1001480	16.07	16.86	14.48	6.78	13.68	13.34	3.54	6.61	19.35			
	THYRO1001481	16.23	13.97	17.19	13.3	15.2	13.73	4.94	6.01	3.76	**		-
	THYRO1001487	39.34	43.94	45.87	41.49	42.62	34.09	36.78	39.23	41.44			
	THYRO1001495	6.21	3.33	12.71	2.18	5.51	4.67	3.43	3.46	4.85			
	THYRO1001498	13.82	15.45	16.61	11.32	20.15	8.37	4.81	6.08	4.31	**		-
	THYRO1001510	9.97	6.87	19.31	8.41	6.21	3.55	4.99	6.45	19.57			
25	THYRO1001512	11.51	8.21	10.34	5.87	6.36	6.84	4.43	19.67	5.22	*		-
	THYRO1001519	12.05	16.47	10.9	4.73	8.69	4.14	4.42	4.28	5.04	*	**	-
	THYRO1001522	10.39	6.84	12.83	6.15	7.71	8	5.13	5.33	7.56			
	THYRO1001523	15.14	10.51	16.01	7.01	9.2	6.38	3.77	3.19	4.5	*	**	-
	THYRO1001526	5.67	5.48	12.84	2.85	5.19	3.09	4.51	3.63	4.01			
	THYRO1001529	70.52	99.68	61.07	73.62	81.82	35.88	29.07	23.9	34.69	*		-
30	THYRO1001534	10.48	7.92	11.72	6.09	7.42	11.24	6.53	6.35	3.17	*		-
	THYRO1001537	5.9	3.05	5.93	3.4	3.75	2.75	3.26	2.87	4.91			
	THYRO1001541	27.84	38.72	38.42	23.51	30.22	18.99	22.01	26.98	14.85			
	THYRO1001549	12.87	9.76	11.61	3.56	6.9	5.41	4.16	22.14	4.44	**		-
	THYRO1001559	143.67	217.09	127.43	126.92	211.99	217.97	165.83	143.91	101.7			
35	THYRO1001563	29.66	25.88	28.83	14.46	17.77	19.17	10.82	18.32	17.35	**	**	-
	THYRO1001570	5.85	5.24	10.72	3.21	3.79	2.31	2.47	4.03	3.05			
	THYRO1001573	10.58	14.52	15.67	7.66	10.98	10.26	4.93	9.17	5.76	*		-
	THYRO1001584	11.71	9.79	13.05	7.75	12.43	7.3	8.19	4.82	4.88	*		-
	THYRO1001593	119.63	87.93	122.57	37.27	54.3	33.56	100.89	84.41	119.61	**		-
	THYRO1001595	9.11	9.13	10.8	7.84	8.88	6.77	4.62	12.97	7.82			
40	THYRO1001596	6.25	3.54	8.97	3.03	4.5	2.76	3.54	3.67	4.02			
	THYRO1001602	7.1	6.21	7.8	6.63	4.96	5.02	4.21	4.12	2.97	**		-
	THYRO1001605	28.22	39.54	25.87	13.48	23.89	22.57	11.83	10.02	13.09	*		-
	THYRO1001608	19.26	17.94	17.77	8.3	22	8.49	8.07	8.36	11.18	**		-
	THYRO1001617	7.36	9.07	12.26	4.4	5.61	3.53	3.83	3.37	4.51	*	*	-
	THYRO1001634	9.8	9.15	14.08	5.65	9.76	4.62	5.62	3.69	4.86	*		-
45	THYRO1001637	6.56	2.42	6.39	2.18	3.8	2.31	2.41	3.7	6.48			
	THYRO1001641	12.87	8.05	12.44	6.03	4.87	6.49	3.32	2.86	2.92	*	**	-
	THYRO1001656	20.03	12.66	30.89	7	10.07	5.22	6.32	7.53	5.64			
	THYRO1001658	7.58	6.85	10.14	4.65	4.77	3.94	3.38	2.8	2.5	*	**	-
	THYRO1001661	150.1	98.3	106.51	135.25	166.2	125.8	74	80.32	53.76			
50	THYRO1001671	10.97	8.43	12.21	5	5.04	3.97	5.12	5.12	3.84	**	**	-
	THYRO1001672	12.9	11.31	11.75	5.85	6.91	5.08	3.69	2.74	2.72	**	**	-
	THYRO1001673	31.04	28.57	26.79	16.85	19.7	19.9	22.8	23.43	23.51	**	*	-
	THYRO1001677	8.63	6.86	9.97	3.55	4.9	4.2	5.4	6.55	6.85	*		-
	THYRO1001683	39.34	16.85	25.87	16.11	18.7	19.17	8.36	10.76	9.09			
	THYRO1001700	12.31	7.03	9.15	3.61	4.23	3.04	2.79	3.63	4.8	*	*	-
55	THYRO1001702	23.7	21.62	17.4	10.57	5.8	11.44	6.01	4.83	2.94	*	**	-
	THYRO1001703	7.22	4.23	5.14	2.63	3.23	1.81	2.37	2.42	2.04	*	*	-
	THYRO1001706	8.38	5.62	8.09	3.72	3.11	3.37	3.24	2.65	1.26	*	**	-
	THYRO1001721	11.69	10.42	16.73	6.09	4.96	4.46	3.92	2.33	3.87	*	**	-
	THYRO1001725	147.69	144.4	144.74	111.99	128.3	86.63	130.43	106.61	93.76	*	*	-

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	THYR01001730	7.74	3.57	7.41	4.48	4.19	3.07	3.64	4.09	4.72			
	THYR01001738	1.57	3.03	2.24	0.97	0.17	0.58	0.7	0.99	1.64	*	-	
	THYR01001743	5.12	3.48	3.39	1.67	2.12	2.94	1.98	2.6	2.48			
5	THYR01001745	30.25	14.84	20.6	6.81	4.65	9.25	12.7	8.09	11.05	*	-	
	THYR01001746	10.78	5.89	7.69	2.83	3.1	3.64	3.64	1.32	2.13	*	-	
	THYR01001770	20.01	12.02	16.57	10.05	13	10.49	5.37	6.07	5.43	*	-	
	THYR01001772	29.2	56.08	29.11	28.47	34.34	15.95	9.21	8.24	9.37	*	-	
	THYR01001778	39.03	35.61	22.42	13.39	32.45	16.04	9.42	8.03	11.2	*	-	
	THYR01001793	9.35	3.26	5.98	4.02	4.49	3.37	4.45	4.26	5.77			
10	THYR01001796	66.96	62.34	52.36	31.61	31.58	30.06	74.83	63.67	78.59	**	-	
	THYR01001800	25.21	17.42	21.74	19.92	16.43	13.71	8.41	10.02	11.59	**	-	
	THYR01001803	12.96	11.11	10.61	7.04	8.3	3.44	5.71	5.48	6.64	*	-	
	THYR01001809	10.44	7.96	6.8	4.59	3.72	3.71	3.62	1.76	1.34	*	-	
	THYR01001817	18.78	13.28	15.51	15.03	13.53	6.93	8.79	4.88	8.37	*	-	
15	THYR01001819	14.15	14.31	9.69	5.8	6.63	6.06	6.27	4.29	5.81	*	-	
	THYR01001828	8.14	8.22	6.65	5.42	7.94	4.29	7.29	4.26	2.47			
	THYR01001854	50.53	32.88	37.71	33.17	34.18	22.81	22.16	27.13	21.15	*	-	
	THYR01001895	9.86	7.83	3.92	4.41	4.53	2.55	3.7	10.54	3.46			
	THYR01001907	27.03	13.41	12.49	9.48	10.54	7.02	4.92	4.41	6.47			
20	TRACH1000006	9.54	7.16	8.08	5.68	4.66	5.53	6.46	4.52	6.76	*	-	
	TRACH1000013	9.02	5.8	8.2	2.58	4.45	3.1	3.07	2.02	4.14	*	-	
	TRACH1000074	13.69	9.32	8.63	4.66	5.76	4.06	6.37	3.07	3.63	*	-	
	TRACH1000095	11.28	8.48	10.55	5.54	3.9	3.41	3.79	4.56	3.68	**	-	
	TRACH1000102	26.86	26.3	20.1	15.81	18.57	15.2	32.52	24.6	27.09	*	-	
	TRACH1000108	88.66	59.61	40.48	28.57	26.39	20.8	69.3	56.08	66.91			
25	TRACH1000126	17.36	13.19	13.78	8.07	9.6	6.46	5.91	5.75	6.51	*	-	
	TRACH1000146	7.25	6.83	5.07	5.29	3.75	3.17	3.49	3.25	4.97	*	-	
	TRACH1000160	11.76	11.24	7.7	4.05	5.59	4.95	5.32	4.22	5.87	*	-	
	TRACH1000184	33.51	45.86	50.29	14.82	25.81	22.15	25.29	16.88	23.76	*	-	
	VESEN1000004	11.35	8.9	8.13	5.46	9.59	6.32	5.53	5.44	6.01	*	-	
30	VESEN1000007	32.64	30.13	26.81	16.7	21.99	18.54	37.62	29.73	33.89	**	-	
	VESEN1000013	13.16	11.68	12.05	7.19	9.9	4.25	7.18	4.46	8.92	*	-	
	VESEN1000028	23.17	20.53	28.94	10.16	15.29	14.76	9.13	12.72	8.48	*	-	
	VESEN1000059	4.76	3.32	5.57	3.56	3.32	3.56	1.16	3.33	1.96			
	VESEN1000100	8.85	5.84	8.92	5.55	6.82	5.48	3.69	5.59	3.98	*	-	
	VESEN1000107	158.28	125.83	134.47	126.46	135.37	133.6	74.61	79.36	82.66	**	-	
35	VESEN1000117	3.74	4.02	10.93	3.48	5.02	4.1	2.18	2.11	2.69			
	VESEN1000122	5.84	5.31	7.17	3.91	7.47	3.29	2.52	3.75	2.41	*	-	
	VESEN1000137	7.93	10.91	7.7	8.31	5.46	4.02	3.34	3.36	5.77	*	-	
	VESEN1000195	12.47	4.75	10.07	4.43	4.22	7.07	3.11	4.32	13.25			
	VESEN1000215	89.55	69.15	78.83	74.46	93.71	81.06	50.08	36.95	43.24	**	-	
	VESEN1000279	16.42	11.12	19.97	7.86	19.23	9.52	8.84	13.86	21.33			
40	VESEN1000363	40.43	29.46	56.48	41.4	53.72	50.13	17.51	33.82	20.25			
	VESEN1000388	4.51	6.13	9.09	5.56	8.45	6.21	3.44	6.29	2.57			
	VESEN1000394	137.33	123.92	135.03	107.32	177.33	115.58	81.85	76.56	86.04	**	-	
	VESEN1000410	7.84	11.73	12.31	7.37	8.85	7.32	5.82	6.16	5.5	*	-	
	VESEN1000411	14.34	16.7	11.87	14.26	14.7	9.52	6.54	4.28	7.07	**	-	
	VESEN1000416	6.65	6.22	8.5	3.16	5.01	4.35	2.06	3.93	7.37	*	-	
45	VESEN1000440	7.1	4.56	7.48	10.06	4.69	9.04	3.62	6.97	6.76			
	VESEN1000452	127.08	114.54	102.58	100.33	106.23	122.79	77.87	58.16	82.71	*	-	
	VESEN1000539	57.4	47.68	67.32	36.3	45.7	42.57	51.56	51.15	50.18			
	VESEN1000554	7.29	12.24	14.13	6.05	4.57	6.75	3.69	3.4	3.85	*	-	
	VESEN1000557	4.5	6.91	10.86	5.64	5.73	4.35	3.05	2.96	4.75			
	VESEN1000575	16	18.27	24.28	11.3	16.07	11.77	13.59	13.83	16.27			
50	VESEN1000585	14.4	14.28	13.38	9.87	13.37	6.72	4.91	4.08	5.01	**	-	
	VESEN1000592	28.09	20.04	22.75	8.98	11.53	7	7.53	8.48	8.84	**	-	
	VESEN1000658	9.27	5.98	6.99	4.92	3.93	3.11	3.31	12.18	6.06	*	-	
	VESEN1000669	7.65	11.62	18.09	8.2	9.11	7.91	4.21	6.96	3.61			
	VESEN1000743	27.12	25.27	28.48	19.46	23.17	19.77	12.01	15.14	12.53	*	-	
	VESEN1000752	23.77	18.91	24.8	11.19	11.63	9.8	14.24	19.48	18.19	**	-	
55	VESEN1000761	7.03	8.3	9.9	5.64	5.41	3.65	3.1	8.25	5.47	*	-	
	VESEN2000039	16.58	20.4	16.46	7.12	12.23	7.45	5.23	4.66	6.91	*	-	
	VESEN2000102	15.76	17.97	17.55	7.45	12.52	8.13	11.35	8.16	13.31	*	-	
	VESEN2000164	69.66	54.85	54.07	18.32	20.39	15.6	15.69	21.51	20.97	**	-	

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	VESEN2000175	7.45	6.95	7.39	3.43	6.1	3.72	4.64	8.1	4.35	*	-	-
	VESEN2000186	18.04	20.73	21.8	11.19	14.77	10.58	8.74	12.84	12.61	**	**	-
	VESEN2000199	11.71	6.48	9.96	8.59	9.24	5.52	6.89	6.26	14.79	*	*	-
5	VESEN2000200	150.21	142.83	144.63	172.94	215.31	128.05	93.38	87.48	97.05	**	-	-
	VESEN2000204	7.05	7.07	9.65	4.56	4.24	3	2.19	4.63	3.19	*	*	-
	VESEN2000218	16.65	12.07	17.29	7.31	8.24	6.16	8.32	5	5.15	**	**	-
	VESEN2000230	12.09	13.48	13.57	4.57	10.45	4.08	3.93	4.19	2.98	*	**	-
	VESEN2000272	8.95	9.01	11.14	4.32	3.66	3.22	4.36	3.53	4.22	**	**	-
10	VESEN2000299	8.61	7.23	11.81	5.04	5.83	4.25	3.6	5.71	4.76	*	*	-
	VESEN2000323	17.3	12.74	15.22	15.36	17.47	14.24	5.84	6.35	4.65	**	-	-
	VESEN2000327	18.5	9.19	14.45	6.81	8.17	7.45	3.2	5.07	5.85	*	-	-
	VESEN2000328	7.53	7.78	8.38	3.45	4.17	4.12	2.35	2.19	1.81	**	**	-
	VESEN2000330	25.07	20.15	22.73	13.34	18.45	13.16	15.63	15.15	15	*	**	-
	VESEN2000336	7.29	9.37	11.82	5.86	9.09	5.78	3.64	3.5	5	*	*	-
15	VESEN2000354	10.99	9.78	10.4	5.27	8.22	4.93	3.58	3.58	2.59	*	**	-
	VESEN2000378	168.58	110.88	139.59	81.44	99.69	74.23	74.17	76.59	54.75	*	*	-
	VESEN2000379	32.08	21.47	28.34	16.72	15.12	13	22.77	26.45	21.84	*	-	-
	VESEN2000397	21.17	10.11	25.4	12.77	12.2	10.8	15.72	16.01	17.99	*	-	-
	VESEN2000416	5.92	5.21	7.48	3.5	6.28	4.01	2.87	3.94	3.48	*	-	-
20	VESEN2000420	8.47	4.35	7.18	4.04	3.81	2.46	2.31	4.27	1.92	*	**	-
	VESEN2000430	8.74	5.76	7.33	2.94	5.32	2.11	1.8	2.27	0.71	*	**	-
	VESEN2000448	14.67	14.58	16.08	4.71	4.34	2.88	3.91	2.23	2.27	**	**	-
	VESEN2000449	46.1	50.29	39.97	32.75	32.82	21.56	37.62	28.99	23.73	*	*	-
	VESEN2000456	45.88	33.52	32.47	18.88	21.08	19.47	15.48	22.28	22.31	*	*	-
	VESEN2000562	6.11	3.13	4.69	5.4	3.95	3.19	3.24	2.45	2.42	*	*	-
25	VESEN2000573	26.67	20.52	18.39	14.29	11.45	8.79	8.94	7.46	12.2	*	*	-
	VESEN2000604	9.02	7.76	4.59	4.65	4.32	4.42	1.84	4.41	1.34	*	-	-
	VESEN2000614	9.59	7.78	6.05	4.77	5.05	4.35	3	3.94	2.87	*	*	-
	VESEN2000638	16.75	10.83	10.74	6.38	9.46	6.26	4.67	4.46	3.5	*	-	-
	VESEN2000641	15.71	14.29	14.25	7.95	7.6	6.71	8.94	7.41	6.6	**	**	-
	VESEN2000645	9.28	11.51	10.66	5.27	8.01	4.95	5.42	4.96	6.81	*	**	-
30	Y79AA1000013	24.66	15.88	15.09	6.08	5.43	5.53	13.59	13.07	18.88	*	-	-
	Y79AA1000030	19.52	16.62	14.47	8.07	7.77	10.99	7.86	7.77	10.02	*	**	-
	Y79AA1000033	29.91	18.65	28.38	16.37	15.72	11.59	28.15	19.64	28.85	*	-	-
	Y79AA1000037	4.94	2.8	4.89	5.26	3.24	0.91	1.44	1.94	2.43	*	-	-
	Y79AA1000041	79.98	53.74	54.67	39.77	36.14	29.21	42.77	30.09	45.97	*	-	-
	Y79AA1000059	9.8	7.3	8.44	4.37	5.08	2.06	5.32	3.01	5.11	*	*	-
35	Y79AA1000065	116.14	101.03	106.53	93.49	124.96	111.44	68.74	63.93	65.56	**	-	-
	Y79AA1000081	7.88	11.03	9.72	7.03	9.28	7.22	5.68	4.38	3.88	**	-	-
	Y79AA1000127	8	5.82	6.2	3.17	4.25	2.35	5.28	6.34	4.47	*	-	-
	Y79AA1000130	20.16	11.01	14.68	13.04	8.43	8.05	14.41	16.35	14.16	*	-	-
	Y79AA1000131	17.14	8.99	11.18	6.93	10.63	6.92	6.82	8.55	6.52	*	-	-
40	Y79AA1000134	6.34	7.52	5.68	7.86	5.61	3.09	4.16	2.2	3.07	*	-	-
	Y79AA1000143	8.89	7.38	8.14	3.93	5.83	3.75	3.23	2.53	3.96	*	**	-
	Y79AA1000144	11.79	8.62	9.18	5.64	6.37	5.56	3.97	3.84	3.36	*	**	-
	Y79AA1000150	28.57	28.05	20.04	12.4	17.77	10.86	24.46	16.09	20.29	*	-	-
	Y79AA1000153	11.32	11.62	7.41	5.89	9.36	6.53	6.84	5.59	6.52	*	-	-
	Y79AA1000166	13.75	6.3	9.45	4.16	5.68	2.88	7.42	8.85	8.76	*	-	-
45	Y79AA1000178	13.15	8.67	7.74	7.91	7.5	4.67	13.52	5.81	9.18	*	-	-
	Y79AA1000181	14.37	9.22	8.77	6.64	8.41	3.93	3.41	3.97	4.65	*	-	-
	Y79AA1000202	22.9	17.78	19.17	14.55	12.31	8.36	18.27	13.59	20.94	*	-	-
	Y79AA1000207	52.28	63.3	44.9	24.04	38.89	23.79	15.85	13.31	14.27	*	**	-
	Y79AA1000214	9.44	4.9	5.66	4.71	4.78	4.18	5.54	2.28	3.2	*	-	-
	Y79AA1000222	11.34	8.61	7.95	5.13	7.04	2.26	4.7	3.53	4.67	*	-	-
50	Y79AA1000226	27.21	25.59	19.24	12.19	15.74	11.35	24.75	16.69	21.48	*	-	-
	Y79AA1000227	9.07	6.57	6.62	3.66	4.45	3.9	7.4	6.45	7.51	*	-	-
	Y79AA1000230	32.97	25.47	29.26	12.55	10.05	6.68	4.18	3.82	4.93	**	**	-
	Y79AA1000231	65.27	41.2	48.87	47.4	47.89	24.64	28.97	32.14	28.29	*	-	-
	Y79AA1000239	74.35	85.68	67.35	68.07	52.75	45.41	64.49	54.97	44.91	*	-	-
	Y79AA1000258	8.42	5.48	5.2	4.36	4.01	3.09	3.34	2.93	4.62	*	-	-
55	Y79AA1000268	80.53	75.19	49.36	22.18	30.03	27.42	30.39	28.87	31.5	*	*	-
	Y79AA1000269	73.43	71.24	52.77	41.13	70.01	36.67	77.91	62.7	65.45	*	-	-
	Y79AA1000270	10.85	7.03	4.1	4.98	7.95	3.4	5.03	5.7	4.72	*	-	-
	Y79AA1000280	25.49	25.11	28.96	8.6	12.9	9.27	5.74	8.76	6.26	**	**	-

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	Y79AA1000285	22.27	16.31	18.63	6.85	10.3	7.36	15.47	22.31	18.91	**	-	-
	Y79AA1000295	4.35	2.68	5.01	1.59	3.76	2.11	2.3	2.59	2.22			
	Y79AA1000307	6.82	4.93	8.12	6.39	9.3	7.36	3	5.88	4.49			
5	Y79AA1000313	4.28	2.34	3.94	1.66	3.1	3.25	1.93	2.47	1.62			
	Y79AA1000314	1.57	1.83	4.11	1.4	1.41	0.98	0.87	0.14	1.73			
	Y79AA1000328	3.78	3.39	5.43	2.09	10.7	2.68	3.27	3.33	3.32			
	Y79AA1000334	9.59	9.06	7.49	5.79	6.64	3.5	5.12	3.62	4.02	*	**	-
	Y79AA1000342	17.48	13.29	18.31	13.02	15.9	13.67	34.2	31.79	30.43	**		+
10	Y79AA1000346	17.08	11.48	18.69	8.72	9.82	6.74	5.35	5.97	4.15	*	**	-
	Y79AA1000347	28.82	26.71	31.26	22.14	31.96	28.74	20.9	20.82	19.69	**		-
	Y79AA1000349	15.95	20.35	20.7	17.44	19.4	18.58	5.37	7.08	5.15	**		-
	Y79AA1000355	11.9	11.6	17.89	14.98	13.32	9.11	5.25	6.54	7.95	*		-
	Y79AA1000368	5.31	4.56	7.88	4.89	6.47	3.77	2.77	3.21	1.95	*		-
	Y79AA1000388	9.85	11.63	11.71	9.62	9.75	4.51	5.03	4.57	5.04	**		-
15	Y79AA1000392	13.05	13.68	11.25	7.92	12.06	6.34	12.1	13.67	13.52			
	Y79AA1000405	100.68	62.31	79.28	103.67	109.59	81.35	71.19	52.24	66.44			
	Y79AA1000410	8.13	6.1	10.22	6.13	5.36	5.28	4.83	4.8	5.17			
	Y79AA1000420	11.1	11.77	13.46	5.41	8.52	5.43	6.77	7.21	5.64	*	**	-
	Y79AA1000423	7.61	9.21	8.96	4.46	6.29	5.4	4.36	2.75	3.4	*	**	-
20	Y79AA1000426	5.75	6.96	10.06	4.68	5.08	3.97	3.38	2.69	2.24	*		-
	Y79AA1000432	5.62	5.18	10.2	4.71	5.75	4.03	2.85	3.99	8.12			
	Y79AA1000453	32.42	33.52	37.01	20.21	25.21	18.7	36.98	32.84	33.05	**		-
	Y79AA1000465	4.43	1.91	3.14	1.7	4.29	1.76	2.57	2.29	2.11			
	Y79AA1000469	35.31	28.37	27.42	30.17	34.28	32.32	21.89	31.66	24.15			
	Y79AA1000480	11.78	8.51	13.38	5.22	5.02	5.9	5.84	10.93	8.28	*		-
25	Y79AA1000502	19.24	16.15	21.16	8.66	14	12.35	16.39	18.08	18.17	*		-
	Y79AA1000521	75.16	71.09	84.73	74.85	78.28	67.85	48.04	51.73	45.89	**		-
	Y79AA1000534	13.31	15.15	20.4	13.25	14.05	10.71	13.15	11.71	11.75			
	Y79AA1000538	12.36	14.67	20.45	9.58	11.27	5.96	3.97	0	4.64	**		-
	Y79AA1000539	15.51	16.32	14.99	9.48	12.74	10.1	5.39	5.2	6.13	*	**	-
	Y79AA1000540	10.2	7.44	12.08	3.41	6.65	4.35	12.15	10.44	10.32	*		-
30	Y79AA1000560	180.34	128.09	149.28	162.08	194.06	150.66	118.75	125.1	108.26			
	Y79AA1000574	12.15	9.72	10.83	5.66	8.8	4.53	10.59	16.21	10.56	*		-
	Y79AA1000584	40.26	35.5	37.1	23.89	28.68	25.51	26.96	34.59	37.41	**		-
	Y79AA1000589	9.65	4.15	9.45	2.79	3.53	2.1	3.54	8.38	4.6			
	Y79AA1000598	34.26	29.42	37.32	17.43	15.95	16.46	24.99	27.55	21.09	**	*	-
	Y79AA1000600	44.58	45.66	51.58	51.4	52.23	39.65	32.06	30.08	26.05	**		-
35	Y79AA1000609	7.91	6.61	8.76	1.95	5.66	3.3	3.74	4.36	7.05	*		-
	Y79AA1000618	20.27	20.13	21.51	6.61	13.31	6.56	19.86	14.92	16.1	**		-
	Y79AA1000627	18.35	16.53	18.66	9.09	10.58	9.21	14.78	8.21	19.69	**		-
	Y79AA1000636	5.21	2.52	7.03	3.36	4.46	4.2	2.54	3.13	1.94			
	Y79AA1000649	19.51	21.35	25.26	12.58	12.75	9.69	16.99	19.63	19.13	**		-
	Y79AA1000656	7.37	5.14	7.46	2.86	2.97	2.28	2.83	3.72	2.99	**	*	-
40	Y79AA1000673	8.38	7.17	11.58	4.74	3.99	5.74	1.87	4.27	2.18	*	*	-
	Y79AA1000674	131.64	157.11	127.73	143.89	140.32	116.2	111.11	118.96	120.08			
	Y79AA1000678	22.12	27.62	25.96	12.61	21.55	13.08	21.7	19.94	19.36	*		-
	Y79AA1000682	14.62	11.86	13.44	6.55	8.13	6.38	12.74	13.35	11.29	**		-
	Y79AA1000683	37.64	24.6	33.28	19.88	16.2	12.73	33.87	33.73	36.17	*		-
45	Y79AA1000697	46.01	35.33	48.41	23.15	27.46	23.15	15.24	20.88	15.95	*	**	-
	Y79AA1000700	3.64	3.69	5.68	3.34	3.06	2.62	3.53	2.27	2.51			
	Y79AA1000702	50.6	33.01	36	23.71	24.96	18.05	18.21	11.97	15.36	*	*	-
	Y79AA1000704	93.86	71.31	88.5	110.92	93.16	106.68	74.22	61.46	46.95			
	Y79AA1000705	6.23	6.74	7.37	1.82	2.22	2.09	2.28	0.26	2.39	**	**	-
	Y79AA1000717	8.36	6.77	8.13	4.96	8.96	4.55	2.44	3.74	2.84	**		-
50	Y79AA1000722	10.83	11.52	10.81	4.97	5.79	3.98	6.28	5.41	5.45	**	**	-
	Y79AA1000724	42.59	35.15	44.52	31.42	30.43	23.04	24.2	29.89	31.56	*	*	-
	Y79AA1000726	8.78	4.43	7.31	5.15	4.77	4.25	2.41	3.94	2.09	*		-
	Y79AA1000734	5.72	4.05	6.45	2.81	2.76	3.46	2.68	2.98	0.98	*	*	-
	Y79AA1000748	7.45	7.72	6.69	2.89	2.82	2.75	2.52	2.6	2.35	**	**	-
	Y79AA1000750	41.52	33.1	33.65	18.03	22.65	18.6	26.15	29.63	22.6	**	*	-
55	Y79AA1000752	9.11	9.26	10.14	4.75	3.47	2.23	2.34	2.01	1.29	**	**	-
	Y79AA1000774	19.25	19.31	26.89	10.74	13.71	10.53	12.54	14.59	12.73	*	*	-
	Y79AA1000776	12.05	9.97	9.69	5.12	6.81	2.36	10.58	10.24	7.92	*		-
	Y79AA1000777	17.61	11.59	13.15	7.32	8.15	7.21	6.02	5.12	6.68	*	*	-

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	Y79AA1000778	20.06	13.62	11.66	10.8	9.69	8.29	13.52	13.51	12.96			
	Y79AA1000782	11.43	7.55	9.19	7.76	8.46	7.38	6.62	5.21	4.82	*	-	-
5	Y79AA1000784	13.14	10.21	12.84	4.67	6.08	6.71	10.7	9.6	9.71	**	-	-
	Y79AA1000794	46.19	39.88	38.82	22.35	24.71	16.75	37.28	33.24	34.17	**	-	-
	Y79AA1000800	7.18	3.91	5.09	0.48	0.36	0.17	2.34	0	0	**	*	-
	Y79AA1000802	11.45	13.12	10.85	5.78	8.8	4.96	3.89	4.75	3.77	*	**	-
	Y79AA1000805	21.22	18.33	12.77	6.7	11.14	4.1	15.87	12.52	16.72	*	-	-
	Y79AA1000814	27.49	21.74	19.65	16.59	17.35	12.96	22	17.22	22.17			
10	Y79AA1000823	14.24	7.73	9.85	4.94	4.36	5.06	6.73	6.96	8.36	*	-	-
	Y79AA1000824	16.24	10	9.76	8.11	9.28	6.16	6.82	5.83	8.72			
	Y79AA1000827	9.71	3.82	4.6	3.63	3.22	2.56	3.51	2.06	2.83			
	Y79AA1000831	7.38	5.79	7.27	4.13	3.32	2.68	4.43	0.57	1.26	**	*	-
	Y79AA1000833	22.35	19.25	16.88	12.38	7.9	8.89	19.38	11.86	18.04	**	-	-
	Y79AA1000850	33.44	40.57	26.99	19.52	21.81	14.62	28.93	23.5	32.01	*	-	-
15	Y79AA1000856	6.26	7.4	4.9	2.81	6.29	2.12	4.31	2.48	3.63	*	-	-
	Y79AA1000862	8.84	4.04	5.05	7.04	4.31	3.07	5.61	5.34	5.05			
	Y79AA1000876	21.17	10.25	11.73	7.67	6.82	6.01	5.79	7.01	6			
	Y79AA1000888	32.02	25.94	21.68	17.64	17.29	12.59	18.41	20.33	23.17	*	-	-
	Y79AA1000902	6.26	5.68	6.17	4.27	4.4	2.72	2.73	2.97	2.19	*	**	-
20	Y79AA1000935	76.11	52.08	52.32	70.65	71.58	69.22	39.77	35.2	32.3	*	-	-
	Y79AA1000959	48.22	40.7	37.08	25.45	33.48	19.11	26.33	21.44	21.93	*	**	-
	Y79AA1000962	46.82	45.31	38.99	22.79	24.29	17.48	60.82	38.12	53.14	**	-	-
	Y79AA1000963	25.33	35.17	19.37	13.71	17.32	12.79	14.75	14.39	13.92			
	Y79AA1000966	41.31	37.86	31.25	27.6	23.69	23.7	32	18.68	25.22	*	-	-
	Y79AA1000967	19.13	9.69	10.03	8.88	7.99	4.65	1.27	8.2	0.25			
25	Y79AA1000968	25.81	16.48	14.41	11.57	12.79	6.94	25.2	19.6	28.68			
	Y79AA1000969	40.02	39.97	33.37	23.55	39.74	36.04	32.93	30.52	18.66			
	Y79AA1000976	22.75	15.17	16.99	14.98	19.84	15.88	14.85	10.98	11.26			
	Y79AA1000978	8.83	7.09	6.8	4.57	5.39	2.66	4.35	3.43	4.33	*	**	-
	Y79AA1000985	8.02	3.9	5.83	4.32	4.39	1.76	4.37	2.17	1.99			
	Y79AA1000989	295.68	243.92	218.77	78.52	138.6	77.87	70.03	46.49	61.43	**	**	-
30	Y79AA1000991	12.26	8.35	10.64	5.63	5.93	8.76	7.23	8.65	6.01			
	Y79AA1001013	42.37	37.07	51.31	24.72	27.17	18.23	24.27	34.59	22.31	*	*	-
	Y79AA1001014	16.53	17.99	19.41	12.93	20.24	14.74	13.35	18.92	15.51			
	Y79AA1001019	8.07	6.21	8.29	4.14	6.05	5.04	2.84	5.3	3.51	*	*	-
	Y79AA1001020	13.89	16.72	13.86	21.03	12.53	10.76	9.5	10.16	11.46	*	-	-
35	Y79AA1001023	7.28	6.24	9.28	4.31	8.03	5.29	3.01	3.87	2.51	*	-	-
	Y79AA1001030	28.41	43.95	33.86	36.62	21.08	22.74	16.86	22.85	18.21	*	-	-
	Y79AA1001035	10.6	13.73	10.93	9.68	10.73	7.69	7.26	7.72	8.91	*	-	-
	Y79AA1001041	14.5	11.14	15.3	8.73	9.98	7.28	9.17	13.51	15.31	*	-	-
	Y79AA1001043	22.79	19.12	22.36	8.78	13.48	10.29	9.42	13.86	17.78	**	*	-
	Y79AA1001048	12.86	13.5	12.88	6.65	11.19	7.59	6.44	7.55	6.3	*	**	-
40	Y79AA1001056	6.67	9.77	12.37	5.42	9.5	6.82	2.1	3.99	2.72	*	-	-
	Y79AA1001061	11.12	17.1	15.18	5.75	10.72	7.78	8.04	10.36	12.77	*	-	-
	Y79AA1001062	4.7	4.96	6.24	2.95	3.71	2.56	2.92	2.19	2.28	*	**	-
	Y79AA1001068	6.22	3.59	5.75	4.34	5.98	4.49	3.29	3.38	3.07			
	Y79AA1001073	17.6	17.56	20.08	5.98	13.24	7.19	16.17	13.71	20.42	*	-	-
	Y79AA1001077	7.3	2.86	6.26	7.08	4.43	3.45	1.86	5.22	1.86			
45	Y79AA1001078	7.29	5.05	6.25	3.73	4.63	2.99	3.3	5.06	3.66	*	-	-
	Y79AA1001081	7.84	5.5	8.85	3.05	3.81	3.52	2.8	3.1	3.74	*	*	-
	Y79AA1001086	36.17	40.23	42.34	24.5	22.27	19	24.36	30.94	32.13	**	*	-
	Y79AA1001089	332.88	366.62	308.34	284.36	390.54	406.65	237.36	376.46	392			
	Y79AA1001090	7.05	4.26	8.66	4.12	3.36	2.71	3.39	1.8	2.5	*	-	-
50	Y79AA1001105	22.53	22.64	23.57	8.51	14.07	9.94	17.11	15.32	16.62	**	**	-
	Y79AA1001142	114.5	98.72	131.88	102.55	114.58	143.24	69.56	60.81	74.51	*	-	-
	Y79AA1001145	98.33	98.57	100.63	125.36	121.38	91.71	78	59.2	74.76	**	-	-
	Y79AA1001162	126.48	83.55	107.65	92.38	93.62	73.32	97.56	124.59	105.84			
	Y79AA1001167	12.61	7.85	13.06	7.92	8.62	6.56	7.15	16.96	9.58			
	Y79AA1001176	75.12	80.1	84.48	76.52	65.54	64.34	46.71	59.03	47.45	**	-	-
	Y79AA1001177	8.46	7.48	10.23	4.06	5.51	3.51	3.45	4.68	2.96	*	**	-
55	Y79AA1001179	54.1	53.61	67.63	28.64	33.09	26.42	13.82	47.33	10.91	**	-	-
	Y79AA1001185	32.79	30.94	36.04	15.68	21.34	16.32	19.9	17.65	25.06	**	**	-
	Y79AA1001201	45.08	50.33	41.06	13.71	31.35	17.81	48.16	43.78	38.95	*	-	-
	Y79AA1001205	18.73	12.88	21.83	8.38	8.46	6.14	7.31	11.86	11.81	*	-	-

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	Y79AA1001211	21.15	21.66	22.83	13.08	12.91	10.43	0.44	20.18	19.17	**	-	-
	Y79AA1001212	128.68	116.33	107.84	151.9	151.84	105.91	80.87	83.57	67.14	**	-	-
	Y79AA1001216	31.68	27.07	33.84	18.3	19.09	14.63	17.05	18.24	23.12	**	*	-
5	Y79AA1001228	7.97	5.25	12.95	3.35	3.4	3.64	3.41	10.17	4.89			
	Y79AA1001233	8.26	6.53	16.79	3.45	3.77	2.51	2.28	3.79	3.13			
	Y79AA1001236	8.84	5.25	11.14	5.02	5.53	3.13	4.08	4.7	2.24			
	Y79AA1001239	74.22	59.48	53.54	45.62	83.11	43.05	50.35	42.44	46.18			
	Y79AA1001240	70.83	49.07	64.4	30.83	35.04	20.32	48.49	59.48	54.67	*	-	-
	Y79AA1001255	8.89	10.29	10.55	7.47	6.78	6.42	0.72	6.35	0.76	**	*	-
10	Y79AA1001264	14.2	10.19	13.36	9.71	10.05	8.67	4.58	4.84	6.39	**	*	-
	Y79AA1001272	15.16	12.6	13.5	3.77	6.76	5.59	8.86	7.59	6.53	**	**	-
	Y79AA1001281	8.87	7.72	6.68	4.17	4.8	3.47	2.65	2.22	2.28	**	**	-
	Y79AA1001299	9.39	10.08	9.6	4.21	5.3	4.49	3.28	3.68	3.29	**	**	-
	Y79AA1001312	40.47	42.72	35.81	17.92	27.92	14.77	29.7	20.85	26.67	*	*	-
15	Y79AA1001319	31.92	23	20.23	23.19	28.4	16.96	30.43	20.02	18			
	Y79AA1001323	32.99	27.82	34.32	14.07	19.03	14.31	25.9	23.32	27.9	**	-	-
	Y79AA1001328	28.33	16.1	28.16	14.56	12.93	12.69	4.94	7.51	4.42	*	-	-
	Y79AA1001343	12.56	8.01	10.99	6.43	7.59	7.49	6.83	9.08	8.27			
	Y79AA1001351	6.64	4.21	8.23	2.99	1.8	1.8	2.08	2.52	1.68	*	*	-
20	Y79AA1001364	8.06	5.02	6.89	3.26	2.98	2.12	4.06	2.93	1.74	*	*	-
	Y79AA1001367	145.27	118.42	143.46	117.7	132.8	94.77	76.65	57.61	66.99	**	-	-
	Y79AA1001384	45.86	52.17	41.89	27.43	34.83	21.42	31.33	29.86	26.76	*	**	-
	Y79AA1001391	10.96	12.22	10.34	2.99	9.55	4.77	7.43	7.31	6.01	**	-	-
	Y79AA1001394	24.73	14.05	14.28	9.7	6.32	9.07	6.42	10.16	9.01			
	Y79AA1001402	12.42	7.77	9.12	5.62	4.8	4.67	4.74	3.87	4.52	*	*	-
25	Y79AA1001410	5.24	2.77	3.09	3.28	1.53	1.95	2.62	0.78	1.99			
	Y79AA1001414	27.49	18.53	20.44	10.78	9.47	10.2	16.16	13.43	11.92	*	*	-
	Y79AA1001426	271.77	221.23	225.78	200.19	221.07	217.77	202.63	211.55	197.64			
	Y79AA1001427	15.18	10.97	10.9	6.77	10.81	5.39	6.71	6.07	6.74	*	-	-
	Y79AA1001430	22.25	17.58	19.52	10.25	13.63	7.85	11.32	11.76	10.84	*	**	-
	Y79AA1001439	6.75	4.58	4.31	2.6	4.23	1.25	2.94	2.35	2.98	*	-	-
30	Y79AA1001485	17.57	9.99	14.92	13.26	10.56	8.25	5.32	10.37	14.36			
	Y79AA1001493	20.47	12.23	13.25	9.02	11.27	6.64	13.37	13.83	16.06			
	Y79AA1001511	14.52	8.05	9.32	8.33	6.58	5.82	5.2	6	5.96			
	Y79AA1001523	10.03	6.72	7.33	6.48	4.81	3.84	4.54	3.21	2.59	*	-	-
	Y79AA1001530	11.44	7.57	8.59	6.64	8.84	5.29	6.2	7.76	5.77			
35	Y79AA1001532	13.55	14.73	11.04	5.35	5.16	4.93	5.08	4.52	6.49	**	**	-
	Y79AA1001533	56.5	68.51	50.9	29.97	36.82	26.92	69.28	61.19	56.58	*	-	-
	Y79AA1001541	8.12	8.52	5.25	4.02	4.89	2.24	4.69	2.24	2.18	*	*	-
	Y79AA1001548	67.38	47.55	44.48	30.61	26.42	21.92	46.07	51.22	51.86	*	-	-
	Y79AA1001555	14.35	9.75	8.13	8.86	4.86	4.97	8.19	7.68	10.98			
	Y79AA1001562	18.44	13.73	12.82	8.99	10.6	7.19	10.2	9.39	15.75	*	-	-
40	Y79AA1001581	24.34	18.91	17.62	9.8	12.04	10.4	15.9	9.96	16.33	*	-	-
	Y79AA1001585	30.32	20.83	22.83	20.22	25.12	15.45	0.69	15.13	0.14	*	-	-
	Y79AA1001592	28.53	25.65	26.36	29.33	16.66	7.28	20.69	8.44	14.72	*	-	-
	Y79AA1001594	23.28	21.85	24.28	14.25	15.59	10.11	22.55	14.53	20.27	**	-	-
	Y79AA1001603	12.47	11.04	10.84	6.8	11.48	6.78	22.63	14.33	27.5			
	Y79AA1001613	25.09	18.27	18.81	23.47	16.84	13.34	20.3	16.35	18.99			
45	Y79AA1001630	22.94	13.91	12.22	13.14	13.53	8.02	11.73	12.98	17.67			
	Y79AA1001647	33.54	24.86	22.66	23.22	25.84	16.49	26.93	21.3	26.55			
	Y79AA1001664	12.2	10.56	13.13	7.78	6.05	5.54	10.34	8.1	11.69	**	-	-
	Y79AA1001665	11.52	9	9.75	6.87	7.31	6.13	5.92	6.12	7.69	*	*	-
	Y79AA1001679	24.51	18.98	17.88	11.13	12.84	9.27	24.02	13.28	18.8	*	-	-
	Y79AA1001692	7.23	6.72	8.1	2.24	2.83	2.63	3.64	2.31	3.06	**	**	-
50	Y79AA1001696	14.23	12.31	9.21	5.29	8.48	4.61	14.27	13.28	13.01	*	-	-
	Y79AA1001705	12.04	11.4	8.55	9.76	11.8	6.21	4.61	5.98	4.57	**	-	-
	Y79AA1001711	13.72	7.72	10.63	6.49	4.11	3.08	6.08	4.06	7.4	*	-	-
	Y79AA1001717	4.71	1.55	3.26	3.34	1.71	0.7	1.49	1.63	1.39			
	Y79AA1001719	22.12	12.72	16.33	9.89	12.72	6.53	12.21	11.1	11.76			
	Y79AA1001727	38.96	27.16	22.35	13.65	17.35	9.31	38.01	28.39	34.23	*	-	-
55	Y79AA1001750	21.5	17.52	18.42	10.15	15.4	8.01	11.94	9.9	11.41	*	**	-
	Y79AA1001760	127.24	115.03	77.78	58.26	73.6	43.62	140.25	100.84	138.73	*	-	-
	Y79AA1001777	6.77	6.32	6.37	2.57	5.24	2.46	5.26	4.15	4.71	*	**	-
	Y79AA1001781	2.86	2.24	2.15	1.61	1.88	2.55	0.74	1.53	1.3	*	-	-

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	Y79AA1001787	5.04	3.62	6.16	2.83	4.49	3.23	3.33	2.97	2.01			
	Y79AA1001793	120.15	97.84	90.95	70.69	108.02	70.38	56.01	50.79	40.18	**	-	
	Y79AA1001795	5.66	5.4	6.21	4.2	5.9	3.1	3.91	2.49	2.28	**	-	
5	Y79AA1001799	15.09	14.95	16.22	8.14	9.02	8.13	5.96	8.67	5.96	**	**	-
	Y79AA1001800	25.64	16.41	26.8	14.68	31.06	13.67	17.04	13.04	14.7			
	Y79AA1001801	18.54	13.81	14.73	8.69	14.72	7.61	10.02	6.35	8.81	*	-	
	Y79AA1001803	4.48	5.85	6.44	4.5	2.73	1.98	4.84	2.96	2.69			
	Y79AA1001805	40.28	26.89	34.51	17.56	11.83	10.76	12.11	14.87	11.59	**	**	-
	Y79AA1001807	42.38	40.49	41.45	39.87	44.56	37.42	30.19	22.76	22.12	**	-	
10	Y79AA1001827	9.32	11.28	9.81	8.01	8.55	6.68	5.41	8.86	5.83	*	*	-
	Y79AA1001846	22.14	19.33	18.59	11.82	17.37	13.61	12.56	15.77	9.7	*	*	-
	Y79AA1001848	8.04	9.99	9.11	5.33	6.98	5.01	6.65	6.63	5.92	*	*	-
	Y79AA1001853	10.87	10.1	9.06	5.77	8.29	4.56	4.63	5.75	4.91	*	**	-
	Y79AA1001863	24.97	27.27	22.17	17.04	22	11.97	13.95	21.02	18.07	*	-	
15	Y79AA1001866	13.46	10.72	11.93	6.28	4.52	4.93	6.56	4.65	4.51	**	**	-
	Y79AA1001874	2.1	1.41	2.93	0.78	1.08	0.95	1.46	1.22	1.08			
	Y79AA1001875	31.78	22.74	37.59	12.11	19.59	18.03	9.16	15	14.61	*	*	-
	Y79AA1001907	517.52	778.32	567.93	750.86	875.67	821.68	479.34	605.65	529.63			
	Y79AA1001908	5.27	6.69	9.96	3.58	5.35	3.25	2.93	3.09	1.48	*	-	
	Y79AA1001923	8.48	16.75	14.8	9.28	7.65	6.34	6.48	6.75	5.36	*	-	
20	Y79AA1001927	18.05	21.6	19.1	12.29	16.25	12.12	14.45	14.01	14.79	*	**	-
	Y79AA1001930	12.23	24.48	15.86	10.91	18.16	6.72	4.54	5.11	5.37	*	*	-
	Y79AA1001932	61.74	56.58	52.19	37.44	49.06	33.54	58.52	51.29	51.59	*	-	
	Y79AA1001933	9.52	6.51	10.88	6.04	6.05	6.44	4.27	11.51	4.91			
	Y79AA1001942	10.76	6.66	7.93	7.97	5.94	4.4	3.29	2.7	3.99	*	-	
25	Y79AA1001963	138.12	106.9	117.87	95.52	130.54	91.9	83.12	67.08	69.04	*	-	
	Y79AA1001968	147.27	91.21	62.32	82.32	49.63	76.26	20.14	2.41	10.4	*	**	-
	Y79AA1001983	12.1	16.25	14.99	5.06	8.59	7.83	3.08	3.73	3.02	*	**	-
	Y79AA1002000	8.87	9.86	16.46	6.28	9.55	3.45	4.66	4.84	4.51	*	-	
	Y79AA1002004	46.17	58.66	37.42	34.61	47	15.44	17.13	16.13	8.67	**	-	
	Y79AA1002008	16.52	21.1	20.83	11.85	16.14	12.02	7.95	15.74	18.89	*	-	
30	Y79AA1002012	13.85	12.54	10.41	5.85	6.84	8.65	8.76	11.21	9.52	**	-	
	Y79AA1002017	15.21	10.94	15.42	6.73	12.23	8.22	1.29	15.64	2.06			
	Y79AA1002022	42.57	32.77	37.11	21.13	22.85	16.91	21.09	21.59	19.22	**	**	-
	Y79AA1002027	10.35	8.04	15.25	2.11	4.6	4.84	5.16	2.67	4.2	*	*	-
	Y79AA1002050	13.21	11.11	14.39	7.26	8.9	5.9	6.9	7.16	7.33	*	**	-
	Y79AA1002058	167.29	130.21	156.91	193.04	186.39	149.35	127.37	93.56	137.15			
35	Y79AA1002060	54.35	78.53	61.68	36.08	41.21	29.16	24.43	9.99	5.28	*	**	-
	Y79AA1002062	49.46	32.53	50.05	16.65	20.72	17.6	35.11	28.1	35.48	*	-	
	Y79AA1002065	113.45	69.34	64.62	65.01	102.96	72.96	82.29	90.04	44.91			
	Y79AA1002067	33.46	37.19	43.9	21.85	20.1	22.68	15.4	10.55	10.37	**	**	-
	Y79AA1002069	5.33	3.94	7.12	3.04	1.49	2.47	3.1	3.24	2.29	*	-	
40	Y79AA1002070	67.39	142.78	83.33	77.38	149.87	86.41	153.3	88.92	78.17			
	Y79AA1002074	1225	1102	498.16	721.59	1162.7	771.32	764.45	491.49	312.45			
	Y79AA1002076	8.24	11.39	15.58	4.01	6.13	3.99	13	9.01	11.16	*	-	
	Y79AA1002083	11.94	6.94	9.48	4.49	4.53	3.15	4.48	1.37	1.78	*	*	-
	Y79AA1002084	20.05	13.84	17.88	7.41	8.36	6.24	10.42	8.8	8.13	**	*	-
	Y79AA1002086	15.57	8.01	9.58	4.16	3.65	3.41	3.6	4.3	3.59	*	*	-
45	Y79AA1002087	265.36	258.38	345.6	296.44	355.85	248.9	347.62	322.78	317.34			
	Y79AA1002089	15.8	12.04	15.08	6.67	9.17	6.14	12.29	9.32	9.91	**	-	
	Y79AA1002093	13.66	12.64	9.33	5.35	6.21	4.47	3.01	2.8	2.57	**	**	-
	Y79AA1002101	6.58	7.04	8.08	3.07	2.77	1.96	3.3	4.71	1.2	**	*	-
	Y79AA1002103	11.98	11.79	10.9	4.11	5.96	4.92	4.54	2.99	2.4	**	**	-
	Y79AA1002115	15.51	18.46	14.58	9.3	11.82	8.45	4.13	9.04	5.86	*	**	-
50	Y79AA1002121	6.93	5.28	6.92	6.7	3.27	4.36	3.68	3.01	3.29	**	-	
	Y79AA1002125	40.85	21.04	26.11	14.22	18.4	17.66	12.21	8.56	11.75	*	-	
	Y79AA1002129	7.76	7.25	11.87	4.36	3.94	3.2	3.76	3.8	4.37	*	-	
	Y79AA1002131	5.89	3.57	4.65	1.58	2.79	2.27	3.32	1.61	2.75	*	-	
	Y79AA1002139	8.48	7.22	6.23	4.06	4.42	2.47	3.44	3.86	2.67	*	**	-
	Y79AA1002144	53.23	47.33	47.13	32.96	42.65	28.86	30.69	36.28	25.23	*	**	-
55	Y79AA1002177	14.09	13.17	13.65	5.87	6.08	5.05	5.82	4.1	4.34	**	**	-
	Y79AA1002183	76.21	99.47	69.64	24.87	40.12	25.67	26.7	15.32	11.38	**	**	-
	Y79AA1002202	29.69	18.4	18.04	8.22	10.65	9.82	13.41	13.22	16.71	*	-	
	Y79AA1002204	4.17	2.23	3.23	5.04	1.05	2.68	3.28	2.4	2.69			

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Table 509

	Y79AA1002206	7.86	6.79	4.86	2.41	3.6	5.74	5.49	1.51	2.8				
	Y79AA1002208	21.91	17.64	15.14	5.6	4.07	5.57	6.81	5.17	2.55	**	**	-	-
5	Y79AA1002209	14.82	11.28	11.86	6.23	4.7	2.82	4.71	1.33	3.18	**	**	-	-
	Y79AA1002210	13.64	7.39	7.59	9.08	4.62	5.18	20.5	2.05	6.37				
	Y79AA1002211	11.76	19.59	13.47	10.43	6.65	6.52	12.32	8.42	11.25				
	Y79AA1002213	40.78	31.99	22.96	18.41	26.57	14.98	45.88	32.4	41.97				
	Y79AA1002215	54.92	41.69	39.55	24.88	24.36	11.26	37.49	23.6	35.98	*		-	-
	Y79AA1002220	17.03	11.5	20.58	7.13	5.68	5.31	4.57	4.8	6.51	*	*	-	-
10	Y79AA1002226	48.55	31.27	31.34	7.35	12.72	13.65	9.19	6.65	11.13	*	**	-	-
	Y79AA1002229	7.88	6.84	5.37	6.02	4.67	2.85	3.67	2.52	3.73	*	*	-	-
	Y79AA1002234	20.83	13.27	12.39	9.34	6.36	3.6	6.9	3.36	5.84	*	*	-	-
	Y79AA1002235	28.03	23.84	21.24	15.07	14.87	9.39	10.75	8.42	13.64	*	**	-	-
	Y79AA1002246	9.72	14.9	10.35	5.25	6.99	4.12	8.31	3.82	6.69	*		-	-
15	Y79AA1002258	12.35	12.02	7.88	7.82	11.57	8.55	9.77	4.5	4.81				
	Y79AA1002279	51.52	49.19	41.11	5.28	2.78	2.07	15.99	20.03	22.13	**	**	-	-
	Y79AA1002292	13.64	7.58	4.14	5.73	4.43	2.94	6.45	6.01	8.36				
	Y79AA1002298	9.43	8.29	4.77	3.29	5.48	4.2	4.42	4.85	3.79				
	Y79AA1002307	9.31	8.07	6.62	3.9	4.4	2.44	5.17	1.76	2.58	*	*	-	-
20	Y79AA1002309	8.88	7.96	8.79	3.32	4.26	2.83	4.23	2.88	3.97	**	**	-	-
	Y79AA1002311	16.51	9.27	11.76	6.9	6.2	3.45	7.45	3.09	6.4	*	*	-	-
	Y79AA1002334	13.05	8.36	7.7	5.13	4.89	3.36	5.91	4.32	5.92	*	*	-	-
	Y79AA1002351	13.61	12.49	9.42	7.1	4.15	6.19	7.95	4.93	5.8	*	*	-	-
	Y79AA1002355	31.74	30.6	21.85	12.21	15.81	9.74	20.54	18.29	18.48	*	*	-	-
25	Y79AA1002361	23.42	15.4	18.02	12.53	10.73	6.85	25.86	17.1	25.5	*		-	-
	Y79AA1002365	12.42	6.37	7.19	3.15	4.11	3.03	4.29	4.74	4.01				
	Y79AA1002373	8.95	6.89	5.46	5.13	4.81	3.4	9.6	4.57	7.84				
	Y79AA1002376	1550.5	2569.2	1680.8	462.62	827.86	616.71	1477.6	1040.3	1062.1	*		-	-
	Y79AA1002378	20.24	17.32	13.54	5.14	9.41	4.23	19.28	11.07	16.88	*		-	-
30	Y79AA1002381	116.11	128.86	74.48	110.66	141.78	92.68	155.95	123.08	170.94				
	Y79AA1002388	33.4	33.3	27.31	13.85	26.75	11.62	21.29	16.32	21.24	*		-	-
	Y79AA1002399	11.13	8.22	7.72	4.28	5.54	4.87	7.56	5.9	6.25	*	*	-	-
	Y79AA1002407	12.66	14.43	18.13	7.72	14.18	6.84	5.83	9.78	4.59	*	*	-	-
	Y79AA1002413	16.98	12.77	14.95	6.14	9.13	4.62	8.44	10.73	7.99	*	*	-	-
	Y79AA1002416	7.52	8.19	8.76	5.47	10.72	5.8	8.2	6.05	6.59				
35	Y79AA1002429	17.73	18.61	8.81	5.82	10.24	4.73	3.65	6.89	5.66	*		-	-
	Y79AA1002431	3.38	3.05	6.2	3.01	5.89	1.6	2.81	2.79	1.69				
	Y79AA1002433	9.94	11.67	9.29	5.11	5.57	3.18	3.49	4.6	3.87	**	**	-	-
	Y79AA1002445	33.47	25.62	23.49	15.99	10.67	7.02	18.92	25.26	13.87	*	*	-	-
	Y79AA1002461	7.94	6.22	7.84	3.36	7.35	4.7	3.49	2.25	3.85	**		-	-
	Y79AA1002466	778.44	338.4	681.02	542.56	499.15	369	592.67	971	768.71				
40	Y79AA1002471	11.38	8.13	15.35	12.81	13.4	11.43	4.94	6.06	4.47	*	*	-	-
	Y79AA1002472	31.22	33.06	31.17	18.15	21.85	9.34	16.29	20.14	20.03	*	**	-	-
	Y79AA1002474	10.68	12.29	10.71	6.77	7.3	7.75	3.17	7.37	4.86	**	*	-	-
	Y79AA1002482	30.09	33.68	36.63	19.02	23.45	17.38	21.9	25.81	23.08	**	*	-	-
	Y79AA1002487	8.33	8.29	7.43	7.28	8.45	6.44	5.34	3.78	3.86	**	**	-	-
45	Y79AA1002490	143.18	106.89	117.63	56.22	71.49	57.31	59.76	51.39	52.37	**	**	-	-
	Y79AA1002493	44.75	41.56	40.36	20.64	28.52	19.33	38.02	46.19	46.7	**	**	-	-
	Z8V6C1006278	5.26	7	5.52	3.16	2.97	2.19	2.99	2.6	2.72	**	**	-	-

50 EXAMPLE 16

Selection of novel cDNA clones from cDNA libraries prepared by oligo-capping method

55 The following 54 clones were newly selected from cDNA libraries prepared by oligo-capping method, based on the criterion that the 5'-end sequence of a cDNA clone contained a coding region which was initiated with ATG codon and which encoded 50 amino acids or more:

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HEMBA1000497, HEMBA1001750, HEMBA1003854, HEMBA1004193, HEMBA1004860,
 HEMBA1005572, HEMBA1006038, HEMBA1006092, HEMBA1006406, HEMBA1006650,
 HEMBA1006812, HEMBB1000672, HEMBB1001197, HEMBB1001871, MAMMA1001252,
 5 MAMMA1002094, NT2RM4000634, NT2RM4000657, NT2RM4000783, NT2RM4000857,
 NT2RM4001178, NT2RM4002420, NT2RP2000198, NT2RP2000551, NT2RP2000660,
 NT2RP2001214, NT2RP2001460, NT2RP2001756, NT2RP2002056, NT2RP2002677,
 NT2RP2002755, NT2RP2002843, NT2RP2003101, NT2RP2003799, NT2RP2004095,
 10 NT2RP2004732, NT2RP2004920, NT2RP2005454, NT2RP2005776, NT2RP2005806,
 NT2RP2005882, NT2RP3001282, NT2RP3001723, NT2RP3002099, NT2RP3003155,
 NT2RP3004028, OVARC1000008, OVARC1000724, OVARC1000751, OVARC1001029,
 PLACE1000814, PLACE1003030, PLACE1005549, PLACE1007218.

15 Among them, the following 23 clones was predicted to contain a coding region encoding 100
 amino acids or more: HEMBA1000497, HEMBA1003854, HEMBA1004193, HEMBA1006812,
 HEMBB1001871, NT2RM4000657, NT2RM4001178, NT2RP2001756, NT2RP2002677,
 NT2RP2002755, NT2RP2002843, NT2RP2004095, NT2RP2004920, NT2RP2005806,
 20 NT2RP3001282, NT2RP3002099, NT2RP3003155, OVARC1000724, OVARC1001029,
 PLACE1000814, PLACE1003030, PLACE1005549, PLACE1007218. This indicates that the
 clones encode proteins.

Table 510 shows maximal ATGprl value determined for each clone. Since the respective
 25 maximal ATGprl values for HEMBA1006812, HEMBB1001871 and NT2RRP3001282 are higher
 than 0.3, the clones would be full-length. Other clones indicated below have maximal ATGprl
 values of 0.3 or less, and this means that the fullness ratios of the clones are low.

However, the sequences can still be full-length:HEMBA1000497, HEMBA1001750,
 30 HEMBA1003854, HEMBA1004193, HEMBA1004860, HEMBA1005572, HEMBA1006038,
 HEMBA1006092, HEMBA1006406, HEMBA1006650, HEMBB1000672, HEMBB1001197,
 MAMMA1001252, MAMMA1002094, NT2RM4000634, NT2RM4000657, NT2RM4000783,
 NT2RM4000857, NT2RM4001178, NT2RM4002420, NT2RP2000198, NT2RP2000551,
 35 NT2RP2000660, NT2RP2001214, NT2RP2001460, NT2RP2001756, NT2RP2002056,
 NT2RP2002677, NT2RP2002755, NT2RP2002843, NT2RP2003101, NT2RP2003799,
 NT2RP2004095, NT2RP2004732, NT2RP2004920, NT2RP2005454, NT2RP2005776,
 NT2RP2005806, NT2RP2005882, NT2RP3001723, NT2RP3002099, NT2RP3003155,
 40 NT2RP3004028, OVARC1000008, OVARC1000724, OVARC1000751, OVARC1001029,
 PLACE1000814, PLACE1003030, PLACE1005549, PLACE1007218

Table 511 (same as Table 2) shows SEQ ID NOs of the nucleotide sequences located at the
 5'-end and 3'-end of each of the 54 clones and the corresponding plasmid clone, which was
 45 obtained herein, containing a polynucleotide as an insert. SEQ ID NO for a 5'-end sequence is
 indicated on the right side of the corresponding Sequence name of 5'-end sequence, and SEQ
 ID NO for a 3'-end sequence is indicated on the right side of the corresponding Sequence name
 of 3'-end sequence.

50 Swiss-Prot was searched for data homologous to the 5' -end sequences of the selected 54
 clones, and GenBank and UniGene were searched for data homologous to the 5' -end and 3'-
 end sequences of the same clones. The search results are indicated as Homology search
 results 1-7 in the last part of this SPECIFICATION.

55 Based on the matching data obtained by the search, 7 clones presumably encode proteins
 belonging to any of the categories of secretory or membrane proteins, glycoproteins, signal

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transduction-associated proteins, transcription-associated proteins, disease-associated proteins, and protein synthesis- and/or protein transport-associated proteins. These were clones exhibiting relatively low homology to any of known proteins belonging to said categories. Here,
5 the term "relatively low homology" means that a nucleotide sequence does not satisfy the conditions under which the nucleotide sequence exhibits "relatively high homology" (which means that, when the nucleotide sequence is compared with the known sequences in Swiss-Prot database, the sequence identity is 60% or higher and the P value is 10^{-10} or less) and
10 that, when the nucleotide sequence is compared with the known sequences in Swiss-Prot database, the sequence to be compared contains 55 nucleotides or more, the sequence identity is 25% or higher, and the P value is 10^{-6} or less.

Among the 7 clones, clones presumably encoding proteins belonging to the category of
15 secretory or membrane proteins are the two clones, HEMBB1001871 and NT2RM4000857 (which also belong to other categories); clones presumably encoding proteins belonging to the category of glycoproteins are the two clones, HEMBB1001871 and NT2RM4000857 (which also belong to other categories);- a clone presumably encoding a protein belonging to the category of
20 signal transduction-associated proteins is PLACE1005549; clones presumably encoding proteins belonging to the category of transcription-associated proteins are the three clones, HEMBA1005572, NT2RP2001756, and NT2RP2005776; a clone presumably encoding a protein belonging to the category of disease-associated proteins is NT2RM4000857 (which also belong
25 to other categories); a clone presumably encoding a protein belonging to the category of protein synthesis- and/or protein transport-associated proteins is HEMBA1001750 (see Examples 12).

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Table 510

The maximal ATGprl value of each clone selected in Example 16

	clone name	name of sequence	maximal ATGprl score
5			
10	HEMBA1000497	F-HEMBA1000497	0.25
	HEMBA1001750	F-HEMBA1001750	0.08
	HEMBA1003854	F-HEMBA1003854	0.23
15	HEMBA1004193	F-HEMBA1004193	0.22
	HEMBA1004860	F-HEMBA1004860	0.29
	HEMBA1005572	F-HEMBA1005572	0.24
	HEMBA1006038	F-HEMBA1006038	0.29
20	HEMBA1006092	F-HEMBA1006092	0.28
	HEMBA1006406	F-HEMBA1006406	0.26
	HEMBA1006650	F-HEMBA1006650	0.22
	HEMBA1006812	F-HEMBA1006812	0.71
25	HEMBA100672	F-HEMBA100672	0.24
	HEMBA1001197	F-HEMBA1001197	0.22
	HEMBA1001871	F-HEMBA1001871	0.94
	MAMMA1001252	F-MAMMA1001252	0.29
30	MAMMA1002094	F-MAMMA1002094	0.28
	NT2RM4000634	F-NT2RM4000634	0.07
	NT2RM4000657	F-NT2RM4000657	0.24
35	NT2RM4000783	F-NT2RM4000783	0.22
	NT2RM4000857	F-NT2RM4000857	0.12
	NT2RM4001178	F-NT2RM4001178	0.27
	NT2RM4002420	F-NT2RM4002420	0.06
40	NT2RP2000198	F-NT2RP2000198	0.15
	NT2RP2000551	F-NT2RP2000551	0.07
	NT2RP2000660	F-NT2RP2000660	0.22
	NT2RP2001214	F-NT2RP2001214	0.26
45	NT2RP2001460	F-NT2RP2001460	0.07
	NT2RP2001756	F-NT2RP2001756	0.17

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	NT2RP2002056	F-NT2RP2002056	0. 12
	NT2RP2002677	F-NT2RP2002677	0. 14
5	NT2RP2002755	F-NT2RP2002755	0. 12
	NT2RP2002843	F-NT2RP2002843	0. 11
	NT2RP2003101	F-NT2RP2003101	0. 13
	NT2RP2003799	F-NT2RP2003799	0. 24
10	NT2RP2004095	F-NT2RP2004095	0. 16
	NT2RP2004732	F-NT2RP2004732	0. 18
	NT2RP2004920	F-NT2RP2004920	0. 15
	NT2RP2005454	F-NT2RP2005454	0. 09
15	NT2RP2005776	F-NT2RP2005776	0. 19
	NT2RP2005806	F-NT2RP2005806	0. 27
	NT2RP2005882	F-NT2RP2005882	0. 11
20	NT2RP3001282	F-NT2RP3001282	0. 39
	NT2RP3001723	F-NT2RP3001723	0. 22
	NT2RP3002099	F-NT2RP3002099	0. 20
	NT2RP3003155	F-NT2RP3003155	0. 29
25	NT2RP3004028	F-NT2RP3004028	0. 13
	OVARC1000008	F-OVARC1000008	0. 23
	OVARC1000724	F-OVARC1000724	0. 27
	OVARC1000751	F-OVARC1000751	0. 28
30	OVARC1001029	F-OVARC1001029	0. 25
	PLACE1000814	F-PLACE1000814	0. 21
	PLACE1003030	F-PLACE1003030	0. 26
35	PLACE1005549	F-PLACE1005549	0. 16
	PLACE1007218	F-PLACE1007218	0. 30

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Table 511

clone name	name of the 5'-end sequence	SEQ ID NO of the 5'-end sequence	name of the 3'-end sequence	SEQ ID NO of the 3'-end sequence
HEMBA1000497	F-HEMBA1000497	16111	R-HEMBA1000497	16165
HEMBA1001750	F-HEMBA1001750	16112	R-HEMBA1001750	16166
HEMBA1003854	F-HEMBA1003854	16113	R-HEMBA1003854	16167
HEMBA1004193	F-HEMBA1004193	16114	R-HEMBA1004193	16168
HEMBA1004860	F-HEMBA1004860	16115	R-HEMBA1004860	16169
HEMBA1005572	F-HEMBA1005572	16116	R-HEMBA1005572	16170
HEMBA1006038	F-HEMBA1006038	16117	R-HEMBA1006038	16171
HEMBA1006092	F-HEMBA1006092	16118	R-HEMBA1006092	16172
HEMBA1006406	F-HEMBA1006406	16119	R-HEMBA1006406	16173
HEMBA1006650	F-HEMBA1006650	16120	R-HEMBA1006650	16174
HEMBA1006812	F-HEMBA1006812	16121	R-HEMBA1006812	16175

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	HEMBB1000672	F-HEMBB1000672	16122	R-HEMBB1000672	16176
	HEMBB1001197	F-HEMBB1001197	16123	R-HEMBB1001197	16177
	HEMBB1001871	F-HEMBB1001871	16124	R-HEMBB1001871	16178
5	MAMMA1001252	F-MAMMA1001252	16125	R-MAMMA1001252	16179
	MAMMA1002094	F-MAMMA1002094	16126	R-MAMMA1002094	16180
	NT2RM4000634	F-NT2RM4000634	16127	R-NT2RM4000634	16181
	NT2RM4000657	F-NT2RM4000657	16128	R-NT2RM4000657	16182
10	NT2RM4000783	F-NT2RM4000783	16129	R-NT2RM4000783	16183
	NT2RM4000857	F-NT2RM4000857	16130	R-NT2RM4000857	16184
	NT2RM4001178	F-NT2RM4001178	16131	R-NT2RM4001178	16185
	NT2RM4002420	F-NT2RM4002420	16132	R-NT2RM4002420	16186
15	NT2RP2000198	F-NT2RP2000198	16133	R-NT2RP2000198	16187
	NT2RP2000551	F-NT2RP2000551	16134	R-NT2RP2000551	16188
	NT2RP2000660	F-NT2RP2000660	16135	R-NT2RP2000660	16189
20	NT2RP2001214	F-NT2RP2001214	16136	R-NT2RP2001214	16190
	NT2RP2001460	F-NT2RP2001460	16137	R-NT2RP2001460	16191
	NT2RP2001756	F-NT2RP2001756	16138	R-NT2RP2001756	16192
	NT2RP2002056	F-NT2RP2002056	16139	R-NT2RP2002056	16193
25	NT2RP2002677	F-NT2RP2002677	16140	R-NT2RP2002677	16194
	NT2RP2002755	F-NT2RP2002755	16141	R-NT2RP2002755	16195
	NT2RP2002843	F-NT2RP2002843	16142	R-NT2RP2002843	16196
	NT2RP2003101	F-NT2RP2003101	16143	R-NT2RP2003101	16197
30	NT2RP2003799	F-NT2RP2003799	16144	R-NT2RP2003799	16198
	NT2RP2004095	F-NT2RP2004095	16145	R-NT2RP2004095	16199
	NT2RP2004732	F-NT2RP2004732	16146	R-NT2RP2004732	16200
	NT2RP2004920	F-NT2RP2004920	16147	R-NT2RP2004920	16201
35	NT2RP2005454	F-NT2RP2005454	16148	R-NT2RP2005454	16202
	NT2RP2005776	F-NT2RP2005776	16149	R-NT2RP2005776	16203
	NT2RP2005806	F-NT2RP2005806	16150	R-NT2RP2005806	16204
	NT2RP2005882	F-NT2RP2005882	16151	R-NT2RP2005882	16205
40	NT2RP3001282	F-NT2RP3001282	16152	R-NT2RP3001282	16206
	NT2RP3001723	F-NT2RP3001723	16153	R-NT2RP3001723	16207
	NT2RP3002099	F-NT2RP3002099	16154	R-NT2RP3002099	16208
	NT2RP3003155	F-NT2RP3003155	16155	R-NT2RP3003155	16209
45	NT2RP3004028	F-NT2RP3004028	16156	R-NT2RP3004028	16210
	OVARC1000008	F-OVARC1000008	16157	R-OVARC1000008	16211
	OVARC1000724	F-OVARC1000724	16158	R-OVARC1000724	16212
	OVARC1000751	F-OVARC1000751	16159	R-OVARC1000751	16213
50	OVARC1001029	F-OVARC1001029	16160	R-OVARC1001029	16214
	PLACE1000814	F-PLACE1000814	16161	R-PLACE1000814	16215
	PLACE1003030	F-PLACE1003030	16162	R-PLACE1003030	16216
	PLACE1005549	F-PLACE1005549	16163	R-PLACE1005549	16217
55	PLACE1007218	F-PLACE1007218	16164	R-PLACE1007218	16218

EXAMPLE 17

- 5 Search for a signal sequence, transmembrane region and functional domain in deduced amino acid sequences

The deduced amino acid sequences from the full-length nucleotide sequences were
 10 examined to predict the presence of a signal sequence in their amino-termini as well as the presence of a transmembrane region. The amino acid sequences were also searched for a protein functional domain (motif). The examinations for a signal sequence in the amino-terminus, for a transmembrane region and for a functional domain were performed by using
 15 PSORT [K. Nakai & M. Kanehisa, Genomics, 14:897-911 (1992)], SOSUI [T. Hirokawa et al., Bioinformatics, 14:378-379 (1998)] (Mitsui Knowledge Industry Co., Ltd.) and Pfam (<http://www.sanger.ac.uk/Software/Pfam/index.shtml>), respectively. When the presence of a signal sequence or a transmembrane region in the amino-terminus was predicted in the amino acid
 20 sequence by PSORT or SOSUI, the protein was predicted to be a secretory protein or a membrane protein. When the amino acid sequence matched a functional domain in the Pfam search for a functional domain, the function of the protein is predictable based on the matching data, for example, by referring to the functional categories in PROSITE (<http://www.expasy.ch/cgi-bin/prosite-list.pl>). The functional domain search can be performed by using
 25 PROSITE instead of Pfam.

Search results obtained by using the respective software programs are indicated below.

Clones whose deduced amino acid sequences were predicted to have signal sequences by
 30 PSORT search are as follows:

HEMBA1001052,	HEMBA1001407,	HEMBA1002486,	HEMBA1002661,	HEMBA1002818,
HEMBA1002876,	HEMBA1003086,	HEMBA1003711,	HEMBA1004752,	HEMBA1005991,
HEMBA1006067,	HEMBA1006173,	HEMBA1006198,	HEMBA1006789,	HEMBA1006921,
35 HEMBB1000054,	HEMBB1000175,	HEMBB1002692,	MAMMA1000798,	MAMMA1002427,
MAMMA1002881,	MAMMA1003035,	NT2RM1000035,	NT2RM1000742,	NT2RM1000811,
NT2RM1000905,	NT2RM1001008,	NT2RM2000287,	NT2RM2000609,	NT2RM2001613,
NT2RM4000634,	NT2RM4000778,	NT2RM4002339,	NT2RM4002460,	NT2RP1000782,
40 NT2RP1000856,	NT2RP1001247,	NT2RP1001546,	NT2RP1001569,	NT2RP2001597,
NT2RP2002537,	NT2RP2004142,	NT2RP2005752,	NT2RP2005812,	NT2RP3001084,
NT2RP3001589,	NT2RP3002163,	NT2RP3002650,	NT2RP3003145,	NT2RP3003242,
NT2RP3003621,	NT2RP3004282,	NT2RP3004503,	NT2RP4000051,	NT2RP4000151,
45 NT2RP4000243,	NT2RP4000259,	NT2RP4000323,	NT2RP4000417,	NT2RP4001064,
NT2RP4001117,	NT2RP4001730,	NT2RP4001739,	NT2RP4002075,	NT2RP5003500,
OVARC1001154,	PLACE1000611,	PLACE1003030,	PLACE1003044,	PLACE1003369,
PLACE1003596,	PLACE1004258,	PLACE1005086,	PLACE1006239,	PLACE1006754,
50 PLACE1006829,	PLACE1007954,	PLACE1008424,	PLACE1008533,	PLACE1008693,
PLACE1010622,	PLACE1010942,	PLACE2000176,	PLACE2000341,	PLACE2000379,
PLACE2000427,	PLACE2000477,	PLACE4000431,	PLACE4000593,	THYRO1000156,
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55 HEMBB1001871,	HEMBB1001925,	MAMMA1000778,	MAMMA1000897,	MAMMA1001080,
NT2RP2004300,	NT2RP3002985,	NT2RP3003059,	OVARC1000689,	OVARC1000890,

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PLACE1005162, PLACE3000399, PLACE3000455, PLACE4000247, PLACE4000259,
PLACE4000494

Clones whose deduced amino acid sequences were predicted to have transmembrane
5 regions by SOSUI search are as follows:

	HEMBA1000005,	HEMBA1000356,	HEMBA1000518,	HEMBA1000531,	HEMBA1000637,
	HEMBA1000719,	HEMBA1000817,	HEMBA1000822,	HEMBA1000870,	HEMBA1000991,
	HEMBA1001052,	HEMBA1001085,	HEMBA1001286,	HEMBA1001351,	HEMBA1001407,
10	HEMBA1001446,	HEMBA1001510,	HEMBA1001515,	HEMBA1001557,	HEMBA1001746,
	HEMBA1002092,	HEMBA1002125,	HEMBA1002150,	HEMBA1002166,	HEMBA1002462,
	HEMBA1002477,	HEMBA1002486,	HEMBA1002609,	HEMBA1002659,	HEMBA1002661,
	HEMBA1002780,	HEMBA1002818,	HEMBA1002876,	HEMBA1002921,	HEMBA1003077,
15	HEMBA1003079,	HEMBA1003086,	HEMBA1003096,	HEMBA1003281,	HEMBA1003286,
	HEMBA1003711,	HEMBA1003742,	HEMBA1003803,	HEMBA1004143,	HEMBA1004146,
	HEMBA1004341,	HEMBA1004461,	HEMBA1004577,	HEMBA1004637,	HEMBA1004752,
	HEMBA1004756,	HEMBA1004850,	HEMBA1004889,	HEMBA1004923,	HEMBA1004930,
20	HEMBA1005029,	HEMBA1005035,	HEMBA1005050,	HEMBA1005552,	HEMBA1005588,
	HEMBA1005616,	HEMBA1005991,	HEMBA1006036,	HEMBA1006067,	HEMBA1006293,
	HEMBA1006492,	HEMBA1006502,	HEMBA1006659,	HEMBA1006758,	HEMBA1006789,
	HEMBA1006921,	HEMBA1006926,	HEMBA1007203,	HEMBA1000050,	HEMBA1000054,
25	HEMBA1000556,	HEMBA1000593,	HEMBA1000631,	HEMBA1000763,	HEMBA1000827,
	HEMBA1000915,	HEMBA1000975,	HEMBA1001112,	HEMBA1001177,	HEMBA1001302,
	HEMBA1001348,	HEMBA1001962,	HEMBA1002142,	HEMBA1002190,	HEMBA1002247,
	HEMBA1002387,	HEMBA1002550,	HEMBA1002600,	HEMBA1002692,	MAMMA1000129,
30	MAMMA1000133,	MAMMA1000277,	MAMMA1000278,	MAMMA1000410,	MAMMA1000416,
	MAMMA1000472,	MAMMA1000714,	MAMMA1000731,	MAMMA1000734,	MAMMA1000798,
	MAMMA1000842,	MAMMA1000956,	MAMMA1001008,	MAMMA1001030,	MAMMA1001139,
	MAMMA1001154,	MAMMA1001388,	MAMMA1001411,	MAMMA1001487,	MAMMA1001751,
35	MAMMA1001771,	MAMMA1002461,	MAMMA1002524,	MAMMA1002598,	MAMMA1002684,
	MAMMA1002769,	MAMMA1002890,	MAMMA1002938,	MAMMA1003146,	NT2RM1000035,
	NT2RM1000037,	NT2RM1000062,	NT2RM1000131,	NT2RM1000257,	NT2RM1000260,
	NT2RM1000355,	NT2RM1000648,	NT2RM1000742,	NT2RM1000800,	NT2RM1000811,
40	NT2RM1000857,	NT2RM1000867,	NT2RM1000882,	NT2RM1001008,	NT2RM1001115,
	NT2RM1001139,	NT2RM2000259,	NT2RM2000395,	NT2RM2000402,	NT2RM2000407,
	NT2RM2000422,	NT2RM2000566,	NT2RM2000581,	NT2RM2000609,	NT2RM2001370,
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45	NT2RM2001671,	NT2RM2001718,	NT2RM2001760,	NT2RM2001785,	NT2RM2001823,
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50	NT2RM4001032,	NT2RM4001054,	NT2RM4001455,	NT2RM4001813,	NT2RM4001930,
	NT2RM4001987,	NT2RM4002054,	NT2RM4002073,	NT2RM4002145,	NT2RM4002146,
	NT2RM4002194,	NT2RM4002339,	NT2RM4002438,	NT2RM4002446,	NT2RM4002452,
	NT2RM4002460,	NT2RM4002493,	NT2RM4002571,	NT2RP1000191,	NT2RP1000358,
55	NT2RP1000418,	NT2RP1000547,	NT2RP1000609,	NT2RP1000677,	NT2RP1000767,
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	NT2RP1001546,	NT2RP1001569,	NT2RP2000032,	NT2RP2000040,	NT2RP2000070,
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	NT2RP2000195,	NT2RP2000248,	NT2RP2000270,	NT2RP2000283,	NT2RP2000289,
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	NT2RP2001581,	NT2RP2001597,	NT2RP2001947,	NT2RP2001991,	NT2RP2002025,
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10	NT2RP2002701,	NT2RP2002740,	NT2RP2002857,	NT2RP2003125,	NT2RP2003297,
	NT2RP2003433,	NT2RP2003446,	NT2RP2003466,	NT2RP2003629,	NT2RP2003777,
	NT2RP2003781,	NT2RP2004041,	NT2RP2004194,	NT2RP2004270,	NT2RP2004681,
	NT2RP2004775,	NT2RP2004799,	NT2RP2004936,	NT2RP2005012,	NT2RP2005159,
15	NT2RP2005227,	NT2RP2005270,	NT2RP2005344,	NT2RP2005509,	NT2RP2005752,
	NT2RP2005781,	NT2RP2005784,	NT2RP2005812,	NT2RP2006069,	NT2RP2006100,
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25	NT2RP3002054,	NT2RP3002108,	NT2RP3002163,	NT2RP3002351,	NT2RP3002455,
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30	NT2RP3003918,	NT2RP3004207,	NT2RP3004454,	NT2RP3004503,	NT2RP4000051,
	NT2RP4000151,	NT2RP4000243,	NT2RP4000259,	NT2RP4000323,	NT2RP4000500,
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35	NT2RP4000989,	NT2RP4001057,	NT2RP4001064,	NT2RP4001079,	NT2RP4001117,
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	OVARC1000700,	OVARC1000722,	OVARC1000751,	OVARC1000850,	OVARC1000924,
	OVARC1000936,	OVARC1000959,	OVARC1000984,	OVARC1001034,	OVARC1001129,
45	OVARC1001381,	OVARC1001391,	OVARC1001453,	OVARC1001476,	OVARC1001506,
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	PLACE1000401,	PLACE1000562,	PLACE1000611,	PLACE1000656,	PLACE1000712,
50	PLACE1000909,	PLACE1000948,	PLACE1001241,	PLACE1001257,	PLACE1001377,
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	PLACE1002794,	PLACE1002851,	PLACE1002908,	PLACE1003045,	PLACE1003238,
55	PLACE1003296,	PLACE1003369,	PLACE1003493,	PLACE1003537,	PLACE1003553,
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	PLACE1004270,	PLACE1004289,	PLACE1004473,	PLACE1004743,	PLACE1004840,

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	PLACE1004969,	PLACE1005086,	PLACE1005206,	PLACE1005313,	PLACE1005530,
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5	PLACE1007014,	PLACE1007111,	PLACE1007243,	PLACE1007274,	PLACE1007282,
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10	PLACE1008715,	PLACE1009045,	PLACE1009319,	PLACE1009338,	PLACE1009368,
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15	PLACE1011492,	PLACE1011646,	PLACE1011749,	PLACE2000034,	PLACE2000111,
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20	PLACE4000581,	PLACE4000593,	PLACE4000650,	THYRO1000394,	THYRO1000395,
	THYRO1000570,	THYRO1000748,	THYRO1000756,	THYRO1001134,	THYRO1001271,
	THYRO1001401,	THYRO1001534,	THYRO1001541,	THYRO1001809,	Y79AA1000258,
	Y79AA1000420,	Y79AA1000469,	Y79AA1000734,	Y79AA1000800,	Y79AA1000976,
25	Y79AA1001023,	Y79AA1001177,	Y79AA1001394,	Y79AA1001603,	Y79AA1001647,
	Y79AA1001846,	Y79AA1001874,	Y79AA1002139,	Y79AA1002351,	Y79AA1002399,
	Y79AA1002416	HEMBA1004055,	HEMBB1001630,	HEMBB1001872,	HEMBB1002044,
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30	MAMMA1002009,	MAMMA1002844,	MAMMA1002947,	MAMMA1003089,	NT2RM1000092,
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35	OVARC1000890,	OVARC1001117,	OVARC1001329,	PLACE1001761,	PLACE1002437,
	PLACE1004793,	PLACE1005611,	PLACE1005898,	PLACE1009935,	PLACE1011896,
	PLACE2000132,	PLACE2000335,	PLACE3000373,	PLACE3000406,	PLACE4000250,
	PLACE4000487,	PLACE4000494,	THYRO1001320,	THYRO1001537,	THYRO1001828,
40	Y79AA1001384				

Names of clones whose deduced amino acid sequences were predicted to have functional domains by Pfam search, and names of the matched functional domains are shown below. When multiple functional domains matched a clone, each domain name was indicated, separated by a double-slash mark, //.

HEMBA1000005//DnaJ, prokaryotic heat shock protein

HEMBA1000020//Tubulin

HEMBA1000129//Helicases conserved C-terminal domain

HEMBA1000156//RNA recognition motif. (aka RRM, RBD, or RNP domain)

HEMBA1000158//Fork head domain, eukaryotic transcription factors //Zinc finger, C2H2 type

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- HEMBA1000303//Src homology domain 3 //Zinc finger, C3HC4 type (RING finger)
- 5 HEMBA1000411//Ank repeat
- HEMBA1000491//Ras family (contains ATP/GTP binding P-loop)
- 10 HEMBA1000531//Heat shock hsp70 proteins
- HEMBA1000561//Zinc finger, C2H2 type
- 15 HEMBA1000608//Src homology domain 3
- HEMBA1000919//WD domain, G-beta repeats
- 20 HEMBA1001043//Ank repeat
- HEMBA1001088//LIM domain containing proteins
- 25 HEMBA1001137//Zinc finger, C2H2 type
- HEMBA1001174//ADP-ribosylation factors (Arf family) (contains ATP/GTP binding P-loop)
- 30 HEMBA1001247//WW/rsp5/WWP domain containing proteins
- HEMBA1001286//Sushi domain
- 35 HEMBA1001510//Basic region plus leucine zipper transcription factors
- HEMBA1001515//Reverse transcriptase (RNA-dependent DNA polymerase)
- 40 HEMBA1001661//Cadherin
- HEMBA1001723//WD domain, G-beta repeats
- 45 HEMBA1001744//Eukaryotic protein kinase domain
- HEMBA1001804//Zinc finger, C2H2 type
- 50 HEMBA1001819//Zinc finger, C2H2 type
- HEMBA1001847//Zinc finger, C2H2 type
- 55 HEMBA1002035//Bromodomain
- HEMBA1002102//Ank repeat

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- HEMBA1002161//Myosin head (motor domain) (contains ATP/GTP binding P-loop)
- 5 HEMBA1002177//GATA family of transcription factors //Zinc finger, C2H2 type
- HEMBA1002212//Eukaryotic protein kinase domain
- 10 HEMBA1002215//LIM domain containing proteins
- HEMBA1002419//RNA recognition motif. (aka RRM, RBD, or RNP domain)
- 15 HEMBA1002547//Kazal-type serine protease inhibitor domain //Laminin EGF-like (Domains III and V)
- HEMBA1002768//Src homology domain 3
- 20 HEMBA1002810//WW/rsp5/WWP domain containing proteins
- HEMBA1002818//EGF-like domain
- 25 HEMBA1002935//Zinc finger, C2H2 type
- HEMBA1002939//Ank repeat
- 30 HEMBA1002973//3'5'-cyclic nucleotide phosphodiesterases
- HEMBA1003077//Fibronectin type III domain
- 35 HEMBA1003250//Eukaryotic protein kinase domain
- HEMBA1003257//Zinc finger, C2H2 type
- 40 HEMBA1003281//IG superfamily
- HEMBA1003291//Eukaryotic protein kinase domain
- 45 HEMBA1003433//Forkhead-associated (FHA) domain
- HEMBA1003545//Homeobox domain //LIM domain containing proteins
- 50 HEMBA1003591//RNA recognition motif. (aka RRM, RBD, or RNP domain)
- HEMBA1003684//Zinc finger, C2H2 type
- 55 HEMBA1003953//Zinc finger, C2H2 type

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HEMBA1004202//Ras family (contains ATP/GTP binding P-loop)

HEMBA1004227//Protein phosphatase 2C

5 HEMBA1004321//Zinc finger, C2H2 type

HEMBA1004356//RNA recognition motif. (aka RRM, RBD, or RNP domain)

10 HEMBA1004408//Peptidyl-prolyl cis-trans isomerases

HEMBA1004596//RNA recognition motif. (aka RRM, RBD, or RNP domain)

15 HEMBA1004734//Ubiquitin-conjugating enzymes

HEMBA1004973//Fibronectin type III domain

20 HEMBA1005009//Actins

HEMBA1005101//RNA recognition motif. (aka RRM, RBD, or RNP domain)

25 HEMBA1005581//EGF-like domain //Laminin G domain

HEMBA1005732//Polyprenyl synthetases

30 HEMBA1005737//EF hand

HEMBA1006248//Zinc finger, C2H2 type

35 HEMBA1006284//Ubiquitin family

HEMBA1006293//IG superfamily

40 HEMBA1006344//Band 4.1 family

HEMBA1006445//Ras family (contains ATP/GTP binding P-loop)

45 HEMBA1006492//Ank repeat

HEMBA1006559//Zinc finger, C3HC4 type (RING finger)

50 HEMBA1006708//WD domain, G-beta repeats

HEMBA1006737//Ank repeat

55 HEMBA1006758//Cadherin

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HEMBA1006941//Thioredoxins

5 HEMBA1007243//Purine/pyrimidine phosphoribosyl transferases

HEMBA1007300//3'5'-cyclic nucleotide phosphodiesterases

10 HEMBB1000083//IG superfamily

HEMBB1000317//EGF-like domain //Thrombospondin type 1 domain

15 HEMBB1000556//Actinin-type actin-binding domain containing proteins //LIM domain containing proteins

HEMBB1000725//Ras family (contains ATP/GTP binding P-loop)

20 HEMBB1000781//Eukaryotic protein kinase domain

HEMBB1000915//Thrombospondin type 1 domain

25 HEMBB1000927//EF hand

HEMBB1000947//Double-stranded RNA binding motif

30 HEMBB1001112//eubacterial secY protein

HEMBB1001175//Ank repeat

35 HEMBB1001234//WW/rsp5WWP domain containing proteins

HEMBB1001282//Ank repeat

40 HEMBB1001294//Ras family (contains ATP/GTP binding P-loop)

HEMBB1001339//Forkhead-associated (FHA) domain

45 HEMBB1001673//Forkhead-associated (FHA) domain //Zinc finger, C3HC4 type (RING finger)

HEMBB1001802//Intermediate filament proteins

50 HEMBB1001839//Zinc finger, C2H2 type

HEMBB1002217//Zinc finger, C2H2 type

55 HEMBB1002342//Thioredoxins

HEMBB1002600//4 transmembrane segments integral membrane proteins

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- MAMMA1000173//Src homology domain 3
- 5 MAMMA1000388//Zinc finger, C2H2 type
- MAMMA1000402//Reverse transcriptase (RNA-dependent DNA polymerase)
- 10 MAMMA1000612//WD domain, G-beta repeats
- MAMMA1000672//Serine carboxypeptidases
- 15 MAMMA1000731//SNF2 and others N-terminal domain
- MAMMA1001008//Eukaryotic aspartyl proteases
- 20 MAMMA1001041//Actinin-type actin-binding domain containing proteins
- MAMMA1001059//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
- 25 MAMMA1001105//Zinc finger, C2H2 type
- MAMMA1001260//Zinc finger, C3HC4 type (RING finger)
- 30 MAMMA1001576//Tubulin
- MAMMA1001735//Tubulin
- 35 MAMMA1001768//ATPases associated with various cellular activities (AAA)
- MAMMA1001837//Zinc finger, C2H2 type
- 40 MAMMA1002170//Ribosomal protein S5
- MAMMA1002385//RNA recognition motif. (aka RRM, RBD, or RNP domain)
- 45 MAMMA1002619//Ubiquitin carboxyl-terminal hydrolases family 2
- MAMMA1002637//Kinesin light chain repeat
- 50 MAMMA1002650//Zinc finger, C2H2 type
- MAMMA1002671//AMP-binding enzymes
- 55 MAMMA1002869//LIM domain containing proteins
- MAMMA1002881//SCP-like extracellular Proteins

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- MAMMA1002937//Zinc finger, C2H2 type
- 5 MAMMA1002938//Multicopper oxidases
- MAMMA1003011//Core histones H2A, H2B, H3 and H4
- 10 MAMMA1003057//WD domain, G-beta repeats
- MAMMA1003127//Myosin head (motor domain) (contains ATP/GTP binding P-loop)
- 15 NT2RM1000086//Zinc finger, C3HC4 type (RING finger)
- NT2RM1000199//CUB domain //Sushi domain
- 20 NT2RM1000256//Glutamine amidotransferases class-II
- NT2RM1000499//Ank repeat
- 25 NT2RM1000555//Cold-shock' DNA-binding domain containing proteins
- NT2RM1000666//Cold-shock' DNA-binding domain containing proteins //Zinc finger, CCHC class
- 30 NT2RM1000772//WD domain, G-beta repeats
- NT2RM1000826//Cold-shock' DNA-binding domain containing proteins
- 35 NT2RM1000850//Ank repeat //Eukaryotic protein kinase domain
- NT2RM1000852//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
- 40 NT2RM1000882//Heme-binding domain in cytochrome b5 and oxidoreductases
- NT2RM1000885//Zinc finger, C3HC4 type (RING finger)
- 45 NT2RM1001059//RNA recognition motif. (aka RRM, RBD, or RNP domain)
- NT2RM1001072//C2 domain //Phosphatidylinositol-specific phospholipase C, X domain
- 50 //Phosphatidylinositol-specific phospholipase C, Y domain
- NT2RM2000092//Ubiquitin carboxyl-terminal hydrolases family 2
- 55 NT2RM2000101//Zinc finger, C3HC4 type (RING finger)
- NT2RM2000191//3'5'-cyclic nucleotide phosphodiesterases

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- NT2RM2000422//Sodium:neurotransmitter symporter family
- 5 NT2RM2000490//C2 domain
- NT2RM2000566//Integrins alpha chain
- 10 NT2RM2000577//tRNA synthetases class I
- NT2RM2000594//C-5 cytosine-specific DNA methylases
- 15 NT2RM2000691//Actins
- NT2RM2000735//Zinc finger, C2H2 type
- 20 NT2RM2000740//Helicases conserved C-terminal domain
- NT2RM2000951//FGGY family of carbohydrate kinases
- 25 NT2RM2001324//LIM domain containing proteins
- NT2RM2001499//Amino acid permeases
- 30 NT2RM2001547//DnaJ, prokaryotic heat shock protein //Thioredoxins
- NT2RM2001613//eubacterial secY protein
- 35 NT2RM2001670//Zinc finger, C2H2 type
- NT2RM2001700//Acyl-CoA dehydrogenases
- 40 NT2RM2001730//Ubiquitin carboxyl-terminal hydrolases family 2
- NT2RM2001813//WD domain, G-beta repeats
- 45 NT2RM2001823//Helicases conserved C-terminal domain //SNF2 and others N-terminal domain
- 50 NT2RM2001896//Cytochrome C oxidase subunit II
- NT2RM2001989//RNA recognition motif. (aka RRM, RBD, or RNP domain)
- 55 NT2RM2001997//Thioredoxins
- NT2RM2002088//KH domain family of RNA binding proteins

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NT2RM2002100//DEAD and DEAH box helicases //Helicases conserved C-terminal domain

NT2RM2002109//IG superfamily

5 NT2RM4000046//Zinc finger, C3HC4 type (RING finger)

NT2RM4000104//Zinc finger, C2H2 type

10 NT2RM4000167//Kinesin motor domain

NT2RM4000191//DEAD and DEAH box helicases //Helicases conserved C-terminal domain

15 NT2RM4000202//Zinc finger, C2H2 type

NT2RM4000229//PH (pleckstrin homology) domain

20 NT2RM4000344//ATPases associated with various cellular activities (AAA)

NT2RM4000356//Ras family (contains ATP/GTP binding P-loop)

25 NT2RM4000471//Aminotransferases class-V

NT2RM4000496//ATPases associated with various cellular activities (AAA)

30 NT2RM4000611//WD domain, G-beta repeats

NT2RM4000657//C2 domain //Phosphatidylinositol-specific phospholipase C, Y domain

35 NT2RM4000712//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2

40 NT2RM4000733//Forkhead-associated (FHA) domain

NT2RM4000734//Zinc finger, C2H2 type

45 NT2RM4000751//Zinc finger, C2H2 type

NT2RM4000795//Carboxylesterases

50 NT2RM4000996//Zinc finger, C2H2 type

NT2RM4001054//eubacterial secY protein

55 NT2RM4001140//Homeobox domain

NT2RM4001178//DEAD and DEAH box helicases

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- NT2RM4001200//Zinc finger, C2H2 type
- 5 NT2RM4001313//Phosphatidylinositol 3- and 4-kinases
- NT2RM4001316//Acyl-CoA dehydrogenases
- 10 NT2RM4001320//Src homology domain 3
- NT2RM4001411//PH (pleckstrin homology) domain //Src homology domain 2
- 15 NT2RM4001454//PH (pleckstrin homology) domain
- NT2RM4001483//Zinc finger, C2H2 type
- 20 NT2RM4001629//Src homology domain 3
- NT2RM4001758//Eukaryotic protein kinase domain
- 25 NT2RM4001810//Zinc finger, C2H2 type
- NT2RM4001813//Lectin C-type domain short and long forms
- 30 NT2RM4001823//Zinc finger, C2H2 type
- NT2RM4001828//Zinc finger, C2H2 type
- 35 NT2RM4001979//Zinc finger, C2H2 type
- NT2RM4001987//IG superfamily
- 40 NT2RM4002013//WD domain, G-beta repeats
- NT2RM4002073//AMP-binding enzymes
- 45 NT2RM4002093//RNA recognition motif. (aka RRM, RBD, or RNP domain)
- NT2RM4002145//IG superfamily
- 50 NT2RM4002287//Fibronectin type III domain
- NT2RM4002527//WD domain, G-beta repeats
- 55 NT2RM4002623//tRNA synthetases class II
- NT2RP1000101//Zinc finger, C2H2 type

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- NT2RP1000202//Ank repeat
- 5 NT2RP1000272//RNA recognition motif. (aka RRM, RBD, or RNP domain)
- NT2RP1000363//PH (pleckstrin homology) domain
- 10 NT2RP1000376//Ank repeat
- NT2RP1000470//DEAD and DEAH box helicases
- 15 NT2RP1000478//Tubulin
- NT2RP1000522//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal
hydrolases family 2
- 20 NT2RP1000677//Kazal-type serine protease inhibitor domain
- NT2RP1000701//WD domain, G-beta repeats
- 25 NT2RP1000733//Elongation factor Tu family (contains ATP/GTP binding P-loop)
- NT2RP1000782//4 transmembrane segments integral membrane proteins
- 30 NT2RP1000833//3'5'-cyclic nucleotide phosphodiesterases
- NT2RP1000856//4 transmembrane segments integral membrane proteins
- 35 NT2RP1000947//Ubiquitin-conjugating enzymes
- NT2RP1000959//60s Acidic ribosomal protein
- 40 NT2RP1000966//RNA recognition motif. (aka RRM, RBD, or RNP domain)
- NT2RP1001033//Tubulin
- 45 NT2RP1001080//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
- NT2RP1001177//Core histones H2A, H2B, H3 and H4
- 50 NT2RP1001247//Transforming growth factor beta like domain
- NT2RP1001294//WD domain, G-beta repeats
- 55 NT2RP1001302//WD domain, G-beta repeats

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- NT2RP1001313//Heme-binding domain in cytochrome b5 and oxidoreductases
- NT2RP1001457//WD domain, G-beta repeats
- 5 NT2RP1001546//4 transmembrane segments integral membrane proteins
- NT2RP2000008//Zinc finger, C2H2 type
- 10 NT2RP2000040//C2 domain
- NT2RP2000045//DnaJ, prokaryotic heat shock protein
- 15 NT2RP2000054//Zinc finger, C3HC4 type (RING finger)
- NT2RP2000070//Cadherin
- 20 NT2RP2000126//Helicases conserved C-terminal domain //SNF2 and others N-terminal domain
- 25 NT2RP2000153//RNA recognition motif. (aka RRM, RBD, or RNP domain)
- NT2RP2000224//PH (pleckstrin, homology) domain
- 30 NT2RP2000257//Mitochondrial carrier proteins
- NT2RP2000329//Adenylate kinases
- 35 NT2RP2000414//RNA recognition motif. (aka RRM, RBD, or RNP domain)
- NT2RP2000448//PH (pleckstrin homology) domain
- 40 NT2RP2000660//ATPases associated with various cellular activities (AAA)
- NT2RP2000668//Eukaryotic protein kinase domain
- 45 NT2RP2000710//tRNA synthetases class II
- NT2RP2000764//Aminotransferases class-V
- 50 NT2RP2000842//7 transmembrane receptor (rhodopsin family)
- NT2RP2000880//Elongation factor Tu family (contains ATP/GTP binding P-loop)
- 55 NT2RP2000931//RNA recognition motif. (aka RRM, RBD, or RNP domain)
- NT2RP2000932//Ank repeat

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NT2RP2001081//C2 domain

5 NT2RP2001174//Zinc finger, C2H2 type

NT2RP2001397//Cyclins

10 NT2RP2001520//Mitochondrial carrier proteins

NT2RP2001597//Zinc finger, C3HC4 type (RING finger)

15 NT2RP2001740//Ubiquitin carboxyl-terminal hydrolases family 2

NT2RP2001748//Polyprenyl synthetases

20 NT2RP2001756//Zinc finger, C2H2 type

NT2RP2001839//Eukaryotic protein kinase domain

25 NT2RP2001900//Actins

NT2RP2001991//Sodium:neurotransmitter symporter family

30 NT2RP2002058//WD domain, G-beta repeats

NT2RP2002124//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal
hydrolases family 2

35 NT2RP2002185//Ubiquitin family

NT2RP2002208//Zinc finger, C3HC4 type (RING finger)

40 NT2RP2002256//Cytochrome P450

NT2RP2002479//ABC transporters

45 NT2RP2002503//Zinc finger, C2H2 type

NT2RP2002520//Ank repeat

50 NT2RP2002591//Zinc finger, C2H2 type

NT2RP2002741//Src homology domain 3

55 NT2RP2002929//WD domain, G-beta repeats

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NT2RP2002939//Zinc finger, C2H2 type

5 NT2RP2002959//Ubiquitin-conjugating enzymes

NT2RP2002980//Ribosomal protein S10

10 NT2RP2003137//Ubiquitin family

NT2RP2003164//Eukaryotic protein kinase domain

15 NT2RP2003228//MCM2/3/5 family

NT2RP2003243//Fibronectin type III domain

20 NT2RP2003272//Ubiquitin family

NT2RP2003307//Kinesin light chain repeat

25 NT2RP2003401//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases, family 2

NT2RP2003433//eubacterial secY protein

30 NT2RP2003480//Zinc finger, C2H2 type

NT2RP2003713//Ubiquitin carboxyl-terminal hydrolases family 2

35 NT2RP2003737//Ubiquitin-conjugating enzymes

NT2RP2003777//Zinc finger, C3HC4 type (RING finger)

40 NT2RP2003840//Ubiquitin-conjugating enzymes

NT2RP2003857//Ank repeat

45 NT2RP2003981//Zinc finger, C3HC4 type (RING finger)

NT2RP2004170//WD domain, G-beta repeats

50 NT2RP2004187//Zinc finger, C2H2 type

NT2RP2004232//Phorbol esters / diacylglycerol binding domain //PH (pleckstrin homology) domain //Eukaryotic protein kinase domain

55 NT2RP2004389//Ribosomal protein S9

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NT2RP2004538//PH (pleckstrin homology) domain

5 NT2RP2004568//DEAD and DEAH box helicases //Helicases conserved C-terminal domain

NT2RP2004710//WW/rsp5WWP domain containing proteins

10 NT2RP2004768//Eukaryotic protein kinase domain

NT2RP2004933//Eukaryotic protein kinase domain

15 NT2RP2004961//Zinc finger, C2H2 type

NT2RP2005003//Zinc finger, C3HC4 type (RING finger)

20 NT2RP2005012//DnaJ, prokaryotic heat shock protein

NT2RP2005126//DEAD and DEAH box helicases //Helicases conserved C-terminal domain

25 NT2RP2005139//Ank repeat

NT2RP2005140//PH (pleckstrin homology) domain

30 NT2RP2005239//Aminotransferases class-V

NT2RP2005288//Regulator of chromosome condensation (RCC1)

35 NT2RP2005293//PH (pleckstrin homology) domain

NT2RP2005325//Homeobox domain //LIM domain containing proteins

40 NT2RP2005344//E1-E2 ATPases

NT2RP2005465//Mitochondrial carrier proteins

45 NT2RP2005525//Forkhead-associated (FHA) domain

NT2RP2005531//Band 4.1 family

50 NT2RP2005557//Bacterial mutT protein

NT2RP2005654//DnaJ, prokaryotic heat shock protein

55 NT2RP2005701//Zinc finger, C3HC4 type (RING finger)

NT2RP2005722//Zinc finger, C2H2 type

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NT2RP2005752//TNFR/NGFR cysteine-rich region

5 NT2RP2005763//DEAD and DEAH box helicases //Helicases conserved C-terminal domain

NT2RP2005767//HMG (high mobility group) box

10 NT2RP2006312//HMG (high mobility group) box

NT2RP2006464//HMG (high mobility group) box

15 NT2RP2006571//Cytochrome P450

NT2RP3000050//Zinc finger, C2H2 type

20 NT2RP3000068//PH (pleckstrin homology) domain

NT2RP3000085//Biotin-requiring enzymes //Carbamoyl-phosphate synthase (CPSase)

25 NT2RP3000299//Src homology domain 3

NT2RP3000359//Adenylate kinases

30 NT2RP3000366//Ras family (contains ATP/GTP binding P-loop)

NT2RP3000403//WW/rsp5/WWP domain containing proteins

35 NT2RP3000487//WW/rsp5/WWP domain containing proteins

NT2RP3000512//Homeobox domain

40 NT2RP3000527//Zinc finger, C2H2 type

NT2RP3000531//IG superfamily

45 NT2RP3000590//Zinc finger, C3HC4 type (RING finger)

NT2RP3000603//Helix-loop-helix DNA-binding domain

50 NT2RP3000605//Zinc finger, C2H2 type

NT2RP3000632//Zinc finger, C2H2 type

55 NT2RP3000742//Phosphatidylinositol-specific phospholipase C, X domain
//Phosphatidylinositol-specific phospholipase C, Y domain

NT2RP3000759//ADP-ribosylation factors (Arf family) (contains ATP/GTP binding P-loop)

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- NT2RP3000825//EGF-like domain
- 5 NT2RP3000869//ATPases associated with various cellular activities (AAA)
- NT2RP3000994//Double-stranded RNA binding motif
- 10 NT2RP3001057//Zinc finger, C2H2 type
- NT2RP3001084//PH (pleckstrin homology) domain
- 15 NT2RP3001120//Zinc finger, C2H2 type
- NT2RP3001140//Thrombospondin type 1 domain
- 20 NT2RP3001150//Forkhead-associated (FHA) domain
- NT2RP3001155//HMG (high mobility group) box
- 25 NT2RP3001214//Zinc finger, C2H2 type
- NT2RP3001268//Zinc finger, C2H2 type
- 30 NT2RP3001338//Zinc finger, C2H2 type
- NT2RP3001355//Mitochondrial carrier proteins
- 35 NT2RP3001398//Zinc finger, C2H2 type
- NT2RP3001426//DnaJ, prokaryotic heat shock protein
- 40 NT2RP3001453//ABC transporters
- NT2RP3001457//PH (pleckstrin homology) domain
- 45 NT2RP3001472//HMG (high mobility group) box
- NT2RP3001495//Alcohol/other dehydrogenases, short chain type //WW/rsp5/WWP domain
containing proteins
- 50 NT2RP3001497//Zinc finger, C3HC4 type (RING finger)
- NT2RP3001724//Helicases conserved C-terminal domain
- 55 NT2RP3001792//RNA recognition motif. (aka RRM, RBD, or RNP domain)

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NT2RP3001943//Zinc finger, C3HC4 type (RING finger)

5 NT2RP3001944//Zinc finger, C3HC4 type (RING finger)

NT2RP3002007//ATPases associated with various cellular activities (AAA)

NT2RP3002054//Low-density lipoprotein receptor domain class A

10 NT2RP3002151//Elongation factor Tu family (contains ATP/GTP binding P-loop)

NT2RP3002399//MCM2/3/5 family

15 NT2RP3002501//Serine/threonine dehydratases

NT2RP3002602//Thioredoxins

20 NT2RP3002628//DnaJ, prokaryotic heat shock protein //Thioredoxins

NT2RP3002663//PH (pleckstrin homology) domain

25 NT2RP3002909//Ank repeat

NT2RP3002953//Cadherin

30 NT2RP3002969//AMP-binding enzymes

NT2RP3003061//Ank repeat

35 NT2RP3003145//Zinc carboxypeptidases

NT2RP3003230//WD domain, G-beta repeats

40 NT2RP3003251//Zinc finger, C3HC4 type (RING finger)

NT2RP3003278//Ank repeat //Zinc finger, C2H2 type

45 NT2RP3003282//PH (pleckstrin homology) domain

NT2RP3003311//PH (pleckstrin homology) domain

50 NT2RP3003385//Ank repeat //Chaperonins clpA/B

NT2RP3003589//Ras family (contains ATP/GTP binding P-loop)

55 NT2RP3003621//CUB domain //Kring domain

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NT2RP3003701//Thrombospondin type 1 domain

5 NT2RP3003716//Fibronectin type III domain

NT2RP3003809//ATPases associated with various cellular activities (AAA)

10 NT2RP3004016//Zinc finger, C3HC4 type (RING finger)

NT2RP3004207//CUB domain //Sushi domain

15 NT2RP3004209//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2

NT2RP3004242//PH (pleckstrin homology) domain

20 NT2RP3004262//DnaJ, prokaryotic heat shock protein

NT2RP3004566//Zinc finger, C2H2 type

25 NT2RP3004569//Ank repeat

NT2RP3004594//HMG (high mobility group) box

30 NT2RP3004617//Zinc finger, C3HC4 type (RING finger)

NT2RP4000259//Glutathione . peroxidases

35 NT2RP4000370//Prokaryotic-type class I peptide chain release factors

NT2RP4000376//WD domain, G-beta repeats

40 NT2RP4000398//Zinc finger, C2H2 type

NT2RP4000455//Forkhead-associated (FHA) domain //Zinc finger, C3HC4 type (RING finger)

45 NT2RP4000457//Ubiquitin carboxyl-terminal hydrolases family 2

NT2RP4000518//DEAD and DEAH box helicases //Helicases conserved C-terminal domain

50 NT2RP4000588//Actinin-type actin-binding domain containing proteins

NT2RP4000614//RNA recognition motif. (aka RRM, RBD, or RNP domain)

55 NT2RP4000648//Forkhead-associated (FHA) domain //Zinc finger, C3HC4 type (RING finger)

NT2RP4000837//Zinc finger, C2H2 type

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NT2RP4000839//WD domain, G-beta repeats

5 NT2RP4000865//Zinc finger, C2H2 type

NT2RP4000907//Fibronectin type III domain //IG superfamily

10 NT2RP4000925//Fibronectin type III domain

NT2RP4000927//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2

15 NT2RP4000973//DnaJ, prokaryotic heat shock protein //Thioredoxins

NT2RP4001079//E1-E2 ATPases

20 NT2RP4001080//RNA recognition motif. (aka RRM, RBD, or RNP domain)

NT2RP4001117//eubacterial secY protein

25 NT2RP4001150//Fibronectin type III domain

NT2RP4001213//Zinc finger, C2H2 type

30 NT2RP4001219//Thioredoxins

NT2RP4001235//Zinc finger, CCHC class

35 NT2RP4001433//Zinc finger, C2H2 type

NT2RP4001498//Ank repeat

40 NT2RP4001568//Ank repeat

NT2RP4001644//Eukaryotic protein kinase domain

45 NT2RP4001725//WD domain, G-beta repeats

NT2RP4001753//Zinc finger, C2H2 type

50 NT2RP4001790//Zinc finger, C2H2 type

NT2RP4001822//4 transmembrane segments integral membrane proteins

55 NT2RP4001823//Fibrinogen beta and gamma chains, C-terminal globular domain

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NT2RP4001893//Ank repeat

5 NT2RP4001896//WD domain, G-beta repeats

NT2RP4001927//WD domain, G-beta repeats

10 NT2RP4001938//Zinc finger, C2H2 type

NT2RP4002047//Elongation factor Tu family (contains ATP/GTP binding P-loop)

15 NT2RP4002078//Zinc finger, C2H2 type

NT2RP4002408//Eukaryotic protein kinase domain

20 NT2RP4002905//Cyclins

NT2RP5003477//WD domain, G-beta repeats

25 OVARC1000006//Core histones H2A, H2B, H3 and H4

OVARC1000085//Proteasome A-type and B-type

30 OVARC1000148//RNA recognition motif. (aka RRM, RBD, or RNP domain)

OVARC1000556//Eukaryotic protein kinase domain

35 OVARC1000649//PH (pleckstrin homology) domain //Src homology domain 2

OVARC1000746//Double-stranded RNA binding motif

40 OVARC1000885//Alcohol/other dehydrogenases, short chain type

OVARC1000937//Cyclins

45 OVARC1000999//Ank repeat

OVARC1001154//Granulins

50 OVARC1001180//Ubiquitin family

OVARC1001306//Helix-loop-helix DNA-binding domain

55 OVARC1001577//RNA recognition motif. (aka RRM, RBD, or RNP domain)

OVARC1001731//Tropomyosins

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OVARC1001943//Zinc finger, C2H2 type

5 OVARC1002050//Spectrin alpha chain, repeated domain

OVARC1002112//Core histones H2A, H2B, H3 and H4

10 OVARC1002138//ATPases associated with various cellular activities (AAA)

OVARC1002182//WD domain, G-beta repeats

15 PLACE1000014//Zinc finger, C3HC4 type (RING finger)

PLACE1000040//Ras family (contains ATP/GTP binding P-loop)

20 PLACE1000050//Zinc finger, C2H2 type

PLACE1000081//PH (pleckstrin homology) domain

25 PLACE1000142//Enoyl-CoA hydratase/isomerase

PLACE1000401//IG superfamily

30 PLACE1000406//RNA recognition motif. (aka RRM, RBD, or RNP domain)

PLACE1000420//Bacterial mutT protein

35 PLACE1000706//Bromodomain

PLACE1000769//KH domain family of RNA binding proteins

40 PLACE1000786//PH (pleckstrin homology) domain

PLACE1000863//Ribosomal protein S4

45 PLACE1000909//Ank repeat

PLACE1000972//Src homology domain 3

50 PLACE1000979//Zinc finger, C2H2 type

PLACE1001304//Zinc finger, C2H2 type

55 PLACE1001387//Src homology domain 3

PLACE1001632//Zinc finger, C2H2 type

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PLACE1001672//Aminotransferases class-III pyridoxal-phosphate

PLACE1001716//Zinc finger, CCHC class

5

PLACE1001739//DEAD and DEAH box helicases //Helicases conserved C-terminal domain

PLACE1001781//Phosphoglucosyltransferase and phosphomannosyltransferase phosphoserine

10

PLACE1001869//FGGY family of carbohydrate kinases

PLACE1002438//Zinc finger, C2H2 type

15

PLACE1002450//Zinc finger, C2H2 type

PLACE1002474//EGF-like domain //von Willebrand factor type A domain

20

PLACE1002499//Zinc finger, C3HC4 type (RING finger)

PLACE1002532//Homeobox domain

25

PLACE1002571//Actins

PLACE1002685//Src homology domain 2

30

PLACE1002722//7 transmembrane receptor (rhodopsin family)

PLACE1002775//Bromodomain

35

PLACE1002834//Zinc finger, C2H2 type

PLACE1003100//Alcohol/other dehydrogenases, short chain type

40

PLACE1003174//Ubiquitin-conjugating enzymes

PLACE1003238//7 transmembrane receptor (rhodopsin family)

45

PLACE1003302//Zinc finger, C2H2 type

PLACE1003334//RNA recognition motif. (aka RRM, RBD, or RNP domain)

50

PLACE1003366//C2 domain

PLACE1003394//Ras family (contains ATP/GTP binding P-loop)

55

PLACE1003420//Mitochondrial carrier proteins

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- PLACE1003493//C1q domain
- 5 PLACE1003519//KH domain family of RNA binding-proteins
- PLACE1003723//Src homology domain 2
- 10 PLACE1003738//Zinc finger, C2H2 type
- PLACE1003888//C2 domain //Phosphatidylinositol-specific phospholipase C, X domain
//Phosphatidylinositol-specific phospholipase C, Y domain
- 15 PLACE1004128//WD domain, G-beta repeats
- PLACE1004358//PH (pleckstrin homology) domain
- 20 PLACE1004428//Acyl-CoA dehydrogenases
- PLACE1004437//Isocitrate and isopropylmalate dehydrogenases
- 25 PLACE1004506//LIM domain containing proteins
- PLACE1004674//EF hand
- 30 PLACE1004918//L-lactate dehydrogenases
- PLACE1005243//Eukaryotic protein kinase domain
- 35 PLACE1005305//Adenylate kinases
- PLACE1005327//Src homology domain 3
- 40 PLACE1005530//Zinc finger, C3HC4 type (RING finger)
- PLACE1005646//Helicases conserved C-terminal domain
- 45 PLACE1005656//Ribonucleotide reductases
- PLACE1005966//WD domain, G-beta repeats
- 50 PLACE1006157//Sushi domain
- PLACE1006196//DEAH and DEAR box helicases //Helicases conserved C-terminal domain
- 55 PLACE1006438//Zinc finger, C2H2 type
- PLACE1006626//Double-stranded RNA binding motif

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- PLACE1006754//IG superfamily
- 5 PLACE1006829//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2
- PLACE1006917//RNA recognition motif. (aka RRM, RBD, or RNP domain)
- 10 PLACE1006956//ABC transporters
- PLACE1006958//Heat shock hsp70 proteins
- 15 PLACE1007375//C2 domain
- PLACE1007488//PH (pleckstrin homology) domain
- 20 PLACE1007511//Intermediate filament proteins
- PLACE1007537//Ank repeat
- 25 PLACE1007544//Zinc finger, C2H2 type
- PLACE1007547//Zinc finger, C3HC4 type (RING finger)
- 30 PLACE1007598//Zinc finger, C2H2 type
- PLACE1007697//ABC transporters
- 35 PLACE1007958//3'5'-cyclic nucleotide phosphodiesterases
- PLACE1007969//RNA recognition motif. (aka RRM, RBD, or RNP domain)
- 40 PLACE1008201//Zinc finger, C2H2 type
- PLACE1008429//Ank repeat
- 45 PLACE1008465//Zinc finger, C2H2 type
- PLACE1008650//WD domain, G-beta repeats
- 50 PLACE1009020//Aminotransferases class-V
- PLACE1009094//von Willebrand factor type C domain
- 55 PLACE1009099//Zinc finger, C2H2 type

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PLACE1009246//LIM domain containing proteins

5 PLACE1009468//WD domain, G-beta repeats

PLACE1009476//DEAD and DEAH box helicases //Helicases conserved C-terminal domain

10 PLACE1009524//PH (pleckstrin homology) domain

PLACE1009596//WD domain, G-beta repeats

15 PLACE1009622//Double-stranded RNA binding motif

PLACE1009861//Cysteine proteases

20 PLACE1009925//Helicases conserved C-terminal domain

PLACE1009992//CUB domain //EGF-like domain //Sushi domain //Trypsin

25 PLACE1010053//Double-stranded RNA binding motif

PLACE1010089//Ubiquitin carboxyl-terminal hydrolases family 2

30 PLACE1010702//Zinc finger, C2H2 type

PLACE1010833//EF hand

35 PLACE1010926//Src homology domain 3

PLACE1010960//Actins

40 PLACE1011041//Src homology domain 3

PLACE1011046//C2 domain //Phosphatidylinositol-specific phospholipase C, X domain
//Phosphatidylinositol-specific phospholipase C, Y domain

45 PLACE1011114//Helicases conserved C-terminal domain

PLACE1011160//Zinc finger, C3HC4 type (RING finger)

50 PLACE1011263//Ank repeat

PLACE1011433//Zinc finger, C2H2 type

55 PLACE1011576//Zinc finger, C2H2 type

PLACE1011923//Eukaryotic protein kinase domain

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- PLACE2000034//Fibronectin type III domain //IG superfamily
- 5 PLACE2000072//Zinc finger, C2H2 type
- PLACE2000111//IG superfamily
- 10 PLACE2000164//WD domain, G-beta repeats
- PLACE2000216//PH (pleckstrin homology) domain
- 15 PLACE2000341//Sodium:solute symporter family
- PLACE2000371//Src homology domain 2
- 20 PLACE2000373//Thrombospondin type 1 domain
- PLACE2000398//IG superfamily
- 25 PLACE2000427//Helicases conserved C-terminal domain
- PLACE2000458//Cadherin
- 30 PLACE3000020//Guanylate cyclases
- PLACE3000169//Zinc finger, C2H2 type
- 35 PLACE4000014//Helicases conserved C-terminal domain
- PLACE4000052//ABC transporters
- 40 PLACE4000192//Zinc finger, C2H2 type
- PLACE4000211//Bromodomain
- 45 PLACE4000431//Helicases conserved C-terminal domain
- PLACE4000522//Ank repeat
- 50 PLACE4000581//EGF-like domain //Sushi domain
- PLACE4000654//Ubiquitin-conjugating enzymes
- 55 THYRO1000072//IG superfamily
- THYRO1000242//Zinc finger, C2H2 type

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- THYRO1000288//Zinc-binding metalloprotease domain
- 5 THYRO1000488//Zinc finger, C3HC4 type (RING finger)
- THYRO1000501//Zinc finger, C3HC4 type (RING finger)
- 10 THYRO1000666//Kinesin motor domain
- THYRO1000748//Src homology domain 3
- 15 THYRO1000926//3' 5'-cyclic nucleotide phosphodiesterases
- THYRO1001661//RNA recognition motif. (aka RRM, RBD, or RNP domain)
- 20 THYRO1001671//Ubiquitin family
- Y79AA1000037//Zinc finger, C3HC4 type (RING finger)
- 25 Y79AA1000214//Core histones H2A, H2B, H3 and H4
- Y79AA1000342//Zinc finger, C2H2 type
- 30 Y79AA1000349//Double-stranded RNA binding motif
- Y79AA1000627//Zinc finger, C2H2 type
- 35 Y79AA1000705//Helicases conserved C-terminal domain
- Y79AA1000752//KH domain family of RNA binding proteins
- 40 Y79AA1000833//Tubulin
- Y79AA1001048//Acyl-CoA dehydrogenases
- 45 Y79AA1001391//Homeobox domain
- Y79AA1001394//ATPases associated with various cellular activities (AAA)
- 50 Y79AA1001493//Ubiquitin-conjugating enzymes
- Y79AA1001613//Zinc finger, C2H2 type
- 55 Y79AA1001874//TNFR/NGFR cysteine-rich region
- Y79AA1002027//Ubiquitin-conjugating enzymes

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- Y79AA1002139//DnaJ, prokaryotic heat shock protein
- 5 Y79AA1002208//Ank repeat
- Y79AA1002246//C2 domain
- 10 Y79AA1002307//Fibronectin type III domain
- Y79AA1002472//Zinc finger, C2H2 type
- 15 HEMBA1003538//CUB domain HEMBA1003645//WD domain, G-beta repeats //Src homology domain 3 HEMBA1005206//Glutathione S-transferases.
- HEMBA1006521//Alcohol/other dehydrogenases, short chain type
- 20 HEMBB1001482//Zinc finger, C2H2 type HEMBB1001915//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2 HEMBB1002044//Cadherin MAMMA1000183//Zinc finger, C2H2 type
- 25 MAMMA1000897//von Willebrand factor type A domain MAMMA1001080//IG superfamily MAMMA1002498//IG superfamily MAMMA1002573//KH domain family of RNA binding proteins MAMMA1002617//Zinc finger, C2H2 type
- 30 NT2RM1000833//eubacterial secY protein NT2RM2001797//Zinc finger, C2H2 type
- NT2RP1001013//Zinc finger, C2H2 type NT2RP2001233//Zinc finger, C2H2 type
- 35 NT2RP2001440//14-3-3 proteins NT2RP2002105//transmembrane receptor (rhodopsin family) NT2RP3001723//Laminin G domain NT2RP3001938//Eukaryotic protein kinase domain NT2RP3002330//Elongation factor Tu family (contains ATP/GTP binding P-loop)
- 40 NT2RP3003133//Zinc finger, C2H2 type
- NT2RP3003500//Eukaryotic protein kinase domain NT2RP3003799//C2 domain
- 45 NT2RP3003800//Eukaryotic protein kinase domain NT2RP3004013//Double-stranded RNA binding motif NT2RP3004125//Zinc finger, C2H2 type
- 50 OVARC1001244//Bromodomain OVARC1001496//D-isomer specific 2-hydroxyacid dehydrogenases PLACE1000007//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2 PLACE1001118//Zinc finger, C2H2 type PLACE1010310//Zinc finger, C2H2 type PLACE1011896//wnt family of developmental signaling proteins PLACE3000124//Src homology domain 2
- 55 PLACE4000100//D-isomer specific 2-hydroxyacid dehydrogenases

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PLACE4000259//Helicases conserved C-terminal domain PLACE4000261//Bromodomain
SKNMC1000013//ABC transporters SKNMC1000091//Basic region plus leucine zipper
transcription factors THYRO1000343//Src homology domain 3 THYRO1000569//Zinc finger,
5 C2H2 type THYRO1001189//Zinc finger, C2H2 type Y79AA1002103//Zinc finger, C2H2 type
PLACE3000350//Eukaryotic protein kinase domain

10 PLACE4000156//Zinc finger, C2H2 type

EXAMPLE 18

15 Classification of cDNA clones into functional categories based on the full-length nucleotide
sequences

Prediction of functions of proteins encoded by the clones and the categorization thereof were
20 performed based on the results of homology search (see Homology search results 6, 12, 13 and
14) of the databases, GenBank, Swiss-Prot and UniGene, for the full-length nucleotide
sequences of 4997 clones and based on the results of domain search (see Example 17) of the
deduced amino acid sequences encoded by the full-length nucleotide sequences. The target
25 4997 clones are listed below:

HEMBA1000005,	HEMBA1000012,	HEMBA1000020,	HEMBA1000030,	HEMBA1000042,
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45 HEMBA1000592,	HEMBA1000594,	HEMBA1000604,	HEMBA1000608,	HEMBA1000622,
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10 Y79AA1002220, Y79AA1002229, Y79AA1002234, Y79AA1002246, Y79AA1002258,
Y79AA1002298, Y79AA1002307, Y79AA1002311, Y79AA1002351, Y79AA1002361,
Y79AA1002399, Y79AA1002407, Y79AA1002416, Y79AA1002431, Y79AA1002433,
Y79AA1002472, Y79AA1002482, Y79AA1002487,

15 Among the 4997 clones, there are 2189 clones that presumably encode proteins belonging to any of the categories of secretory or membrane proteins, glycoprotein-associated proteins, signal transduction-associated proteins, transcription-associated proteins, disease-associated proteins, enzymes and/or metabolism-associated proteins, ATP- and/or GTP-binding proteins,
20 nuclear proteins, DNA- and/or RNA-binding proteins, RNA synthesis-associated proteins, protein synthesis- and/or protein transport-associated proteins, cytoskeleton-associated proteins, cell division- and/or cell proliferation-associated proteins, embryogenesis- and/or development-associated proteins, or cellular defense-associated proteins.

25 The clones that presumably encode proteins belonging to the category of secretory or membrane proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "growth factor", "cytokine", "hormone", "signal", "transmembrane", "membrane", "extracellular matrix", "receptor", "G-protein coupled receptor", "ionic channel",
30 "voltage-gated channel", "calcium channel", "cell adhesion", "collagen", or "connective tissue"; those which matched the data, suggesting that the proteins are secretory or membrane proteins; or those which matched the full-length sequences of GenBank or UniGene database with similar description; and, further, those predicted to have an N-terminal signal sequence or
35 a transmembrane region as a result of domain search for the amino acid sequences deduced from the full-length nucleotide sequences.

The clones that presumably encode proteins belonging to the category of glycoprotein-associated proteins are those which matched the full-length sequences of Swiss-Prot database
40 with the keywords "glycoprotein"; those which matched the data, suggesting that the proteins are glycoprotein; or those which matched the full-length sequences of GenBank or UniGene database with similar description.

45 The clones that presumably encode proteins belonging to the category of signal transduction-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "serine/threonine-protein kinase", "tyrosine-protein kinase", or "SH3 domain"; those which matched the data, suggesting that the proteins are signal transduction-associated
50 proteins (for example, "ADP-ribosylation factor"); or those which matched the full-length sequences of GenBank or UniGene database with similar description.

The clones that presumably encode proteins belonging to the category of transcription-associated proteins are those which matched the full-length sequences of Swiss-Prot database
55 with the keywords "transcription regulation", "zinc finger", or "homeobox"; those which matched the data, suggesting that the proteins are transcription-associated proteins; or those which matched the full-length sequences of GenBank or UniGene database with similar description.

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The clones that presumably encode proteins belonging to the category of disease-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "disease mutation" or "syndrome"; those which matched the data, suggesting that the proteins are disease-associated proteins; or those which matched the full-length sequences of Swiss-Prot database and GenBank or UniGene database where the matched sequences of genes or proteins which had been registered in the database of Online Mendelian Inheritance in Man (OMIM) (<http://www.ncbi.nlm.nih.gov/Omim/>), which is a database of human genes and diseases.

The clones that presumably encode proteins belonging to the category of enzymes and/or metabolism-associated proteins are those which showed the terms "metabolism", "oxidoreductase", or "E.C. No. (Enzyme commission number)" in the matching data.

The clones that presumably encode proteins belonging to the category of ATP- and/or GTP-binding proteins are those which matched the data with the terms "ATP-binding" or "GTP-binding".

The clones that presumably encode proteins belonging to the category of nuclear proteins are those which matched the data with the terms "nuclear protein".

The clones that presumably encode proteins belonging to the category of DNA- and/or RNA-binding proteins are those which matched the data with the terms "DNA-binding" or "RNA-binding".

The clones that presumably encode proteins belonging to the category of RNA synthesis-associated proteins are those which matched the data with the terms "RNA splicing", "RNA processing", "RNA helicase", or "polyadenylation".

The clones that presumably encode proteins belonging to the category of protein synthesis- and/or protein transport-associated proteins are those which matched the data with the terms "translation regulation", "protein biosynthesis", "amino-acid biosynthesis", "ribosomal protein", "protein transport", or "signal recognition particle".

The clones that presumably encode proteins belonging to the category of cytoskeleton-associated proteins are those which matched the data with the terms "structural protein", "cytoskeleton", "actin-binding", or "microtubules".

The clones that presumably encode proteins belonging to the category of cell division- and/or cell proliferation-associated proteins are those which matched the data with the terms "cell division", "cell cycle", "mitosis", "chromosomal protein", "cell growth", or "apoptosis".

The clones that presumably encode proteins belonging to the category of embryogenesis- and/or development-associated proteins are those which matched the data with the terms "developmental protein".

The clones that presumably encode proteins belonging to the category of cellular defense-associated proteins are those which matched the data with the terms "heat shock", "DNA repair", or "DNA damage".

When a clone belonged to the above-mentioned multiple functional categories, the clone was classified into the multiple categories. However, the functions of the protein encoded by the clone are not limited to the functions of the categories into which the clone was classified, and therefore, additional functions can be found for the protein by further analyses.

The following 796 clones are categorized into secretory or membrane proteins.
HEMBA1000356, HEMBA1000518, HEMBA1000531, HEMBA1000637, HEMBA1000719,
HEMBA1000817, HEMBA1000822, HEMBA1000852, HEMBA1000870, HEMBA1000991,

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	HEMBA1001052,	HEMBA1001071,	HEMBA1001085,	HEMBA1001286,	HEMBA1001351,
	HEMBA1001407,	HEMBA1001446,	HEMBA1001515,	HEMBA1001557,	HEMBA1001569,
	HEMBA1001661,	HEMBA1001734,	HEMBA1001746,	HEMBA1001866,	HEMBA1002125,
5	HEMBA1002150,	HEMBA1002166,	HEMBA1002417,	HEMBA1002462,	HEMBA1002475,
	HEMBA1002477,	HEMBA1002486,	HEMBA1002609,	HEMBA1002659,	HEMBA1002661,
	HEMBA1002780,	HEMBA1002818,	HEMBA1002876,	HEMBA1002921,	HEMBA1003071,
	HEMBA1003077,	HEMBA1003079,	HEMBA1003086,	HEMBA1003096,	HEMBA1003281,
10	HEMBA1003286,	HEMBA1003538,	HEMBA1003711,	HEMBA1003742,	HEMBA1003803,
	HEMBA1004055,	HEMBA1004143,	HEMBA1004146,	HEMBA1004207,	HEMBA1004341,
	HEMBA1004461,	HEMBA1004577,	HEMBA1004637,	HEMBA1004752,	HEMBA1004756,
	HEMBA1004850,	HEMBA1004889,	HEMBA1004923,	HEMBA1004930,	HEMBA1005029,
15	HEMBA1005035,	HEMBA1005050,	HEMBA1005552,	HEMBA1005576,	HEMBA1005581,
	HEMBA1005588,	HEMBA1005616,	HEMBA1005699,	HEMBA1005991,	HEMBA1006036,
	HEMBA1006038,	HEMBA1006067,	HEMBA1006173,	HEMBA1006198,	HEMBA1006293,
	HEMBA1006310,	HEMBA1006492,	HEMBA1006502,	HEMBA1006583,	HEMBA1006659,
20	HEMBA1006758,	HEMBA1006789,	HEMBA1006921,	HEMBA1006926,	HEMBA1006976,
	HEMBA1007203,	HEMBA1007301,	HEMBA1000037,	HEMBA1000050,	HEMBA1000054,
	HEMBA1000175,	HEMBA1000317,	HEMBA1000556,	HEMBA1000593,	HEMBA1000631,
	HEMBA1000763,	HEMBA1000827,	HEMBA1000915,	HEMBA1000975,	HEMBA1001112,
25	HEMBA1001151,	HEMBA1001177,	HEMBA1001302,	HEMBA1001348,	HEMBA1001564,
	HEMBA1001630,	HEMBA1001871,	HEMBA1001872,	HEMBA1001925,	HEMBA1001962,
	HEMBA1002042,	HEMBA1002044,	HEMBA1002142,	HEMBA1002190,	HEMBA1002193,
	HEMBA1002247,	HEMBA1002383,	HEMBA1002387,	HEMBA1002550,	HEMBA1002600,
30	HEMBA1002692,	MAMMA1000045,	MAMMA1000129,	MAMMA1000133,	MAMMA1000277,
	MAMMA1000278,	MAMMA1000410,	MAMMA1000416,	MAMMA1000472,	MAMMA1000672,
	MAMMA1000684,	MAMMA1000714,	MAMMA1000734,	MAMMA1000778,	MAMMA1000798,
	MAMMA1000842,	MAMMA1000859,	MAMMA1000897,	MAMMA1000956,	MAMMA1001008,
35	MAMMA1001030,	MAMMA1001041,	MAMMA1001073,	MAMMA1001080,	MAMMA1001139,
	MAMMA1001154,	MAMMA1001322,	MAMMA1001388,	MAMMA1001411,	MAMMA1001487,
	MAMMA1001751,	MAMMA1001754,	MAMMA1001771,	MAMMA1002009,	MAMMA1002427,
	MAMMA1002428,	MAMMA1002461,	MAMMA1002524,	MAMMA1002573,	MAMMA1002598,
40	MAMMA1002655,	MAMMA1002684,	MAMMA1002769,	MAMMA1002844,	MAMMA1002881,
	MAMMA1002890,	MAMMA1002938,	MAMMA1002947,	MAMMA1003035,	MAMMA1003089,
	MAMMA1003146,	MAMMA1003150,	NT2RM1000035,	NT2RM1000037,	NT2RM1000062,
45	NT2RM1000080,	NT2RM1000092,	NT2RM1000131,	NT2RM1000199,	NT2RM1000257,
	NT2RM1000260,	NT2RM1000355,	NT2RM1000430,	NT2RM1000563,	NT2RM1000648,
	NT2RM1000742,	NT2RM1000770,	NT2RM1000800,	NT2RM1000811,	NT2RM1000833,
	NT2RM1000857,	NT2RM1000867,	NT2RM1000882,	NT2RM1000905,	NT2RM1001008,
	NT2RM1001115,	NT2RM1001139,	NT2RM2000259,	NT2RM2000260,	NT2RM2000287,
50	NT2RM2000395,	NT2RM2000402,	NT2RM2000407,	NT2RM2000422,	NT2RM2000490,
	NT2RM2000522,	NT2RM2000566,	NT2RM2000581,	NT2RM2000609,	NT2RM2000821,
	NT2RM2001370,	NT2RM2001393,	NT2RM2001499,	NT2RM2001547,	NT2RM2001613,
	NT2RM2001648,	NT2RM2001659,	NT2RM2001671,	NT2RM2001688,	NT2RM2001698,
55	NT2RM2001718,	NT2RM2001753,	NT2RM2001760,	NT2RM2001785,	NT2RM2001930,
	NT2RM2001950,	NT2RM2001997,	NT2RM2001998,	NT2RM2002049,	NT2RM2002145,
	NT2RM4000233,	NT2RM4000433,	NT2RM4000457,	NT2RM4000486,	NT2RM4000496,

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	NT2RM4000520,	NT2RM4000634,	NT2RM4000674,	NT2RM4000700,	NT2RM4000764,
	NT2RM4000778,	NT2RM4000795,	NT2RM4000820,	NT2RM4000857,	NT2RM4001032,
	NT2RM4001054,	NT2RM4001116,	NT2RM4001455,	NT2RM4001666,	NT2RM4001810,
5	NT2RM4001813,	NT2RM4001930,	NT2RM4001987,	NT2RM4002054,	NT2RM4002073,
	NT2RM4002145,	NT2RM4002146,	NT2RM4002189,	NT2RM4002194,	NT2RM4002251,
	NT2RM4002339,	NT2RM4002438,	NT2RM4002446,	NT2RM4002452,	NT2RM4002460,
	NT2RM4002493,	NT2RM4002558,	NT2RM4002565,	NT2RM4002571,	NT2RM4002594,
10	NT2RP1000130,	NT2RP1000191,	NT2RP1000326,	NT2RP1000358,	NT2RP1000413,
	NT2RP1000418,	NT2RP1000547,	NT2RP1000609,	NT2RP1000677,	NT2RP1000767,
	NT2RP1000782,	NT2RP1000856,	NT2RP1001113,	NT2RP1001247,	NT2RP1001286,
	NT2RP1001310,	NT2RP1001311,	NT2RP1001313,	NT2RP1001385,	NT2RP1001449,
15	NT2RP1001546,	NT2RP1001569,	NT2RP2000032,	NT2RP2000040,	NT2RP2000056,
	NT2RP2000070,	NT2RP2000091,	NT2RP2000114,	NT2RP2000120,	NT2RP2000173,
	NT2RP2000175,	NT2RP2000195,	NT2RP2000257,	NT2RP2000270,	NT2RP2000283,
	NT2RP2000288,	NT2RP2000289,	NT2RP2000459,	NT2RP2000516,	NT2RP2000660,
20	NT2RP2000842,	NT2RP2000892,	NT2RP2001081,	NT2RP2001268,	NT2RP2001295,
	NT2RP2001366,	NT2RP2001378,	NT2RP2001576,	NT2RP2001581,	NT2RP2001597,
	NT2RP2001613,	NT2RP2001947,	NT2RP2001991,	NT2RP2002025,	NT2RP2002066,
	NT2RP2002078,	NT2RP2002105,	NT2RP2002312,	NT2RP2002325,	NT2RP2002385,
25	NT2RP2002479,	NT2RP2002537,	NT2RP2002643,	NT2RP2002701,	NT2RP2002740,
	NT2RP2002857,	NT2RP2003125,	NT2RP2003297,	NT2RP2003433,	NT2RP2003446,
	NT2RP2003466,	NT2RP2003506,	NT2RP2003513,	NT2RP2003629,	NT2RP2003668,
	NT2RP2003760,	NT2RP2003777,	NT2RP2003781,	NT2RP2004041,	NT2RP2004142,
30	NT2RP2004194,	NT2RP2004270,	NT2RP2004300,	NT2RP2004392,	NT2RP2004655,
	NT2RP2004681,	NT2RP2004775,	NT2RP2004799,	NT2RP2004936,	NT2RP2004959,
	NT2RP2005012,	NT2RP2005159,	NT2RP2005227,	NT2RP2005270,	NT2RP2005344,
	NT2RP2005465,	NT2RP2005509,	NT2RP2005752,	NT2RP2005781,	NT2RP2005784,
35	NT2RP2005812,	NT2RP2006069,	NT2RP2006100,	NT2RP2006141,	NT2RP2006184,
	NT2RP2006261,	NT2RP2006565,	NT2RP2006571,	NT2RP2006573,	NT2RP3000092,
	NT2RP3000109,	NT2RP3000134,	NT2RP3000207,	NT2RP3000333,	NT2RP3000341,
	NT2RP3000393,	NT2RP3000439,	NT2RP3000441,	NT2RP3000531,	NT2RP3000685,
40	NT2RP3000825,	NT2RP3000826,	NT2RP3000852,	NT2RP3000919,	NT2RP3001084,
	NT2RP3001096,	NT2RP3001126,	NT2RP3001140,	NT2RP3001176,	NT2RP3001260,
	NT2RP3001282,	NT2RP3001355,	NT2RP3001383,	NT2RP3001426,	NT2RP3001453,
	NT2RP3001497,	NT2RP3001538,	NT2RP3001589,	NT2RP3001642,	NT2RP3001708,
45	NT2RP3001716,	NT2RP3001727,	NT2RP3001739,	NT2RP3001799,	NT2RP3001943,
	NT2RP3001944,	NT2RP3002002,	NT2RP3002007,	NT2RP3002014,	NT2RP3002054,
	NT2RP3002108,	NT2RP3002163,	NT2RP3002351,	NT2RP3002455,	
	NT2RP3002549,	NT2RP3002602,	NT2RP3002628,	NT2RP3002650,	NT2RP3002687,
50	NT2RP3002701,	NT2RP3002810,	NT2RP3002869,	NT2RP3002969,	NT2RP3002985,
	NT2RP3003008,	NT2RP3003059,	NT2RP3003071,	NT2RP3003101,	NT2RP3003145,
	NT2RP3003197,	NT2RP3003203,	NT2RP3003242,	NT2RP3003302,	NT2RP3003353,
	NT2RP3003409,	NT2RP3003576,	NT2RP3003621,	NT2RP3003665,	NT2RP3003672,
55	NT2RP3003701,	NT2RP3003716,	NT2RP3003799,	NT2RP3003828,	NT2RP3003914,
	NT2RP3003918,	NT2RP3003992,	NT2RP3004051,	NT2RP3004148,	NT2RP3004155,
	NT2RP3004207,	NT2RP3004282,	NT2RP3004454,	NT2RP3004480,	NT2RP3004503,

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	NT2RP4000008,	NT2RP4000051,	NT2RP4000151,	NT2RP4000212,	NT2RP4000243,
	NT2RP4000259,	NT2RP4000323,	NT2RP4000417,	NT2RP4000500,	NT2RP4000524,
	NT2RP4000556,	NT2RP4000560,	NT2RP4000588,	NT2RP4000713,	NT2RP4000724,
5	NT2RP4000817,	NT2RP4000833,	NT2RP4000878,	NT2RP4000907,	NT2RP4000925,
	NT2RP4000928,	NT2RP4000973,	NT2RP4000989,	NT2RP4001057,	NT2RP4001064,
	NT2RP4001079,	NT2RP4001117,	NT2RP4001138,	NT2RP4001149,	NT2RP4001150,
	NT2RP4001174,	NT2RP4001219,	NT2RP4001274,	NT2RP4001313,	NT2RP4001345,
10	NT2RP4001372,	NT2RP4001373,	NT2RP4001379,	NT2RP4001498,	NT2RP4001547,
	NT2RP4001571,	NT2RP4001574,	NT2RP4001644,	NT2RP4001656,	NT2RP4001677,
	NT2RP4001730,	NT2RP4001739,	NT2RP4001803,	NT2RP4001822,	NT2RP4001823,
	NT2RP4001950,	NT2RP4001975,	NT2RP4002052,	NT2RP4002075,	NT2RP5003500,
15	NT2RP5003506,	NT2RP5003522,	NT2RP5003534,	OVARC1000060,	OVARC1000335,
	OVARC1000682,	OVARC 1000689,	OVARC 1000700,	OVARC 1000722,	OVARC1000751,
	OVARC 1000850,	OVARC1000890,	OVARC1000924,	OVARC1000936,	OVARC1000959,
	OVARC1000984,	OVARC1000999,	OVARC1001034,	OVARC1001055,	OVARC1001117,
20	OVARC1001129,	OVARC1001154,	OVARC1001329,	OVARC1001381,	OVARC1001391,
	OVARC1001453,	OVARC1001476,	OVARC1001506,	OVARC1001610,	OVARC1001702,
	OVARC1001703,	OVARC1001713,	OVARC1001745,	OVARC1001767,	OVARC1002127,
	OVARC1002138,	OVARC1002158,	OVARC1002165,	PLACE1000014,	PLACE1000213,
25	PLACE1000401,	PLACE1000562,	PLACE1000611,	PLACE1000656,	PLACE1000712,
	PLACE1000793,	PLACE1000909,	PLACE1000948,	PLACE1000977,	PLACE1001241,
	PLACE1001377,	PLACE1001517,	PLACE1001610,	PLACE1001761,	PLACE1001771,
	PLACE1001817,	PLACE1001983,	PLACE1002046,	PLACE1002140,	PLACE1002213,
30	PLACE1002395,	PLACE1002437,	PLACE1002500,	PLACE1002583,	PLACE1002714,
	PLACE1002722,	PLACE1002782,	PLACE1002794,	PLACE1002851,	PLACE1002908,
	PLACE1003030,	PLACE1003044,	PLACE1003045,	PLACE1003238,	PLACE1003296,
	PLACE1003369,	PLACE1003420,	PLACE1003493,	PLACE1003537,	PLACE1003553,
35	PLACE1003596,	PLACE1003760,	PLACE1003768,	PLACE1003771,	PLACE1003903,
	PLACE1004149,	PLACE1004197,	PLACE1004203,	PLACE1004258,	PLACE1004270,
	PLACE1004277,	PLACE1004289,	PLACE1004473,	PLACE1004629,	PLACE1004646,
	PLACE1004743,	PLACE1004751,	PLACE1004793,	PLACE1004840,	PLACE1004969,
40	PLACE1005086,	PLACE1005162,	PLACE1005206,	PLACE1005313,	PLACE1005467,
	PLACE1005530,	PLACE1005595,	PLACE1005611,	PLACE1005623,	PLACE1005763,
	PLACE1005884,	PLACE1005890,	PLACE1005898,	PLACE1005934,	PLACE1005953,
	PLACE1006157,	PLACE1006225,	PLACE1006239,	PLACE1006288,	PLACE1006492,
45	PLACE1006534,	PLACE1006678,	PLACE1006754,	PLACE1006901,	PLACE1006935,
	PLACE1006956,	PLACE1007111,	PLACE1007243,	PLACE1007274,	PLACE1007282,
	PLACE1007317,	PLACE1007375,	PLACE1007386,	PLACE1007409,	PLACE1007416,
	PLACE1007484,	PLACE1007583,	PLACE1007632,	PLACE1007645,	PLACE1007649,
50	PLACE1007852,	PLACE1007877,	PLACE1007954,	PLACE1008273,	PLACE1008309,
	PLACE1008331,	PLACE1008402,	PLACE1008424,	PLACE1008429,	PLACE1008531,
	PLACE1008532,	PLACE1008533,	PLACE1008568,	PLACE1008643,	PLACE1008693,
	PLACE1008715,	PLACE1009045,	PLACE1009094,	PLACE1009298,	PLACE1009319,
55	PLACE1009338,	PLACE1009368,	PLACE1009493,	PLACE1009639,	
	PLACE1009659,	PLACE1009708,	PLACE1009731,	PLACE1009845,	PLACE1009861,
	PLACE1009935,	PLACE1009992,	PLACE1010089,	PLACE1010231,	PLACE1010321,

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	PLACE1010362,	PLACE1010599,	PLACE1010622,	PLACE1010662,	PLACE1010811,
	PLACE1010917,	PLACE1010942,	PLACE1010954,	PLACE1011090,	PLACE1011214,
	PLACE1011221,	PLACE1011371,	PLACE1011399,	PLACE1011492,	PLACE1011646,
5	PLACE1011749,	PLACE1011896,	PLACE2000034,	PLACE2000062,	PLACE2000111,
	PLACE2000132,	PLACE2000176,	PLACE2000187,	PLACE2000216,	PLACE2000335,
	PLACE2000341,	PLACE2000373,	PLACE2000379,	PLACE2000398,	PLACE2000399,
	PLACE2000425,	PLACE2000438,	PLACE2000458,	PLACE2000477,	PLACE3000020,
10	PLACE3000218,	PLACE3000226,	PLACE3000242,	PLACE3000244,	PLACE3000339,
	PLACE3000373,	PLACE3000399,	PLACE3000406,	PLACE3000413,	PLACE3000455,
	PLACE4000052,	PLACE4000063,	PLACE4000129,	PLACE4000247,	PLACE4000250,
	PLACE4000259,	PLACE4000300,	PLACE4000387,	PLACE4000431,	PLACE4000487,
15	PLACE4000494,	PLACE4000522,	PLACE4000548,	PLACE4000581,	PLACE4000593,
	PLACE4000650,	THYRO1000156,	THYRO1000327,	THYRO1000394,	THYRO1000395,
	THYRO1000570,	THYRO1000748,	THYRO1000756,	THYRO1000783,	THYRO1001134,
	THYRO1001271,	THYRO1001287,	THYRO1001320,	THYRO1001401,	THYRO1001534,
20	THYRO1001537,	THYRO1001541,	THYRO1001828,	Y79AA1000258,	Y79AA1000420,
	Y79AA1000469,	Y79AA1000734,	Y79AA1000800,	Y79AA1000976,	Y79AA1001023,
	Y79AA1001177,	Y79AA1001384,	Y79AA1001394,	Y79AA1001603,	Y79AA1001647,
	Y79AA1001846,	Y79AA1001874,	Y79AA1002139,	Y79AA1002246,	Y79AA1002351,
25	Y79AA1002399,	Y79AA1002416,			

The following 141 clones are categorized into glycoproteins-associated proteins.

	HEMBA1000156,	HEMBA1000518,	HEMBA1000852,	HEMBA1001071,	HEMBA1001286,
	HEMBA1001661,	HEMBA1001734,	HEMBA1001866,	HEMBA1003071,	HEMBA1003077,
30	HEMBA1003281,	HEMBA1003538,	HEMBA1003679,	HEMBA1003866,	HEMBA1005576,
	HEMBA1005581,	HEMBA1005699,	HEMBA1006038,	HEMBA1006976,	HEMBA1007301,
	HEMBB1000317,	HEMBB1000915,	HEMBB1001871,	HEMBB1001872,	HEMBB1002193,
	MAMMA1000672,	MAMMA1000897,	MAMMA1001030,	MAMMA1001388,	MAMMA1002329,
35	MAMMA1002428,	MAMMA1002573,	MAMMA1003150,	NT2RM1000648,	NT2RM1001115,
	NT2RM2000260,	NT2RM2000407,	NT2RM2000422,	NT2RM2000490,	NT2RM2001499,
	NT2RM2001659,	NT2RM2001930,	NT2RM4000820,	NT2RM4000857,	NT2RM4001810,
	NT2RM4001813,	NT2RM4001987,	NT2RM4002145,	NT2RM4002189,	NT2RM4002251,
40	NT2RM4002460,	NT2RM4002558,	NT2RP1000677,	NT2RP1000782,	NT2RP1000856,
	NT2RP1001546,	NT2RP2000056,	NT2RP2000070,	NT2RP2001295,	NT2RP2001378,
	NT2RP2001597,	NT2RP2001991,	NT2RP2002025,	NT2RP2002078,	NT2RP2002385,
	NT2RP2004587,	NT2RP2004732,	NT2RP2005531,	NT2RP3000207,	NT2RP3000531,
45	NT2RP3000825,	NT2RP3001140,	NT2RP3002810,	NT2RP3003672,	NT2RP3003701,
	NT2RP3003716,	NT2RP3003914,	NT2RP3004148,	NT2RP4000212,	NT2RP4000417,
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50	OVARC1000288,	OVARC1000682,	OVARC1001055,	OVARC1001506,	OVARC1001713,
	OVARC1002127,	PLACE1000213,	PLACE1000401,	PLACE1002437,	PLACE1002583,
	PLACE1002722,	PLACE1003045,	PLACE1003238,	PLACE1003258,	PLACE1003493,
	PLACE1004197,	PLACE1004793,	PLACE1005953,	PLACE1005955,	PLACE1006157,
55	PLACE1006239,	PLACE1006368,	PLACE1006534,	PLACE1006754,	PLACE1006956,
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PLACE2000373, PLACE2000398, PLACE2000399, PLACE2000438, PLACE2000458,
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 PLACE4000548, PLACE4000581, THYRO1000327, THYRO1000756, THYRO1001287,
 5 Y79AA1001603, Y79AA1001874

The following 129 clones are categorized into signal transduction-associated proteins.

HEMBA1000303, HEMBA1000369, HEMBA1000608, HEMBA1000657, HEMBA1000919,
 HEMBA1001019, HEMBA1001174, HEMBA1001822, HEMBA1001921, HEMBA1002139,
 10 HEMBA1002212, HEMBA1002341, HEMBA1002417, HEMBA1002768, HEMBA1003250,
 HEMBA1003291, HEMBA1003645, HEMBA1004286, HEMBA1005737, HEMBA1006130,
 HEMBA1006708, HEMBB1000083, HEMBB1000266, HEMBB1000632, HEMBB1000781,
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 15 MAMMA1002842, MAMMA1003057, NT2RM1000702, NT2RM1000772, NT2RM1001072,
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 NT2RM2002128, NT2RM4000229, NT2RM4000354, NT2RM4000611, NT2RM4000798,
 NT2RM4001411, NT2RM4001412, NT2RM4001629, NT2RM4001758, NT2RM4002013,
 20 NT2RM4002527, NT2RP1000018, NT2RP1000701, NT2RP1001294, NT2RP1001302,
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 25 NT2RP3000845, NT2RP3001646, NT2RP3001857, NT2RP3001938, NT2RP3002004,
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 30 NT2RP4001896, NT2RP4001927, NT2RP4002408, NT2RP5003477, OVARC1000013,
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 35 PLACE1005243, PLACE1008000, PLACE1008244, PLACE1008650, PLACE1009468,
 PLACE1009596, PLACE1009708, PLACE1009845, PLACE1010926, PLACE1011041,
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 THYRO1000748, THYRO1001120, Y79AA1000328, Y79AA1002431

40 The following 309 clones are categorized into transcription -associated proteins.

HEMBA1000158, HEMBA1000201, HEMBA1000216, HEMBA1000555, HEMBA1000561,
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 HEMBA1001635, HEMBA1001804, HEMBA1001809, HEMBA1001819, HEMBA1001847,
 45 HEMBA1001869, HEMBA1002035, HEMBA1002092, HEMBA1002177, HEMBA1002770,
 HEMBA1002935, HEMBA1003408, HEMBA1003545, HEMBA1003568, HEMBA1003662,
 HEMBA1003684, HEMBA1003760, HEMBA1003953, HEMBA1004097, HEMBA1004321,
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 50 HEMBA1005219, HEMBA1005359, HEMBA1005513, HEMBA1005528, HEMBA1005548,
 HEMBA1005558, HEMBA1005931, HEMBA1006158, HEMBA1006248, HEMBA1006278,
 HEMBA1006283, HEMBA1006347, HEMBA1006359, HEMBA1006559, HEMBA1006941,
 HEMBB1000789, HEMBB1001011, HEMBB1001314, HEMBB1001482, HEMBB1001673,
 55 HEMBB1001749, HEMBB1001839, HEMBB1001908, HEMBB1002134, HEMBB1002217,
 HEMBB1002342, HEMBB1002607, MAMMA1000183, MAMMA1000388, MAMMA1001105,

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	MAMMA1001222,	MAMMA1001260,	MAMMA1001627,	MAMMA1001633,	MAMMA1001743,
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5	NT2RM1001092,	NT2RM2000013,	NT2RM2000452,	NT2RM2000735,	NT2RM2000740,
	NT2RM2001035,	NT2RM2001105,	NT2RM2001575,	NT2RM2001670,	NT2RM2001716,
	NT2RM2001771,	NT2RM2002091,	NT2RM4000024,	NT2RM4000046,	NT2RM4000104,
	NT2RM4000202,	NT2RM4000531,	NT2RM4000595,	NT2RM4000733,	NT2RM4000734,
10	NT2RM4000741,	NT2RM4000751,	NT2RM4000996,	NT2RM4001092,	NT2RM4001140,
	NT2RM4001200,	NT2RM4001483,	NT2RM4001592,	NT2RM4001783,	NT2RM4001823,
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15	NT2RP2000126,	NT2RP2000297,	NT2RP2000420,	NT2RP2001174,	NT2RP2001233,
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	NT2RP2002464,	NT2RP2002503,	NT2RP2002520,	NT2RP2002591,	NT2RP2002880,
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	NT2RP2005139,	NT2RP2005325,	NT2RP2005496,	NT2RP2005701,	NT2RP2005722,
	NT2RP2005776,	NT2RP2005942,	NT2RP2006238,	NT2RP2006436,	NT2RP3000050,
25	NT2RP3000320,	NT2RP3000512,	NT2RP3000527,	NT2RP3000590,	NT2RP3000603,
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30	NT2RP3002876,	NT2RP3003133,	NT2RP3003193,	NT2RP3003251,	NT2RP3003313,
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	NT2RP4000398,	NT2RP4000455,	NT2RP4000648,	NT2RP4000837,	NT2RP4000865,
35	NT2RP4000997,	NT2RP4001029,	NT2RP4001080,	NT2RP4001213,	NT2RP4001433,
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40	OVARC1001271,	OVARC1001417,	OVARC1001436,	PLACE1000133,	PLACE1000583,
	PLACE1000706,	PLACE1000786,	PLACE1000979,	PLACE1001118,	PLACE1001238,
	PLACE1001294,	PLACE1001304,	PLACE1001383,	PLACE1001602,	PLACE1001632,
	PLACE1002171,	PLACE1002438,	PLACE1002450,	PLACE1002532,	PLACE1002775,
45	PLACE1002834,	PLACE1003302,	PLACE1003605,	PLACE1003738,	PLACE1003885,
	PLACE1004471,	PLACE1005584,	PLACE1005803,	PLACE1005966,	PLACE1006167,
	PLACE1006318,	PLACE1006438,	PLACE1006482,	PLACE1007239,	PLACE1007346,
	PLACE1007488,	PLACE1007547,	PLACE1007598,	PLACE1007955,	PLACE1008132,
50	PLACE1008201,	PLACE1009099,	PLACE1009246,	PLACE1009308,	PLACE1009398,
	PLACE1009798,	PLACE1010134,	PLACE1010702,	PLACE1010771,	PLACE1010870,
	PLACE1011160,	PLACE1011433,	PLACE1011576,	PLACE3000009,	PLACE3000169,
	PLACE3000254,	PLACE4000128,	PLACE4000156,	PLACE4000192,	PLACE4000211,
55	PLACE4000261,	PLACE4000450,	PLACE4000489,	THYRO1000085,	THYRO1000121,
	THYRO1000242,	THYRO1000488,	THYRO1000501,	THYRO1000569,	THYRO1001100,
	THYRO1001189,	THYRO1001809,	Y79AA1000013,	Y79AA1000033,	Y79AA1000037,

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Y79AA1000342, Y79AA1000627, Y79AA1000705, Y79AA1001299, Y79AA1001312,
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5 The following 392 clones are categorized into disease-associated proteins.

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10 HEMBA1002267, HEMBA1002419, HEMBA1002469, HEMBA1002547, HEMBA1002555,
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15 HEMBA1004202, HEMBA1004248, HEMBA1004275, HEMBA1004321, HEMBA1004353,
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20 HEMBA1006737, HEMBA1006807, HEMBA1006877, HEMBA1007121, HEMBA1007243,
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HEMBB1001282, HEMBB1001339, HEMBB1001482, HEMBB1001564, HEMBB1001802,
HEMBB1001905, HEMBB1001908, HEMBB1002217, HEMBB1002477, MAMMA1000388,
25 MAMMA1000731, MAMMA1001305, MAMMA1001633, MAMMA1001868, MAMMA1002170,
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30 NT2RM1000826, NT2RM1000850, NT2RM1001003, NT2RM1001092, NT2RM1001102,
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35 NT2RM2001698, NT2RM2001803, NT2RM2001839, NT2RM4000155, NT2RM4000471,
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55 NT2RP2005288, NT2RP2005315, NT2RP2005325, NT2RP2005336, NT2RP2005358,
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	NT2RP2006456,	NT2RP3000050,	NT2RP3000068,	NT2RP3000085,	NT2RP3000299,
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	NT2RP3001057,	NT2RP3001081,	NT2RP3001216,	NT2RP3001307,	NT2RP3001338,
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	NT2RP3003251,	NT2RP3003282,	NT2RP3003313,	NT2RP3003327,	NT2RP3003409,
10	NT2RP3003672,	NT2RP3003831,	NT2RP3004016,	NT2RP3004078,	NT2RP3004209,
	NT2RP3004258,	NT2RP3004490,	NT2RP3004534,	NT2RP3004569,	NT2RP3004572,
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15	NT2RP4001213,	NT2RP4001276,	NT2RP4001407,	NT2RP4001433,	NT2RP4001483,
	NT2RP4001575,	NT2RP4001760,	NT2RP4001861,	NT2RP4002078,	NT2RP4002791,
	OVARC1000014,	OVARC1000139,	OVARC1000520,	OVARC1000722,	OVARC1000771,
	OVARC1000834,	OVARC1001051,	OVARC1001113,	OVARC1001244,	OVARC1001372,
20	OVARC1001417,	OVARC1001496,	OVARC1001506,	OVARC1001577,	
	OVARC1001726,	OVARC1001766,	OVARC1001809,	OVARC1002165,	PLACE1000133,
	PLACE1000383,	PLACE1000420,	PLACE1000583,	PLACE1000588,	PLACE1001171,
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25	PLACE1002474,	PLACE1002685,	PLACE1002782,	PLACE1002834,	PLACE1002908,
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30	PLACE1004506,	PLACE1004510,	PLACE1004674,	PLACE1004777,	PLACE1004814,
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	PLACE1007140,	PLACE1007239,	PLACE1007257,	PLACE1007511,	PLACE1007598,
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35	PLACE1009113,	PLACE1009158,	PLACE1009444,	PLACE1009524,	PLACE1010529,
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	PLACE2000015,	PLACE2000072,	PLACE2000216,	PLACE2000399,	PLACE2000438,
	PLACE2000458,	PLACE3000242,	PLACE4000009,	PLACE4000014,	PLACE4000156,
40	PLACE4000369,	SKNMC1000046,	SKNMC1000050,	THYRO1000034,	THYRO1000327,
	THYRO1000343,	THYRO1000358,	THYRO1000501,	THYRO1000662,	THYRO1000684,
	THYRO1000748,	THYRO1000934,	THYRO1001120,	THYRO1001189,	THYRO1001204,
	THYRO1001458,	THYRO1001617,	THYRO1001671,	Y79AA1000346,	Y79AA1000469,
45	Y79AA1000560,	Y79AA1000734,	Y79AA1000782,	Y79AA1001391,	Y79AA1001548,
	Y79AA1001594,	Y79AA1001711,	Y79AA1001874,	Y79AA1002204,	Y79AA1002210,
	Y79AA1002258,	Y79AA1002472,	Y79AA1002482,		

Among them, Swiss-Prot database search and GenBank or UniGene database search revealed that the following 380 clones matched the data of genes or proteins which had been registered in the database of Online Mendelian Inheritance in Man (OMIM) (<http://www.ncbi.nlm.nih.gov/Omim/>), which is a database of human genes and diseases. (The corresponding OMIM numbers are parenthetically indicated following the clone names.)

55	HEMBB1000985(147485),	HEMBB1001068(603142),	HEMBB1001282(182900),
	HEMBB1001339(300080),	HEMBB1001482(603971),	HEMBB1001564(603931),
	HEMBB1001802(125660),	HEMBB1001905(190370),	HEMBB1001908(601408),

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	HEMBB1002217(603971),	HEMBB1002477(604439),	MAMMA1000388(604865),
	MAMMA1000731(602118),	MAMMA1001305(602732),	MAMMA1001633(600834),
	MAMMA1001868(190370),	MAMMA1002170(603624),	MAMMA1002198(600538),
5	MAMMA1002268(603730),	MAMMA1002485(603665),	MAMMA1002530(603602),
	MAMMA1002858(601064),	MAMMA1002869(602567),	MAMMA1002881(602692),
	MAMMA1003047(603566),	MAMMA1003146(603094),	MAMMA1003166(604061),
	NT2RM1000001(601169),	NT2RM1000153(600417),	NT2RM1000252(604108),
10	NT2RM1000555(191510),	NT2RM1000770(300061),	NT2RM1000826(191510),
	NT2RM1000850(182900),	NT2RM1001003(604785),	NT2RM1001092(603971),
	NT2RM1001102(604533),	NT2RM2000191(602973),	NT2RM2000363(151410),
	NT2RM2000594(602900),	NT2RM2000624(601940),	NT2RM2000714(179555),
15	NT2RM2000821(600959),	NT2RM2001035(604913),	NT2RM2001575(109092),
	NT2RM2001652(604141),	NT2RM2001664(603722),	NT2RM2001668(602952),
	NT2RM2001698(604327),	NT2RM2001803(603722),	NT2RM2001839(603420),
	NT2RM4000155(187790),	NT2RM4000471(603485),	NT2RM4000486(168730),
20	NT2RM4000657(602142),	NT2RM4000751(602277),	NT2RM4000996(603971),
	NT2RM4001629(601114),	NT2RM4001810(155760),	NT2RM4001819(176873),
	NT2RM4001876(179555),	NT2RM4001940(603887),	NT2RM4002066(300188),
	NT2RM4002093(600693),	NT2RM4002146(602603),	NT2RM4002161(254780),
25	NT2RM4002558(604194),	NT2RM4002571(602274),	NT2RP1000086(602219),
	NT2RP1000574(601740),	NT2RP1000825(602732),	
	NT2RP1000833(602973),	NT2RP1000959(180510),	NT2RP1000966(164035),
	NT2RP1001013(194558),	NT2RP1001185(243500),	NT2RP1001482(600586),
30	NT2RP1001665(114180),	NT2RP2000070(600976),	NT2RP2000147(603535),
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	THYRO1000748(300023),	THYRO1000934(179035),	THYRO1001120(602582),
	THYRO1001189(603971),	THYRO 1001204(603169),	
10	THYRO1001458(160776),	THYRO1001617(602744),	THYRO1001671(603281),
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15	Y79AA1001874(600315),	Y79AA1002204(605033),	Y79AA1002210(191161),
	Y79AA1002472(603971),	Y79AA1002482(603971),	

The following 425 clones presumably belong to enzymes and/or metabolism-associated proteins.

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	HEMBA1002973,	HEMBA1003046,	HEMBA1003136,	HEMBA1003179,	HEMBA1003250,
25	HEMBA1003291,	HEMBA1003408,	HEMBA1003538,	HEMBA1003679,	HEMBA1003680,
	HEMBA1004199,	HEMBA1004227,	HEMBA1004408,	HEMBA1004509,	HEMBA1004734,
	HEMBA1004768,	HEMBA1005394,	HEMBA1005513,	HEMBA1005737,	HEMBA1005815,
	HEMBA1006031,	HEMBA1006272,	HEMBA1006278,	HEMBA1006291,	HEMBA1006309,
30	HEMBA1006347,	HEMBA1006485,	HEMBA1006521,	HEMBA1006624,	HEMBA1006885,
	HEMBA1006976,	HEMBA1007121,	HEMBA1007224,	HEMBA1007243,	HEMBA1007300,
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	HEMBB1001346,	HEMBB1001429,	HEMBB1001443,	HEMBB1001915,	HEMBB1001950,
35	HEMBB1002042,	MAMMA1000020,	MAMMA1000085,	MAMMA1000672,	MAMMA1000713,
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45	NT2RM2000504,	NT2RM2000577,	NT2RM2000594,	NT2RM2000951,	NT2RM2001238,
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35	OVARC1000915,	OVARC1001107,	OVARC1001713,	OVARC1001762,	OVARC1001809,
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 10 Y79AA1001827, Y79AA1002027, Y79AA1002209, Y79AA1002211, Y79AA1002361,
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The following 217 clones presumably belong to a group of cDNAs encoding ATP- and/or GTP-binding proteins.

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 10 THYRO1000072, THYRO1001458, Y79AA1000833, Y79AA1000962, Y79AA1001394,
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The following 320 clones presumably belong to nuclear proteins.

HEMBA1000005, HEMBA1000158, HEMBA1000216, HEMBA1000561, HEMBA1000591,
 15 HEMBA1001088, HEMBA1001137, HEMBA1001405, HEMBA1001510, HEMBA1001579,
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 20 HEMBA1003684, HEMBA1003690, HEMBA1003760, HEMBA1004203, HEMBA1004321,
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 25 HEMBB1001056, HEMBB1001242, HEMBB1001482, HEMBB1001915, HEMBB1002134,
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 MAMMA1002869, MAMMA1002937, MAMMA1003011, NT2RM1000086, NT2RM1000187,
 30 NT2RM1000666, NT2RM1000885, NT2RM1000894, NT2RM1001059, NT2RM1001092,
 NT2RM2000013, NT2RM2000588, NT2RM2000624, NT2RM2000735, NT2RM2000740,
 NT2RM2001105, NT2RM2001635, NT2RM2001670, NT2RM2001771, NT2RM2001823,
 NT2RM2001936, NT2RM2001989, NT2RM2002004, NT2RM2002088, NT2RM2002091,
 35 NT2RM4000024, NT2RM4000046, NT2RM4000104, NT2RM4000202, NT2RM4000215,
 NT2RM4000290, NT2RM4000531, NT2RM4000751, NT2RM4000996, NT2RM4001092,
 NT2RM4001140, NT2RM4001200, NT2RM4001483, NT2RM4001566, NT2RM4001592,
 NT2RM4001597, NT2RM4001783, NT2RM4001823, NT2RM4001828, NT2RM4001858,
 40 NT2RM4001979, NT2RP1000035, NT2RP1000111, NT2RP1000493, NT2RP1000574,
 NT2RP1000630, NT2RP1000902, NT2RP1000915, NT2RP1000958, NT2RP1000966,
 NT2RP1001013, NT2RP1001177, NT2RP2000008, NT2RP2000076, NT2RP2000126,
 NT2RP2000153, NT2RP2000161, NT2RP2000248, NT2RP2000258, NT2RP2000297,
 45 NT2RP2000420, NT2RP2000931, NT2RP2001233, NT2RP2001420, NT2RP2001756,
 NT2RP2001869, NT2RP2002079, NT2RP2002270, NT2RP2002503, NT2RP2002591,
 NT2RP2002880, NT2RP2002939, NT2RP2002993, NT2RP2003137, NT2RP2003157,
 NT2RP2003277, NT2RP2003286, NT2RP2003308, NT2RP2003347, NT2RP2003714,
 50 NT2RP2003912, NT2RP2004013, NT2RP2004187, NT2RP2004689, NT2RP2004920,
 NT2RP2005393, NT2RP2005436, NT2RP2005496, NT2RP2005539, NT2RP2005701,
 NT2RP2005767, NT2RP2005776, NT2RP2005933, NT2RP2005942, NT2RP2006043,
 NT2RP2006436, NT2RP3000031, NT2RP3000050, NT2RP3000397, NT2RP3000512,
 55 NT2RP3000527, NT2RP3000590, NT2RP3000603, NT2RP3000632, NT2RP3000917,
 NT2RP3001057, NT2RP3001107, NT2RP3001120, NT2RP3001253, NT2RP3001338,
 NT2RP3001384, NT2RP3001398, NT2RP3001427, NT2RP3001428,

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	NT2RP3001472,	NT2RP3001646,	NT2RP3001671,	NT2RP3001792,	NT2RP3001855,
	NT2RP3002056,	NT2RP3002165,	NT2RP3002399,	NT2RP3002876,	NT2RP3003193,
	NT2RP3003212,	NT2RP3003555,	NT2RP3004016,	NT2RP3004206,	NT2RP3004424,
5	NT2RP3004428,	NT2RP3004566,	NT2RP3004617,	NT2RP4000078,	NT2RP4000111,
	NT2RP4000210,	NT2RP4000398,	NT2RP4000481,	NT2RP4000518,	NT2RP4000997,
	NT2RP4001148,	NT2RP4001206,	NT2RP4001213,	NT2RP4001433,	NT2RP4001568,
	NT2RP4001638,	NT2RP4001696,	NT2RP4001753,	NT2RP4001938,	NT2RP4002058,
10	NT2RP4002078,	NT2RP4002081,	NT2RP4002791,	OVARC1000006,	OVARC1000087,
	OVARC1000091,	OVARC1000241,	OVARC1000326,	OVARC1000556,	OVARC1000846,
	OVARC1001038,	OVARC1001180,	OVARC1001232,	OVARC1001271,	OVARC1001306,
	OVARC1001436,	OVARC1002112,	PLACE1000133,	PLACE1000184,	PLACE1000406,
15	PLACE1000583,	PLACE1000596,	PLACE1000979,	PLACE1001118,	PLACE1001383,
	PLACE1001632,	PLACE1002171,	PLACE1002433,	PLACE1002438,	PLACE1002532,
	PLACE1002775,	PLACE1002816,	PLACE1002834,	PLACE1003100,	PLACE1003190,
	PLACE1003302,	PLACE1003519,	PLACE1003521,	PLACE1003605,	PLACE1003704,
20	PLACE1003738,	PLACE1003885,	PLACE1003923,	PLACE1004302,	PLACE1004471,
	PLACE1004564,	PLACE1004814,	PLACE1004902,	PLACE1005287,	PLACE1005876,
	PLACE1005966,	PLACE1006167,	PLACE1006438,	PLACE1006482,	PLACE1006829,
	PLACE1006878,	PLACE1006917,	PLACE1007014,	PLACE1007547,	PLACE1007598,
25	PLACE1007688,	PLACE1007969,	PLACE1008044,	PLACE1008132,	PLACE1008603,
	PLACE1009099,	PLACE1009130,	PLACE1009308,	PLACE1009398,	PLACE1010134,
	PLACE1010194,	PLACE1010702,	PLACE1010720,	PLACE1010870,	PLACE1011056,
	PLACE1011433,	PLACE1011664,	PLACE2000014,	PLACE2000427,	PLACE3000009,
30	PLACE3000169,	PLACE4000014,	PLACE4000156,	PLACE4000192,	PLACE4000261,
	PLACE4000326,	PLACE4000489,	SKNMC1000011,	THYRO1000085,	THYRO1000242,
	THYRO1000585,	THYRO1001100,	THYRO1001189,	THYRO1001809,	Y79AA1000037,
	Y79AA1000214,	Y79AA1000231,	Y79AA1000589,	Y79AA1000752,	Y79AA1001391,
35	Y79AA1001613,	Y79AA1001705,	Y79AA1001963,	Y79AA1002431,	Y79AA1002472,
	Y79AA1002482				

The following 292 clones presumably belong to DNA- and/or RNA-binding proteins.

	HEMBA1000158,	HEMBA1000216,	HEMBA1000561,	HEMBA1000591,	HEMBA1000851,
40	HEMBA1001088,	HEMBA1001137,	HEMBA1001405,	HEMBA1001510,	HEMBA1001804,
	HEMBA1001809,	HEMBA1001819,	HEMBA1001847,	HEMBA1001869,	HEMBA1002177,
	HEMBA1002935,	HEMBA1003408,	HEMBA1003545,	HEMBA1003568,	HEMBA1003591,
	HEMBA1003662,	HEMBA1003684,	HEMBA1003760,	HEMBA1003783,	HEMBA1003805,
45	HEMBA1003953,	HEMBA1004321,	HEMBA1004354,	HEMBA1004389,	HEMBA1004479,
	HEMBA1004669,	HEMBA1004847,	HEMBA1004973,	HEMBA1005202,	HEMBA1005359,
	HEMBA1005931,	HEMBA1006248,	HEMBA1006278,	HEMBA1006283,	HEMBA1006359,
	HEMBA1006652,	HEMBA1007087,	HEMBA1007194,	HEMBA1007264,	HEMBA100789,
50	HEMBA1001011,	HEMBA1001482,	HEMBA1001736,	HEMBA1001749,	HEMBA1001839,
	HEMBA1002217,	MAMMA1000183,	MAMMA1000284,	MAMMA1000731,	MAMMA1001105,
	MAMMA1001222,	MAMMA1001260,	MAMMA1001743,	MAMMA1001837,	MAMMA1002385,
	MAMMA1002617,	MAMMA1002869,	MAMMA1002937,	MAMMA1003011,	NT2RM1000086,
55	NT2RM1000539,	NT2RM1000555,	NT2RM1000666,	NT2RM1000691,	NT2RM1000826,
	NT2RM1000885,	NT2RM1001059,	NT2RM1001092,	NT2RM2000371,	NT2RM2000624,
	NT2RM2000735,	NT2RM2001105,	NT2RM2001424,	NT2RM2001575,	NT2RM2001605,

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NT2RM2001670, NT2RM2001771, NT2RM2001823, NT2RM2001989, NT2RM2002004,
 NT2RM2002014, NT2RM2002088, NT2RM2002091, NT2RM4000046, NT2RM4000104,
 NT2RM4000167, NT2RM4000191, NT2RM4000202, NT2RM4000531, NT2RM4000595,
 5 NT2RM4000733, NT2RM4000751, NT2RM4000996, NT2RM4001092, NT2RM4001140,
 NT2RM4001178, NT2RM4001200, NT2RM4001483, NT2RM4001592, NT2RM4001783,
 NT2RM4001823, NT2RM4001828, NT2RM4001858, NT2RM4001880, NT2RM4001979,
 NT2RM4002093, NT2RM4002109, NT2RP1000470, NT2RP1000493, NT2RP1000574,
 10 NT2RP1000902, NT2RP1000966, NT2RP1001013, NT2RP1001073, NT2RP1001080,
 NT2RP2000008, NT2RP2000153, NT2RP2000258, NT2RP2000297, NT2RP2001127,
 NT2RP2001174, NT2RP2001233, NT2RP2001511, NT2RP2001756, NT2RP2001869,
 NT2RP2002079, NT2RP2002099, NT2RP2002503, NT2RP2002591, NT2RP2002939,
 15 NT2RP2003157, NT2RP2003329, NT2RP2003347, NT2RP2003480, NT2RP2003522,
 NT2RP2003564, NT2RP2003714, NT2RP2004187, NT2RP2004568, NT2RP2004920,
 NT2RP2005003, NT2RP2005139, NT2RP2005168, NT2RP2005436, NT2RP2005496,
 NT2RP2005701, NT2RP2005763, NT2RP2005776, NT2RP2005942, NT2RP2006043,
 20 NT2RP2006436, NT2RP2006464, NT2RP3000050, NT2RP3000512, NT2RP3000527,
 NT2RP3000562, NT2RP3000590, NT2RP3000603, NT2RP3000624, NT2RP3000632,
 NT2RP3000994, NT2RP3001057, NT2RP3001107, NT2RP3001120, NT2RP3001150,
 NT2RP3001155, NT2RP3001338, NT2RP3001398, NT2RP3001472, NT2RP3001672,
 25 NT2RP3001688, NT2RP3001724, NT2RP3001792, NT2RP3001855, NT2RP3002165,
 NT2RP3002399, NT2RP3002876, NT2RP3003138, NT2RP3003193, NT2RP3003251,
 NT2RP3003327, NT2RP3003555, NT2RP3004013, NT2RP3004078, NT2RP3004428,
 NT2RP3004490, NT2RP3004566, NT2RP3004594, NT2RP3004617, NT2RP3004618,
 30 NT2RP4000111, NT2RP4000398, NT2RP4000455, NT2RP4000518, NT2RP4000648,
 NT2RP4000865, NT2RP4000929, NT2RP4001080, NT2RP4001095, NT2RP4001213,
 NT2RP4001433, NT2RP4001568, NT2RP4001696, NT2RP4001753, NT2RP4001838,
 NT2RP4001938, NT2RP4002078, OVARC1000006, OVARC1000087, OVARC1000241,
 35 OVARC1000746, OVARC1000846, OVARC1001232, OVARC1001271, OVARC1001306,
 OVARC1001987, OVARC1002112, PLACE1000406, PLACE1000583, PLACE1000979,
 PLACE1001118, PLACE1001632, PLACE1001739, PLACE1002438, PLACE1002532,
 PLACE1002775, PLACE1002834, PLACE1003302, PLACE1003519, PLACE1003605,
 40 PLACE1003704, PLACE1003738, PLACE1003885, PLACE1004471, PLACE1004564,
 PLACE1004814, PLACE1005584, PLACE1005876, PLACE1005951, PLACE1006196,
 PLACE1006482, PLACE1006488, PLACE1006531, PLACE1006917, PLACE1007346,
 PLACE1007547, PLACE1007598, PLACE1007688, PLACE1007969, PLACE1008132,
 45 PLACE1009099, PLACE1009246, PLACE1009398, PLACE1009476, PLACE1009622,
 PLACE1010053, PLACE1010194, PLACE1010702, PLACE1010870, PLACE1011056,
 PLACE1011114, PLACE1011433, PLACE2000427, PLACE3000009, PLACE3000169,
 PLACE4000014, PLACE4000156, PLACE4000192, PLACE4000261, PLACE4000489,
 50 SKNMC1000091, THYRO1000085, THYRO1000242, THYRO1000501, THYRO1001100,
 THYRO1001189, THYRO1001809, Y79AA1000037, Y79AA1000349, Y79AA1000752,
 Y79AA1001211, Y79AA1001312, Y79AA1001391, Y79AA1001613, Y79AA1002103,
 Y79AA1002472, Y79AA1002482,

55 The following 66 clones presumably belong to the category of RNA synthesis-associated proteins.

HEMBA1000591, HEMBA1001579, HEMBA1003179, HEMBA1003591, HEMBA1006278,

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HEMBB1000226, NT2RM1000187, NT2RM1000852, NT2RM2000624, NT2RM2001989,
 NT2RM2002100, NT2RM4000191, NT2RM4001178, NT2RM4002093, NT2RP1000035,
 NT2RP1000272, NT2RP1000470, NT2RP1001080, NT2RP2000153, NT2RP2002928,
 5 NT2RP2003157, NT2RP2004568, NT2RP2005126, NT2RP2005436, NT2RP2005539,
 NT2RP2005605, NT2RP2005776, NT2RP2005942, NT2RP2006043, NT2RP2006238,
 NT2RP3000361, NT2RP3000397, NT2RP3001671, NT2RP3004504, NT2RP4000078,
 NT2RP4000111, NT2RP4000481, NT2RP4000518, NT2RP4000614, NT2RP4000929,
 10 NT2RP4001696, NT2RP4002058, OVARC1001232, OVARC1001577, PLACE1000406,
 PLACE1000596, PLACE1000755, PLACE1001739, PLACE1003704,
 PLACE1003885, PLACE1004564, PLACE1004814, PLACE1004902, PLACE1005373,
 PLACE1005646, PLACE1005876, PLACE1006196, PLACE1006626, PLACE1006878,
 15 PLACE1006917, PLACE1009476, PLACE1009925, PLACE1010194, PLACE1011114,
 THYRO1000121, Y79AA1001963,

The following 183 clones presumably belong to protein synthesis-associated and/or protein transport-associated proteins.

20 HEMBA1000012, HEMBA1000141, HEMBA1000592, HEMBA1003617, HEMBA1003773,
 HEMBA1004202, HEMBA1004276, HEMBA1004734, HEMBA1004847, HEMBA1004929,
 HEMBA1004930, HEMBA1005047, HEMBA1005202, HEMBA1006031, HEMBA1006272,
 HEMBA1006474, HEMBA1006652, HEMBA1006914, HEMBA1006973, HEMBA1007224,
 25 HEMBB1000915, HEMBB1001112, HEMBB1001137, HEMBB1001736, HEMBB1001831,
 HEMBB1001915, MAMMA1000085, MAMMA1000734, MAMMA1001008, MAMMA1002170,
 MAMMA1002219, MAMMA1002236, MAMMA1002619, NT2RM1000661, NT2RM1000833,
 NT2RM2000092, NT2RM2000504, NT2RM2000577, NT2RM2000821, NT2RM2001201,
 30 NT2RM2001592, NT2RM2001613, NT2RM2001648, NT2RM2001730, NT2RM2001760,
 NT2RM2002055, NT2RM4000155, NT2RM4000169, NT2RM4000344, NT2RM4000356,
 NT2RM4000421, NT2RM4000712, NT2RM4001054, NT2RM4001203, NT2RM4001382,
 NT2RM4001444, NT2RM4002062, NT2RM4002205, NT2RM4002623, NT2RP1000326,
 35 NT2RP1000522, NT2RP1000547, NT2RP1000746, NT2RP1000947, NT2RP1001569,
 NT2RP2000147, NT2RP2000710, NT2RP2000880, NT2RP2000943, NT2RP2001290,
 NT2RP2001392, NT2RP2001601, NT2RP2001613, NT2RP2001660, NT2RP2001740,
 NT2RP2002124, NT2RP2002606, NT2RP2002862, NT2RP2002959, NT2RP2002980,
 40 NT2RP2003137, NT2RP2003158, NT2RP2003391, NT2RP2003394, NT2RP2003401,
 NT2RP2003433, NT2RP2003704, NT2RP2003713, NT2RP2003737, NT2RP2003760,
 NT2RP2003981, NT2RP2004366, NT2RP2004389, NT2RP2004791, NT2RP2005012,
 NT2RP2005116, NT2RP2005360, NT2RP2005763, NT2RP2005784, NT2RP3000366,
 45 NT2RP3000759, NT2RP3000968, NT2RP3001113, NT2RP3001690, NT2RP3002045,
 NT2RP3002151, NT2RP3002529, NT2RP3002671, NT2RP3003301, NT2RP3003846,
 NT2RP3003876, NT2RP3004209, NT2RP4000370, NT2RP4000457, NT2RP4000879,
 NT2RP4000927, NT2RP4001041, NT2RP4001117, NT2RP4001313, NT2RP4001315,
 50 NT2RP4001574, NT2RP4001592, OVARC1000013, OVARC1000071, OVARC1000085,
 OVARC1000465, OVARC1000564, OVARC1000771, OVARC1000862, OVARC1001171,
 OVARC1001180, OVARC1001342, PLACE1000007, PLACE1000061, PLACE1000081,
 PLACE1000492, PLACE1000863, PLACE1001092, PLACE1001748, PLACE1002090,
 55 PLACE1003174, PLACE1003915, PLACE1004104, PLACE1004270, PLACE1004743,
 PLACE1005557, PLACE1005813, PLACE1006170, PLACE1006488, PLACE1006829,
 PLACE1007706, PLACE1007729, PLACE1008273, PLACE1008402, PLACE1008790,

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PLACE1008813, PLACE1009094, PLACE1009130, PLACE1009477, PLACE1009721,
 PLACE1009845, PLACE1010074, PLACE1010547, PLACE1011109, PLACE1011229,
 PLACE1011477, PLACE1012031, PLACE2000404, PLACE3000059, PLACE3000121,
 5 PLACE4000269, PLACE4000654, SKNMC1000011, THYRO1000983, THYRO1001003,
 THYRO1001313, Y79AA1000560, Y79AA1000784, Y79AA1000968, Y79AA1001493,
 Y79AA1001875, Y79AA1002027, Y79AA1002209,

The following 130 clones presumably belong to cytoskeletal-associated proteins.

10 HEMBA1000156, HEMBA1000168, HEMBA1000411, HEMBA1000588, HEMBA1001043,
 HEMBA1001651, HEMBA1001661, HEMBA1002102, HEMBA1002161, HEMBA1002939,
 HEMBA1003235, HEMBA1003581, HEMBA1004499, HEMBA1004534, HEMBA1004697,
 HEMBA1004929, HEMBA1004972, HEMBA1005582, HEMBA1005595, HEMBA1006344,
 15 HEMBA1006737, HEMBB1001175, HEMBB1001282, HEMBB1001562,
 HEMBB1001802, MAMMA1000824, MAMMA1001041, MAMMA1001576, MAMMA1001679,
 MAMMA1001735, MAMMA1002297, MAMMA1002351, MAMMA1002622, MAMMA1002637,
 MAMMA1003127, NT2RM1000850, NT2RM1000898, NT2RM2000030, NT2RM2000260,
 20 NT2RM2000691, NT2RM2001324, NT2RM4000169, NT2RM4000229, NT2RM4000515,
 NT2RM4001217, NT2RP1000202, NT2RP1000348, NT2RP1000460, NT2RP1000478,
 NT2RP1001033, NT2RP1001294, NT2RP1001302, NT2RP2000070, NT2RP2000812,
 NT2RP2000814, NT2RP2001168, NT2RP2001245, NT2RP2001634, NT2RP2001900,
 25 NT2RP2003307, NT2RP2003394, NT2RP2004041, NT2RP2004242, NT2RP2004538,
 NT2RP2004587, NT2RP2004681, NT2RP2004732, NT2RP2004978, NT2RP2005491,
 NT2RP2005531, NT2RP2005712, NT2RP2006275, NT2RP3000753, NT2RP3001113,
 NT2RP3001216, NT2RP3001239, NT2RP3001272, NT2RP3001554, NT2RP3001690,
 30 NT2RP3001799, NT2RP3002688, NT2RP3003061, NT2RP3003185, NT2RP3003230,
 NT2RP3004569, NT2RP3004578, NT2RP4001004, NT2RP4001086, NT2RP4001256,
 NT2RP4001567, NT2RP4001927, OVARC1000001, OVARC1000106, OVARC1000437,
 OVARC1000520, OVARC1000679, OVARC1001731, OVARC1002050, PLACE1001104,
 35 PLACE1002571,
 PLACE1002591, PLACE1002655, PLACE1002714, PLACE1003625, PLACE1005287,
 PLACE1006552, PLACE1007946, PLACE1008426, PLACE1010148, PLACE1010547,
 PLACE1010743, PLACE1010896, PLACE1010960, PLACE1011310, PLACE1011922,
 40 PLACE2000216, PLACE2000274, PLACE2000371, PLACE2000458, PLACE3000145,
 PLACE3000416, PLACE4000009, THYRO1000132, THYRO1001405, THYRO1001458,
 Y79AA1000368, Y79AA1000794, Y79AA1000833, Y79AA1000962, Y79AA1002208,

The following 54 clones presumably belong to cell division-associated and/or cell proliferation-associated proteins.

45 HEMBA1001019, HEMBA1001595, HEMBA1002363, HEMBA1002997, HEMBA1003136,
 HEMBA1003369, HEMBA1004131, HEMBA1004354, HEMBA1005621, HEMBB1000037,
 HEMBB1000264, MAMMA1001768, MAMMA1002769, NT2RM1000354, NT2RM1000430,
 50 NT2RM1000874, NT2RM2001256, NT2RM2001743, NT2RM2001896, NT2RM2002145,
 NT2RM4000215, NT2RM4001714, NT2RP1000163, NT2RP1000333, NT2RP1000439,
 NT2RP2000346, NT2RP2001397, NT2RP2002595, NT2RP2003177, NT2RP2003596,
 NT2RP2003912, NT2RP2004396, NT2RP2005037, NT2RP2005520, NT2RP2005669,
 55 NT2RP2005835, NT2RP3001730, NT2RP3002081, NT2RP4000210, NT2RP4000415,
 NT2RP4001414, NT2RP4001634, OVARC1000013, OVARC1000937, PLACE1001383,

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PLACE1002433, PLACE1004316, PLACE1005287, PLACE1008808, PLACE1010720,
PLACE1010833, Y79AA1000748, Y79AA1001236, Y79AA1001394,

5 The following 36 clones presumably belong to the category of embryogenesis- and/or development-associated proteins.

HEMBA1000518, HEMBA1001847, HEMBA1001869, HEMBA1003545, HEMBA1004973,
HEMBA1002442, MAMMA1001837, NT2RM2001670, NT2RM4000046, NT2RM4000531,
NT2RM4001140, NT2RM4001858, NT2RP2002078, NT2RP2004187, NT2RP2006436,
10 NT2RP3000603, NT2RP3000994, NT2RP3001580, NT2RP3001708, NT2RP3003071,
NT2RP3004472, NT2RP3004617, NT2RP4000246, NT2RP4001567, OVARC1000304,
OVARC1000746, PLACE1000793, PLACE1002532, PLACE1003258, PLACE1003625,
PLACE1004460, PLACE1009622, PLACE4000558, THYRO1000085, Y79AA1001391,
15 Y79AA1001692,

The following 30 clones presumably belong to cellular defense-associated proteins.

HEMBA1000005, HEMBA1000531, HEMBA1003417, HEMBA1006253, NT2RM4000354,
NT2RM4001880, NT2RP1000333, NT2RP1000493, NT2RP2000006, NT2RP2000045,
20 NT2RP2000809, NT2RP2001536, NT2RP2002464, NT2RP2004920,
NT2RP2005037, NT2RP3000590, NT2RP3001426, NT2RP3002062, NT2RP3002785,
NT2RP3004262, NT2RP4001555, NT2RP4001638, PLACE1006958, PLACE1008275,
PLACE1009113, PLACE1011858, PLACE4000014, THYRO1000684, Y79AA1002139,
25 Y79AA1002229,

Although it is unclear whether or not 261 clones out of clones other than the above-mentioned clones belong to any of the above-described categories, these clones are predicted to have some functions, based on the homology search using the full-length sequences thereof. The clone names and the gene definitions found in the result of homology search are shown below, separated with a double-slash mark, //.

35 HEMBA1000030//Homo sapiens ARF GTPase-activating protein GIT1 mRNA, complete cds.

HEMBA1000307//CARNITINE DEFICIENCY-ASSOCIATED PROTEIN EXPRESSED IN VENTRICLE 1

40

HEMBA1000333//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.

45 HEMBA1000488//RING CANAL PROTEIN (KELCH PROTEIN).

HEMBA1000523//TESTIS-SPECIFIC PROTEIN PBS13.

50 HEMBA1001197//Homo sapiens rap2 interacting protein x mRNA, complete cds.

HEMBA1001302//Homo sapiens calcium binding protein precursor, mRNA, complete cds.

55 HEMBA1001455//Mus musculus transposon-derived Buster2 transposase-like protein gene, partial cds.

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- HEMBA1001675//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS9.
- 5 HEMBA1001714//Homo sapiens mRNA for ATPase inhibitor precursor, complete cds.
- HEMBA1001744//SCY1 PROTEIN.
- 10 HEMBA1001967//Homo sapiens NY-REN-57 antigen mRNA, partial cds.
- HEMBA1002151//Rattus norvegicus p34 mRNA, complete cds.
- 15 HEMBA1002215//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].
- HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74.
- 20 HEMBA1002777//Fugu rubripes BAW (BAW) mRNA, complete cds.
- HEMBA1003098//Homo sapiens NY-REN-6 antigen mRNA, partial cds.
- 25 HEMBA1003199//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.
- HEMBA1003615//Homo sapiens ART-4 mRNA, complete cds.
- 30 HEMBA1003836//MOB1 PROTEIN (MPS1 BINDER 1).
- HEMBA1004295//Homo sapiens NY-REN-25 antigen mRNA, partial cds.
- 35 HEMBA1004573//Homo sapiens mRNA for HELG protein.
- HEMBA1004604//Homo sapiens COP9 complex subunit 7a mRNA, complete cds.
- 40 HEMBA1004795//CDC4-LIKE PROTEIN (FRAGMENT).
- HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.
- 45 HEMBA1005201//Homo sapiens CGI-07 protein mRNA, complete cds.
- HEMBA1005206//Drosophila simulans anon73B1 gene and Su(P) gene.
- 50 HEMBA1005530//Homo sapiens anaphase-promoting complex subunit 7 (APC7) mRNA, complete cds.
- 55 HEMBA1005666//Homo sapiens mRNA for DIPB protein.
- HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.

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- HEMBA1006268//Homo sapiens HQOO24c mRNA, complete cds.
- 5 HEMBA1006398//Human L1 element L1.6 putative p150 gene, complete cds.
- HEMBA1006445//Homo sapiens putative tumor supressor NOEY2 mRNA, complete cds.
- 10 HEMBA1007174//Homo sapiens epsin 2b mRNA, complete cds.
- HEMBA1007251//Homo sapiens F-box protein FBX29 (FBX29) mRNA, partial cds.
- 15 HEMBB1000036//Homo sapiens CGI-51 protein mRNA, complete cds.
- HEMBB1000144//GUANYLATE CYCLASE ACTIVATING PROTEIN 2 (GCAP 2) (RETINAL
GUANYLYL CYCLASE ACTIVATOR PROTEIN P24).
- 20 HEMBB1000973//Mus musculus schlafen3 (Sfn3) mRNA, complete cds.
- HEMBB1001058//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds
- 25 HEMBB1001234//65 KD YES-ASSOCIATED PROTEIN (YAP65).
- HEMBB1001288//COPPER HOMEOSTASIS PROTEIN CUTC.
- 30 HEMBB1001331//Mus musculus mRNA for hepatoma-derived growth factor, complete cds,
strain:BALB/c.
- 35 HEMBB1001384//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.
- HEMBB1002266//NEURONAL PROTEIN.
- 40 HEMBB1002510//GYP7 PROTEIN.
- HEMBB1002705//Homo sapiens CGI-27 protein mRNA, complete cds.
- 45 MAMMA1000055//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TEST)].
- MAMMA1000625//GYP7 PROTEIN.
- 50 MAMMA1001075//Homo sapiens CGI-72 protein mRNA, complete cds.
- MAMMA1001181//ABC1 PROTEIN HOMOLOG PRECURSOR.
- 55 MAMMA1001259//Mus musculus F-box protein FBX18 mRNA, partial cds.
- MAMMA1001730//Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein

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NSG-x mRNA, partial cds.

MAMMA1002143//Homo sapiens Cdc42 effector protein 4 mRNA, complete cds.

5

MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.

MAMMA1002972//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS27.

10

MAMMA1003113//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.

NT2RM1000118//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).

15

NT2RM1000186//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).

20

NT2RM1000244//Homo sapiens TRAF4 associated factor 1 mRNA, partial cds.

NT2RM1000421//RIBONUCLEASE INHIBITOR.

25

NT2RM1000499//Caenorhabditis elegans mRNA for centaurin gamma 1A.

NT2RM1000623//RIBONUCLEASE INHIBITOR.

30

NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.

NT2RM2000502//Rattus norvegicus W3O7 mRNA, complete cds.

35

NT2RM2000599//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds.

NT2RM2000718//Homo sapiens endocrine regulator mRNA, complete cds.

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NT2RM2001065//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.

NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).

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NT2RM2001983//Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds.

NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.

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NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12.

NT2RM4000030//LAS1 PROTEIN.

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NT2RM4000139//R.norvegicus trg mRNA.

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- NT2RM4000156//H. sapiens HPBRIL-7 gene.
- 5 NT2RM4000386//Mus musculus ODZ3 (Odz3) mRNA, partial cds.
- NT2RM4000590//RING CANAL PROTEIN (KELCH PROTEIN).
- 10 NT2RM4001047//MO25 PROTEIN.
- NT2RM4001155//ADRENAL MEDULLA 50 KD PROTEIN.
- 15 NT2RM4001256//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.
- NT2RM4001320//Homo sapiens mRNA for Neuroblastoma, complete cds.
- 20 NT2RM4001340//UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4 PROTEIN).
- NT2RM4001347//Homo sapiens NY-REN-25 antigen mRNA, partial cds.
- 25 NT2RM4001371//Homo sapiens IDN3 mRNA, partial cds.
- NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.
- 30 NT2RM4001611//SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3).
- NT2RM4001731//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds.
- 35 NT2RM4001969//R.norvegicus mRNA for IP63 protein.
- NT2RM4002034//Homo sapiens hiwi mRNA, partial cds.
- 40 NT2RM4002075//RING CANAL PROTEIN (KELCH PROTEIN).
- NT2RM4002226//GTPASE ACTIVATING PROTEIN ROTUND.
- 45 NT2RP1000040//Mus musculus donson protein (Donson) mRNA, partial cds.
- NT2RP1000363//R.norvegicus LL5 mRNA.
- 50 NT2RP1000481//Homo sapiens antigen NY-CO-3 (NY-CO-3) mRNA, partial cds.
- NT2RP1000513//Human NifU-like protein (hNifU) mRNA, partial cds.
- 55 NT2RP1000733//Human mRNA for GSPT1-TK protein,complete cds.
- NT2RP1000860//Homo sapiens KLO4P mRNA, complete cds.

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NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).

5 NT2RP1001011//Drosophila melanogaster putative 43 kDa protein (TH1) mRNA, complete cds.

NT2RP1001395//Homo sapiens COP9 complex subunit 7a mRNA, complete cds.

10

NT2RP1001457//Homo sapiens partial mRNA for beta-transducin family protein (putative).

NT2RP1001494//MALE STERILITY PROTEIN 2.

15

NT2RP2000054//Homo sapiens putative ring zinc finger protein NY-REN-43 antigen mRNA, complete cds.

20

NT2RP2000067//Mus musculus ODZ3 (Odz3) mRNA, partial cds.

NT2RP2000133//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.

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NT2RP2000157//MLO2 PROTEIN.

NT2RP2000764//NIFS PROTEIN.

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NT2RP2000965//Homo sapiens mRNA for fls353, complete cds.

NT2RP2001839//SCY1 PROTEIN.

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NT2RP2001883//Homo sapiens CGI-01 protein mRNA, complete cds.

NT2RP2001976//Mus musculus calmodulin-binding protein SHA1 (Sha1) mRNA, complete cds.

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NT2RP2001985//Homo sapiens high-risk human papilloma viruses E6 oncoproteins targeted protein E6TP1 alpha mRNA, complete cds.

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NT2RP2002185//Homo sapiens ubiquilin mRNA, complete cds.

NT2RP2002442//HESA PROTEIN.

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NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds.

NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds.

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NT2RP2002986//Homo sapiens mRNA for Kelch motif containing protein, complete cds.

NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.

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- NT2RP2003265//Homo sapiens CGI-53 protein mRNA, complete cds.
- 5 NT2RP2003272//Homo sapiens ubiquilin mRNA, complete cds.
- NT2RP2003857//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN).
- 10 NT2RP2003871//Homo sapiens transposon-derived Buster1 transposase-like protein gene, complete cds.
- 15 NT2RP2004425//Mus musculus axotrophin mRNA, complete cds.
- NT2RP2004476//Homo sapiens cyclin L ania-6a mRNA, complete cds.
- 20 NT2RP2004710//Mus musculus formin binding protein 30 mRNA, complete cds.
- NT2RP2004816//H58 PROTEIN.
- 25 NT2RP2005441//Homo sapiens hypothalamus protein HT002 mRNA, complete cds.
- NT2RP2005490//Mus musculus D3Mm3e (D3Mm3e) mRNA, complete cds.
- 30 NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.
- NT2RP2005654//CYSTEINE STRING PROTEIN (CCCS1).
- 35 NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.
- NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.
- 40 NT2RP2005841//Homo sapiens mRNA for ALEX3, complete cds.
- NT2RP2006598//Homo sapiens retinoid x receptor interacting protein mRNA, complete cds.
- 45 NT2RP3000047//NPL4 PROTEIN.
- NT2RP3000233//RING CANAL PROTEIN (KELCH PROTEIN).
- 50 NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.
- 55 NT2RP3000869//Drosophila melanogaster AAA family protein Bor (bor) mRNA, complete cds.
- NT2RP3001399//SSU72 PROTEIN.

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- NT2RP3001407//SCY1 PROTEIN.
- 5 NT2RP3001457//Drosophila melanogaster Melted (melt) mRNA, partial cds.
- NT2RP3001587//Human anthracycline-associated resistance ARX mRNA, complete cds.
- 10 NT2RP3001712//Homo sapiens HP1-BP74 protein mRNA, complete cds.
- NT2RP3001819//RING CANAL PROTEIN (KELCH PROTEIN).
- 15 NT2RP3001854//Homo sapiens novel retinal pigment epithelial cell protein (NORPEG) mRNA, complete cds.
- NT2RP3001931//Rattus norvegicus clone C48 CDK5 activator-binding protein mRNA,
- 20 complete cds.
- NT2RP3002273//SCD6 PROTEIN.
- 25 NT2RP3002631//Homo sapiens Ran binding protein 11 mRNA, complete cds.
- NT2RP3002682//Homo sapiens CGI-145 protein mRNA, complete cds.
- 30 NT2RP3002770//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.
- NT2RP3002818//INSERTION ELEMENT IS2A HYPOTHETICAL 48.2 KD PROTEIN.
- 35 NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEIN).
- NT2RP3002972//Halocynthia roretzi mRNA for HrPET-1, complete cds.
- 40 NT2RP3003032//Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds.
- NT2RP3003290//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.
- 45 NT2RP3003411//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.
- NT2RP3003491//Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA,
- 50 complete cds.
- NT2RP3003500//SCY1 PROTEIN.
- 55 NT2RP3003726//Homo sapiens spermatogenesis associated PD1 mRNA, complete cds.
- NT2RP3004348//R. norvegicus mRNA for cytosolic resiniferatoxin-binding protein.

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- NT2RP3004507//MOB1 PROTEIN (MPS1 BINDER 1).
- 5 NT2RP4000129//Xenopus laevis F-box protein 28 (Fbx28) mRNA, partial cds.
- NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1).
- 10 NT2RP4000528//NPL4 PROTEIN.
- NT2RP4000737//Mus musculus F-box protein FBL10 mRNA, partial cds.
- 15 NT2RP4000979//Homo sapiens putative HIV-1 infection related protein mRNA, partial cds.
- NT2RP4001010//Rattus norvegicus PSD-95/SAP90-associated protein-4 mRNA, complete cds.
- 20 NT2RP4001207//Homo sapiens Ran binding protein 11 mRNA, complete cds.
- NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN).
- 25 NT2RP4001260//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.
- NT2RP4001339//Homo sapiens mRNA for AMMERC1 protein.
- 30 NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.
- 35 NT2RP4001474//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.
- NT2RP4001966//Mus musculus ODZ3 (Odz3) mRNA, partial cds.
- 40 NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN).
- OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds.
- 45 OVARC1000876//MOB1 PROTEIN (MPS1 BINDER 1).
- OVARC1001065//Homo sapiens CGI-12 protein mRNA, complete cds.
- 50 OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857O7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).
- OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds.
- 55 OVARC1001555//NGG1-INTERACTING FACTOR 3.

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OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B).

OVARG1001943//Mus musculus DEBT-91 mRNA, complete cds.

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PLACE1000004//Homo sapiens IDN3-B mRNA, complete cds.

PLACE1000066//SSU72 PROTEIN.

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PLACE1000610//MSN5 PROTEIN.

PLACE1000636//MALE STERILITY PROTEIN 2.

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PLACE1000769//Homo sapiens CGI-18 protein mRNA, complete cds.

PLACE1000987//Rattus norvegicus late gestation lung 2 protein (Lgl2) mRNA, complete cds.

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PLACE1001036//Homo sapiens mRNA for alpha integrin binding protein 63, partial.

PLACE1001845//Mus musculus cyclin ania-6a mRNA, complete cds.

25

PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.

PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.

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PLACE1003602//Homo sapiens mRNA expressed in placenta.

PLACE1003611//Homo sapiens anaphase-promoting complex subunit 4 (APC4) mRNA, complete cds.

35

PLACE1004256//Mus musculus short coiled coil protein SCOCO (Scoc) mRNA, complete cds.

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PLACE1004550//Homo sapiens CGI-20 protein mRNA, complete cds.

PLACE1004868//MALE STERILITY PROTEIN 2.

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PLACE1004930//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds

PLACE1005052//Homo sapiens CGI-16 protein mRNA, complete cds.

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PLACE1005102//RING CANAL PROTEIN (KELCH PROTEIN).

PLACE1005176//Homo sapiens hypothalamus protein HT001 mRNA, complete cds.

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PLACE1005187//APAG PROTEIN.

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PLACE1005331//Homo sapiens 7h3 protein mRNA, partial cds.

5 PLACE1005727//Homo sapiens STRIN protein (STRIN) mRNA, complete cds.

PLACE1006003//Homo sapiens CGI-94 protein mRNA, complete cds.

10 PLACE1006335//Homo sapiens NY-REN-50 antigen mRNA, partial cds.

PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds.

15 PLACE1006506//Homo sapiens anaphase-promoting complex subunit 4 (APC4) mRNA, complete cds.

PLACE1007105//Homo sapiens muskelin (MKLN1) mRNA, complete cds.

20 PLACE1007537//Homo sapiens ankyrin repeat-containing protein ASB-2 mRNA, complete cds.

PLACE1007705//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.

25 PLACE1007791//Homo sapiens IDN3-B mRNA, complete cds.

PLACE1007897//Homo sapiens FLASH mRNA, complete cds.

30 PLACE1008080//Homo sapiens mRNA for HEXIM1 protein, complete cds.

PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN).

35 PLACE1008398//GENE 33 POLYPEPTIDE.

PLACE1008465//Homo sapiens mRNA for rapa-1 (rapa gene).

40 PLACE1008627//Homo sapiens mRNA for cysteine-rich protein.

PLACE1009020//NIFS PROTEIN.

45 PLACE1009060//BRO1 PROTEIN.

PLACE1009186//Homo sapiens small zinc finger-like protein (TIM9b) mRNA, complete cds.

50 PLACE1009443//Mus musculus F-box protein FBL8 mRNA, complete cds.

PLACE1009571//Homo sapiens PTD002 mRNA, complete cds.

55 PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.

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PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN).

PLACE1010261//SEGREGATION DISTORTER PROTEIN.

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PLACE1010310//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).

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PLACE1010522//Homo sapiens mRNA for DEPP (decidual protein induced by progesterone), complete cds.

PLACE1010579//Homo sapiens CED-6 protein (CED-6) mRNA, complete cds.

15

PLACE1010628//Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds.

PLACE1010661//TESTIS-SPECIFIC PROTEIN PBS13.

20

PLACE1010761//Homo sapiens mRNA for cisplatin resistance-associated overexpressed protein, complete cds.

25

PLACE1011185//INSERTION ELEMENT IS1 PROTEIN INSB.

PLACE1011340//Homo sapiens IDN3-B mRNA, complete cds.

30

PLACE1011586//Rattus norvegicus clone C53 CDK5 activator-binding protein mRNA, complete cds.

PLACE2000246//RING CANAL PROTEIN (KELCH PROTEIN).

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PLACE2000411//Homo sapiens epsin 2b mRNA, complete cds.

PLACE3000477//Homo sapiens phosphoprotein pp75 mRNA, partial cds.

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THYRO1000173//Homo sapiens AP-mu chain family member mu1B (HSMU1B) mRNA, complete cds.

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THYRO1000401//Human TcD37 homolog (HTcD37) mRNA, partial cds.

THYRO1000666//Mus musculus mRNA for kinesin like protein 9.

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THYRO1001033//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521.

THYRO1001347//Homo sapiens RAN binding protein 16 mRNA, complete cds.

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THYRO1001656//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.

THYRO1001703//NIFR3-LIKE PROTEIN.

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THYRO1001721//RING CANAL PROTEIN (KELCH PROTEIN).

5 Y79AA1000059//Homo sapiens aryl-hydrocarbon interacting protein-like 1 (AIPL1) gene, complete cds.

Y79AA1000181//Homo sapiens CGI-01 protein mRNA, complete cds.

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Y79AA1000268//Mus musculus Nip2l mRNA, complete cds.

Y79AA1000313//CALPHOTIN.

15

Y79AA1000540//CELL POLARITY PROTEIN TEA1.

Y79AA1000966//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.

20

Y79AA1000985//Human centrosomal protein kendrin mRNA, complete cds.

Y79AA1001323//Mus musculus mRNA for GSG1, complete cds.

25

Y79AA1001402//Homo sapiens paraneoplastic cancer-testis-brain antigen (MA4) mRNA, partial cds.

30

Y79AA1001679//Homo sapiens lambda-crystallin mRNA, complete cds.

Y79AA1001923//Homo sapiens F-box protein Fbx22 (FBX22) gene, partial cds. Y79AA1002083//H. sapiens mRNA for MUF1 protein.

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Y79AA1002307//Homo sapiens astrotactin2 (ASTN2) mRNA, complete cds.

Y79AA1002311//R. norvegicus mRNA for cytosolic resiniferatoxin-binding protein.

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Y79AA1002487//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.

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Among the clones other than the above-mentioned, there were 36 clones that were similarly classified into the functional categories based on the results of functional domain search using the Pfam program. These clones were categorized as follows.

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Clones presumably belonging to the category of secretory or membrane proteins are two clones, MAMMA1002498 and NT2RM4002287; a clone presumably belonging to the category of glycoproteins-associated proteins is a clone MAMMA1002498; clones presumably belonging to the category of signal transduction-associated proteins are 11 clones, HEMBA1001247, NT2RM2001813, NT2RM4001454, NT2RP2005140, NT2RP2005293, NT2RP3000487, NT2RP3003311, PLACE1000972, PLACE1003723, PLACE1005327, and PLACE3000124; clones presumably belonging to the category of transcription-associated proteins are 12 clones,

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HEMBA1003257, NT2RM2000101, NT2RM2001797, NT2RP1000101, NT2RP2002208, NT2RP3001214, NT2RP3003278, NT2RP4001235, PLACE1000050, PLACE1001716, PLACE1002499, and PLACE1007544; clones presumably belonging to the category of enzymes and/or metabolism-associated proteins are 2 clones, HEMBA1005732 and MAMMA1000402; clones presumably belonging to the category of DNA- and/or RNA-binding proteins are 4 clones, HEMBA1004596, OVARC1000148, PLACE1003334, and THYRO1001661; a clone presumably belonging to the category of protein synthesis- and/or protein transport-associated proteins is a clone, HEMBA1006284.

So far, useful information for presuming the functions is unavailable for the remaining 2511 clones. Their functions will possibly be revealed by further analyses. Names of the clones are listed below.

So far, useful information for presuming the functions are unavailable for the remaining 2511 clones. Their functions will possibly be revealed by further analyses. Names of the clones are listed below.

HEMBA1000042,	HEMBA1000046,	HEMBA1000050,	HEMBA1000076,	HEMBA1000193,
HEMBA1000213,	HEMBA1000227,	HEMBA1000231,	HEMBA1000243,	HEMBA1000244,
HEMBA1000251,	HEMBA1000264,	HEMBA1000280,	HEMBA1000282,	HEMBA1000288,
HEMBA1000290,	HEMBA1000302,	HEMBA1000327,	HEMBA1000338,	HEMBA1000351,
HEMBA1000357,	HEMBA1000376,	HEMBA1000387,	HEMBA1000392,	HEMBA1000396,
HEMBA1000428,	HEMBA1000442,	HEMBA1000456,	HEMBA1000459,	HEMBA1000460,
HEMBA1000469,	HEMBA1000497,	HEMBA1000501,	HEMBA1000504,	HEMBA1000505,
HEMBA1000508,	HEMBA1000519,	HEMBA1000520,	HEMBA1000534,	HEMBA1000545,
HEMBA1000557,	HEMBA1000568,	HEMBA1000575,	HEMBA1000594,	HEMBA1000604,
HEMBA1000622,	HEMBA1000636,	HEMBA1000655,	HEMBA1000673,	HEMBA1000682,
HEMBA1000686,	HEMBA1000702,	HEMBA1000722,	HEMBA1000726,	HEMBA1000727,
HEMBA1000749,	HEMBA1000752,	HEMBA1000769,	HEMBA1000773,	HEMBA1000774,
HEMBA1000843,	HEMBA1000867,	HEMBA1000869,	HEMBA1000872,	HEMBA1000876,
HEMBA1000908,	HEMBA1000918,	HEMBA1000934,	HEMBA1000942,	HEMBA1000943,
HEMBA1000946,	HEMBA1000960,	HEMBA1000968,	HEMBA1000971,	HEMBA1000972,
HEMBA1000975,	HEMBA1000985,	HEMBA1000986,	HEMBA1001008,	HEMBA1001009,
HEMBA1001020,	HEMBA1001022,	HEMBA1001024,	HEMBA1001026,	HEMBA1001051,
HEMBA1001060,	HEMBA1001080,	HEMBA1001094,	HEMBA1001099,	HEMBA1001109,
HEMBA1001121,	HEMBA1001122,	HEMBA1001123,	HEMBA1001133,	HEMBA1001140,
HEMBA1001208,	HEMBA1001213,	HEMBA1001226,	HEMBA1001235,	
HEMBA1001281,	HEMBA1001299,	HEMBA1001303,	HEMBA1001310,	HEMBA1001319,
HEMBA1001323,	HEMBA1001326,	HEMBA1001327,	HEMBA1001330,	HEMBA1001361,
HEMBA1001375,	HEMBA1001377,	HEMBA1001383,	HEMBA1001388,	HEMBA1001391,
HEMBA1001398,	HEMBA1001411,	HEMBA1001413,	HEMBA1001415,	HEMBA1001432,
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	THYRO1000777,	THYRO1000787,	THYRO1000793,	THYRO1000796,	THYRO1000805,
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 MAMMA1002721, NT2RP2002070,

Homology Search Result Data 1.

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The result of the homology search of the SwissProt using the 5'-end sequence.
 Data include

25

the name of clone,

definition of the top hit data,

30

the P-value: the length of the compared sequence: identity (%), and

the organism and the Accession No. of the top hit data, as in the order separated by //.

35

Data are not shown for the clones in which the P-value was higher than 1.

40

The P-value is a score obtained statistically by taking into account the possible similarity
 between two sequences. In general, the smaller P-value reflects the higher similarity. (Altschul,
 S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J. (1990) "Basic local alignment
 search tool." J. Mol. Biol. 215:403-410; Gish, W. & States, D.J. (1993) "Identification of protein coding regions by database similarity search." Nature Genet. 3:
 266-272).

45

F-HEMBA1000005//DNAJ PROTEIN HOMOLOG MTJ1.//1.8e-85:244:75//MUS MUSCULUS
 (MOUSE).//Q61712

50

F-HEMBA1000012//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINETRNAS
 LIGASE) (LEURS).//7.6e-57:231:53//CAENORHABDITIS ELEGANS.//Q09996

55

F-HEMBA1000020//TUBULIN BETA CHAIN.//1.0e-92:143:80//AJELLOMYCES CAPSULATA
 (HISTOPLASMA CAPSULATUM).//P41742

F-HEMBA1000030//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//0.021:136:

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33//PLASMODIUM KNOWLESII (STRAIN NURI).//P04922

5 F-HEMBA1000042//METALLOTHIONEIN 10-II (MT-10-II).//0.71:64:32//MYTILUS EDULIS (BLUE MUSSEL).//P80247

F-HEMBA1000046//PROTEIN Q300.//0.92:40:37//MUS MUSCULUS (MOUSE).//Q02722

10 F-HEMBA1000050//COMPETENCE PROTEIN S.//0.50:28:35//BACILLUS SUBTILIS.//P80355

F-HEMBA1000076//ATP SYNTHASE E CHAIN, MITOCHONDRIAL (EC 3.6.1.34).//0.86:41:41//HOMO SAPIENS (HUMAN).//P56385

15 F-HEMBA1000111

20 F-HEMBA1000129//UVSW PROTEIN (DAR PROTEIN).//0.023:68:33//BACTERIOPHAGE T4.//P20703

F-HEMBA1000141//YSY6 PROTEIN.//0.90:29:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38374

25 F-HEMBA1000150//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//8.4e-16:47:70//HOMO SAPIENS (HUMAN).//P39193

30 F-HEMBA1000156//IMMEDIATE-EARLY PROTEIN.//8.1e-07:143:28//HERPESVIRUS SAIMIRI (STRAIN 11).//Q01042

35 F-HEMBA1000158//HYPOTHETICAL PROTEIN KIAA0192 (FRAGMENT).//7.9e-11:129:40//HOMO SAPIENS (HUMAN).//Q93074

40 F-HEMBA1000168//INSULIN RECEPTOR SUBSTRATE-2 (IRS-2) (4PS).//0.00055:86:36//MUS MUSCULUS (MOUSE).//P81122

F-HEMBA1000180//VPU PROTEIN (U ORF PROTEIN).//0.22:73:28//CHIMPANZEE IMMUNODEFICIENCY VIRUS (SIV(CPZ)) (CIV).//P17286

45 F-HEMBA1000185//RAS-1 PROTEIN.//5.1e-10:121:29//NEUROSPORA CRASSA.//P22126

F-HEMBA1000193//PROLINE-RICH PEPTIDE P-B.//0.00078:56:41//HOMO SAPIENS (HUMAN).//P02814

50 F-HEMBA1000201//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.00061:49:42//MUS MUSCULUS (MOUSE).//P05142

55 F-HEMBA1000213

F-HEMBA1000216//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT

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INTERACTING PROTEIN).//1.6e-59:115:53//MUS MUSCULUS (MOUSE).//Q61221

- 5 F-HEMBA1000227//SUPPRESSOR PROTEIN SRP40.//0.00059:135:22//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST).//P32583
- 10 F-HEMBA1000231//HYPOTHETICAL 60.7 KD PROTEIN C56F8.17C IN CHROMOSOME
I.//0.024:60:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10264
- F-HEMBA1000243//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.0038:125:34//HOMO
SAPIENS (HUMAN).//P08547
- 15 F-HEMBA1000244//HYPOTHETICAL 123.6 KD PROTEIN IN POR2-COX5B INTERGENIC
REGION.//3.1e-17:149:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40480
- 20 F-HEMBA1000251
- F-HEMBA1000264//PROBABLE E5 PROTEIN.//1.0:49:36//HUMAN PAPILLOMAVIRUS TYPE
58.//P26552
- 25 F-HEMBA1000280//SHORT NEUROTOXIN 1 (TOXIN C-6).//0.98:58:31//NAJA NAJA KAOUTHIA
(MONOCLED COBRA) (NAJA NAJA SIAMENSIS).//P14613
- 30 F-HEMBA1000282//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.14:26:65//HOMO SAPIENS
(HUMAN).//P39188
- F-HEMBA1000288
- 35 F-HEMBA1000290//HYPOTHETICAL 14 KD PROTEIN IN TVRI-6 REPETITIVE REGION.//3.8e-
06:98:39//HOMO SAPIENS (HUMAN).//P10516
- 40 F-HEMBA1000302
- F-HEMBA1000303//HYPOTHETICAL 104.4 KD PROTEIN F54G8.4 IN CHROMOSOME
III.//1.3e-05:69:42//CAENORHABDITIS ELEGANS.//Q03601
- 45 F-HEMBA1000304//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//0.021:18:83//HOMO
SAPIENS (HUMAN).//P39194
- 50 F-HEMBA1000307//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT).//7.1e-06:235:
25//HYDRA ATTENUATA (HYDRA) (HYDRA VULGARIS).//P39922
- F-HEMBA1000327
- 55 F-HEMBA1000333//SRP1 PROTEIN.//1.0:159:30//SCHIZOSACCHAROMYCES POMBE
(FISSION YEAST).//Q10193

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F-HEMBA1000338//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/8.8e-26:36:83//HOMO SAPIENS (HUMAN).//P39193

5 F-HEMBA1000351

F-HEMBA1000355//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.99:22:50//HOMO SAPIENS (HUMAN).//P02811

10

F-HEMBA1000356//IMMEDIATE-EARLY PROTEIN IE180.//0.11:82:36//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675

15 F-HEMBA1000357//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/2.1e-35:105:74//HOMO SAPIENS (HUMAN).//P39192

20 F-HEMBA1000366//HYPOTHETICAL TRANSCRIPTIONAL REGULATOR AF1627.//1.0:28:42//ARCHAEOGLOBUS FULGIDUS.//O28646

25 F-HEMBA1000369//PRESYNAPTIC DENSITY PROTEIN 95 (PSD-95).//0.013:140:26//HOMO SAPIENS (HUMAN).//P78352

30 F-HEMBA1000376//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//6.8e-08:66:42//MUS MUSCULUS (MOUSE).//P11369

F-HEMBA1000387//HYPOTHETICAL 63.2 KD PROTEIN C1F3.09 IN CHROMOSOME I.//1.5e-15:177:32//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10414

35 F-HEMBA1000390//PARATHYMOSIN.//0.0071:61:29//HOMO SAPIENS (HUMAN).//P20962

40 F-HEMBA1000392//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.1e-30:92:69//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1000396//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.9e-23:64:57//HOMO SAPIENS (HUMAN).//P08547

45 F-HEMBA1000411

F-HEMBA1000418

50 F-HEMBA1000422//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/8.3e-10:90:53//HOMO SAPIENS (HUMAN).//P39188

55 F-HEMBA1000428//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.1e-12:72:55//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1000434

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- F-HEMBA1000442//GENE 11 PROTEIN.//1.0:28:46//SPIROPLASMA VIRUS SPV1-R8A2 B.//P15902
- 5 F-HEMBA1000456//26S PROTEASOME REGULATORY SUBUNIT MTS4 (19S REGULATORY CAP REGION OF 26S PROTEASE SUBUNIT 2).//0.077:118:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87048
- 10 F-HEMBA1000459//HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE (EC 2.7.1.-) (HRI).//4.8e-62:102:78//ORYCTOLAGUS CUNICULUS (RABBIT).//P33279
- 15 F-HEMBA1000460//LYSIS PROTEIN (E PROTEIN) (GPE).//1.0:24:50//BACTERIOPHAGE ALPHA-3.//P31280
- F-HEMBA1000464
- 20 F-HEMBA1000469//PILI PROTEIN.//1.0:27:44//PSEUDOMONAS AERUGINOSA.//P43502
- F-HEMBA1000488//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//1.1e-07:90:38//HOMO SAPIENS (HUMAN).//Q13105
- 25 F-HEMBA1000490//PLECTIN.//0.74:254:25//RATTUS NORVEGICUS (RAT).//P30427
- 30 F-HEMBA1000491//RAS-RELATED PROTEIN M-RAS.//3.0e-14:100:36//RATTUS NORVEGICUS (RAT).//P97538
- F-HEMBA1000501//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.5e-20:81:54//HOMO SAPIENS (HUMAN).//P39194
- 35 F-HEMBA1000504
- 40 F-HEMBA1000505//NEURON-SPECIFIC X11 PROTEIN (FRAGMENT).//0.00028:128:32//HOMO SAPIENS (HUMAN).//Q02410
- 45 F-HEMBA1000508//CHITIN SYNTHASE 3 (EC 2.4.1.16) (CHITIN-UDP ACETYL-GLUCOSAMINYL TRANSFERASE 3).//0.61:132:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P29465
- F-HEMBA1000518
- 50 F-HEMBA1000519//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.8e-37:68:75//HOMO SAPIENS (HUMAN).//P39189
- 55 F-HEMBA1000520//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//5.2e-09:75:49//HOMO SAPIENS (HUMAN).//P39192

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F-HEMBA1000523//TESTIS-SPECIFIC PROTEIN PBS13.//1.5e-35:257:36//MUS MUSCULUS (MOUSE).//Q01755

5 F-HEMBA1000531//HEAT SHOCK PROTEIN 70 B2.//1.6e-14:72:44//ANOPHELES ALBIMANUS (NEW WORLD MALARIA MOSQUITO).//P41827

10 F-HEMBA1000534//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//9.7e-32:96:78//HOMO SAPIENS (HUMAN).//P39193

15 F-HEMBA1000540//LANTIBIOTIC LACTICIN 481 PRECURSOR (LACTOCOCCIN DR).//1.0:12:75//LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS).//P36499

F-HEMBA1000542//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.0089:79:31//MUS MUSCULUS (MOUSE).//P15265

20 F-HEMBA1000545//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.0e-83:256:66//HOMO SAPIENS (HUMAN).//P08547

25 F-HEMBA1000555//TRANSLATION INITIATION FACTOR IF-2.//3.6e-06:252:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39730

F-HEMBA1000557

30 F-HEMBA1000561//ZINC FINGER PROTEIN 81 (FRAGMENT).//9.1 e-18:200:28//HOMO SAPIENS (HUMAN).//P51508

35 F-HEMBA1000563

F-HEMBA1000568

40 F-HEMBA1000569//GPI-ANCHORED PROTEIN P137.//1.0e-40:137:54//HOMO SAPIENS (HUMAN).//Q14444

F-HEMBA1000575

45 F-HEMBA1000588

50 F-HEMBA1000591//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.1e-17:41:92//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1000592//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//0.18:128:23//HOMO SAPIENS (HUMAN).//Q02224

55 F-HEMBA1000594//HYPOTHETICAL 29.3 KD PROTEIN B0280.6 IN CHROMOSOME III.//0.93:24:54//CAENORHABDITIS ELEGANS.//P41997

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F-HEMBA1000604//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00010:49:55//HOMO SAPIENS (HUMAN).//P39188

5 F-HEMBA1000608//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT).//1.8e-55:179:61//HOMO SAPIENS (HUMAN).//O43295

10 F-HEMBA1000622//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-21:94:62//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1000636//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//0.34:73:36//VOLVOX CARTERI.//P21997

15 F-HEMBA1000637//BASIC PROLINE-RICH PEPTIDE IB-1.//0.0057:76:38//HOMO SAPIENS (HUMAN).//P04281

20 F-HEMBA1000655

F-HEMBA1000657//ZINC FINGER PROTEIN GCS1.//1.5e-07:66:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P35197

25 F-HEMBA1000662//METALLOTHIONEIN-II (MT-II).//0.79:33:39//CRICETULUS GRISEUS (CHINESE HAMSTER).//P02799

30 F-HEMBA1000673//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/3.1e-17:86:59//HOMO SAPIENS (HUMAN).//P39193

35 F-HEMBA1000682//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//3.0e-13:45:44//MUS MUSCULUS (MOUSE).//P11369

40 F-HEMBA1000686//HYPOTHETICAL 48.0 KD PROTEIN C1B3.08 IN CHROMOSOME I.//4.5e-07:79:34//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O13873

F-HEMBA1000702

45 F-HEMBA1000705//PROTEIN Q300.//0.80:25:44//MUS MUSCULUS (MOUSE).//Q02722

F-HEMBA1000719//MYOSIN IC HEAVY CHAIN.//0.0026:115:44//ACANTHAMOEBA CASTELLANI (AMOEB).//P10569

50

F-HEMBA1000722

55 F-HEMBA1000726//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/7.4e-32:83:77//HOMO SAPIENS (HUMAN).//P39191

F-HEMBA1000727//ZINC FINGER PROTEIN CTH2 (YTIS11 PROTEIN).//0.73:26:

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46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P47977

F-HEMBA1000747

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F-HEMBA1000749//HYPOTHETICAL PROTEIN HI1484.//1.0:42:35//HAEMOPHILUS INFLUENZAE.//P44211

10

F-HEMBA1000752//RETROVIRUS-RELATED ENV POLYPROTEIN.//1.0e-08:84:39//HOMO SAPIENS (HUMAN).//P10267

F-HEMBA1000769

15

F-HEMBA1000773//PAIRED BOX PROTEIN PAX-4.//1.0:107:33//HOMO SAPIENS (HUMAN) //O43316

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F-HEMBA1000774//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.3e-23:92:63//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1000791

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F-HEMBA1000817//PROLACTIN RECEPTOR PRECURSOR (PRL-R).//0.079:87:29//CERVUS ELAPHUS (RED DEER).//Q28235

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F-HEMBA1000822

F-HEMBA1000827//HYPOTHETICAL 8.4 KD PROTEIN.//0.98:48:39//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20546

35

F-HEMBA1000843//HYPOTHETICAL 7.3 KD PROTEIN D1044.5 IN CHROMOSOME III.//0.92:46:34//CAENORHABDITIS ELEGANS.//P41953

40

F-HEMBA1000851//HOMEBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC HOMEBOX PROTEIN 2).//0.048:39:51//HOMO SAPIENS (HUMAN).//P52951

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F-HEMBA1000852//ARYLSULFATASE D PRECURSOR (EC 3.1.6.-) (ASD).//4.0e-24:29:100//HOMO SAPIENS (HUMAN).//P51689

F-HEMBA1000867

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F-HEMBA1000869//PROBABLE E5 PROTEIN.//0.99:70:27//HUMAN PAPILLOMAVIRUS TYPE 18.//P06792

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F-HEMBA1000870//MYOTOXIN 3 PRECURSOR (CROTAMINE 3).//0.79:43:32//CROTALUS DURISSUS TERRIFICUS (SOUTH AMERICAN RATTLESNAKE).//P24333

F-HEMBA1000872//GAR2 PROTEIN.//0.89:70:31//SCHIZOSACCHAROMYCES POMBE

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(FISSION YEAST).//P41891

- 5 F-HEMBA1000876//DEFENSIN.//0.89:34:38//ALLOMYRINA DICHOTOMA.//Q10745
- F-HEMBA1000908//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)
./0.69:43:37//HOMO SAPIENS (HUMAN).//P30808
- 10 F-HEMBA1000910//MELANOMA-ASSOCIATED ANTIGEN B3 (MAGE-B3 ANTIGEN).//5.1e-08:
44:38//HOMO SAPIENS (HUMAN).//O15480
- 15 F-HEMBA1000918//60S RIBOSOMAL PROTEIN L37-A (YL35) (FRAGMENT).//1.0:19:
52//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P22667
- F-HEMBA1000919//69 KD PARAFLAGELLAR ROD PROTEIN (69 KD PFR PROTEIN) (PFR-
A/PFR-B).//0.29:116:30//TRYPANOSOMA BRUCEI BRUCEI.//P22225
- 20 F-HEMBA1000934
- 25 F-HEMBA1000942//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.85:27:59//HOMO SAPIENS
(HUMAN).//P39188
- F-HEMBA1000943
- 30 F-HEMBA1000946//STO-2 PROTEIN.//0.82:82:30//CAENORHABDITIS ELEGANS.//Q19958
- F-HEMBA1000960//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/0.0097:29:72//HOMO
SAPIENS (HUMAN).//P39192
- 35 F-HEMBA1000968//METALLOTHIONEIN 20-III ISOFORMS A AND B (MT-20-III A AND MT-20-
IIIB).//0.047:45:37//MYTILUS EDULIS (BLUE MUSSEL).//P80253
- 40 F-HEMBA1000971//HYPOTHETICAL BHLF1 PROTEIN.//0.038:172:31//EPSTEIN-BARR VIRUS
(STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
- 45 F-HEMBA1000972
- F-HEMBA1000974//HYPOTHETICAL PROTEIN MG441.//0.98:66:28//MYCOPLASMA
GENITALIUM.//P47679
- 50 F-HEMBA1000975//COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGEN)
(FRAGMENT).//0.028:57:36//HOMO SAPIENS (HUMAN).//P25067
- 55 F-HEMBA1000985
- F-HEMBA1000986//SUBMANDIBULAR GLAND SECRETORY GLX-RICH PROTEIN CB
PRECURSOR (GRP-CB) (CONTIGUOUS REPEAT POLYPEPTIDE) (CRP).//0.13:91:

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34//RATTUS NORVEGICUS (RAT).//P08462

5 F-HEMBA1000991//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN
D2013.2 IN CHROMOSOME II.//5.6e-05:37:45//CAENORHABDITIS ELEGANS.//Q18964

10 F-HEMBA1001007//HYPOTHETICAL PROTEIN KIAA0179.//0.27:72:41//HOMO SAPIENS
(HUMAN).//Q14684

F-HEMBA1001008//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.4e-25:61:70//HOMO
SAPIENS (HUMAN).//P39194

15 F-HEMBA1001009//CUTICLE COLLAGEN 34.//0.044:214:29//CAENORHABDITIS
ELEGANS.//P34687

20 F-HEMBA1001017//SYNDECAN-3 PRECURSOR (N-SYNDECAN) (NEUROGLYCAN).//5.0e-
85:191:84//RATTUS NORVEGICUS (RAT).//P33671

F-HEMBA1001019

25 F-HEMBA1001020//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/6.7e-24:49:73//HOMO
SAPIENS (HUMAN).//P39188

30 F-HEMBA1001022

F-HEMBA1001024//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.0e-11:61:59//HOMO
SAPIENS (HUMAN).//P08547

35 F-HEMBA1001026//HYPOTHETICAL PROTEIN BB0073.//0.94:63:34//BORRELIA
BURGDORFERI (LYME DISEASE SPIROCHETE).//O51100

40 F-HEMBA1001043//INVOLUCRIN.//0.0036:238:25//SAGUINUS OEDIPUS (COTTON-TOP
TAMARIN).//P24712

45 F-HEMBA1001051//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/3.3e-32:95:75//HOMO
SAPIENS (HUMAN).//P39189

F-HEMBA1001052//CURROMYCIN RESISTANCE PROTEIN.//1.0:31:38//STREPTOMYCES
HYGROSCOPICUS.//P16961

50 F-HEMBA1001059//N-ACETYL GALACTOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.4)
(N- ACETYL GALACTOSAMINE-6-SULFATE SULFATASE) (GALACTOSE-6-SULFATE
SULFATASE) (GALNAC6S SULFATASE) (CHONDROITINSULFATASE) (CHONDROITINASE)
//3.2e-132:249:94//HOMO SAPIENS (HUMAN).//P34059

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F-HEMBA1001060

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F-HEMBA1001071//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.//8.3e-23:51:
96//HOMO SAPIENS (HUMAN).//P02461

5 F-HEMBA1001077//AUTOIMMUNE REGULATOR (APECED PROTEIN).//3.4e-06:37:56//HOMO
SAPIENS (HUMAN).//O43918

10 F-HEMBA1001080//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACTOR
ICP34.5).//0.0012:70:38//HERPES SIMPLEX VIRUS (TYPE 1 / STRAW MGH-10).//P37319

15 F-HEMBA1001085//SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PPS)
(PROTEIN PHOSPHATASE T) (PPT) (FRAGMENT).//0.00018:76:32//MUS MUSCULUS
(MOUSE).//Q60676

20 F-HEMBA1001088//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS
PROTEIN).//3.5e-50:176:57//HOMO SAPIENS (HUMAN).//P48059

F-HEMBA1001094

25 F-HEMBA1001099//LIGHT-HARVESTING PROTEIN B800/850/890, ALPHA-2 CHAIN (EHA-
ALPHA-2) (ANTENNA PIGMENT PROTEIN, ALPHA-2 CHAIN) (FRAGMENT).//1.0:15:
60//ECTOTHIORHODOSPIRA HALOPHILA.//P80101

30 F-HEMBA1001109/////ALU SUBFAMILY SB WARNING ENTRY !!!!!//6.7e-37:102:82//HOMO
SAPIENS (HUMAN).//P39189

35 F-HEMBA1001121//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.036:49:46//HOMO
SAPIENS (HUMAN).//P08547

F-HEMBA1001122

40 F-HEMBA1001123

45 F-HEMBA1001133//HYPOTHETICAL 9.4 KD PROTEIN (ORF2).//0.86:29:41//FELINE
IMMUNODEFICIENCY VIRUS (ISOLATE SAN DIEGO) (FIV), AND FELINE
IMMUNODEFICIENCY VIRUS (ISOLATE PETALUMA) (FIV).//P19033

F-HEMBA1001137//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.0e-22:
103:52//HOMO SAPIENS (HUMAN).//P51523

50 F-HEMBA1001140//COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR.//0.032:94:36//HOMO
SAPIENS (HUMAN).//P53420

F-HEMBA1001172

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F-HEMBA1001174//ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5.//2.9e-78:179:
79//RATTUS NORVEGICUS (RAT).//P51646

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5 F-HEMBA1001197//MAJOR PRION PROTEIN PRECURSOR (PRP) (PRP27-30) (PRP33-35C)
(FRAGMENT).//0.051:96:32//CERCOCEBUS ATERRIMUS, AND MACACA SYLVANUS
(BARBARY APE).//Q95145

F-HEMBA1001208

10 F-HEMBA1001213

F-HEMBA1001226//PROTEASOME COMPONENT C8 (EC 3.4.99.46) (MACROPAIN SUBUNIT
C8) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8).//1.5e-08:24:91//HOMO
15 SAPIENS (HUMAN).//P25788

F-HEMBA1001235//FIBRONECTIN (FN) (FRAGMENT).//0.76:50:38//ORYCTOLAGUS
CUNICULUS (RABBIT).//Q28749

20 F-HEMBA1001247//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//0.00052:16:
81//VOLVOX CARTERI.//P21997

25 F-HEMBA1001257//2-ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-.-).//1.6e-68:178:
77//RATTUS NORVEGICUS (RAT).//P70473

F-HEMBA1001265//MANNAN ENDO-1,4-BETA-MANNOSIDASE A PRECURSOR (EC 3.2.1.78)
30 (BETA- MANNANASE A) (1,4-BETA-D-MANNAN MANNANOHYDROLASE A).//0.67:23:
60//PIROMYCES SP.//P55296

F-HEMBA1001281//HYPOTHETICAL 8.9 KD PROTEIN YCF34 (ORF76).//0.83:48:
35 35//PORPHYRA PURPUREA.//P51229

F-HEMBA1001286//COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR.//1.3e-
07:185:29//CAVIA PORCELLUS (GUINEA PIG).//Q60401

40 F-HEMBA1001289//METABOTROPIC GLUTAMATE RECEPTOR 3 PRECURSOR.//0.00018:
159:30//RATTUS NORVEGICUS (RAT).//P31422

45 F-HEMBA1001294

F-HEMBA1001299//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//5.3e-07:27:77//HOMO
SAPIENS (HUMAN).//P39195

50 F-HEMBA1001302//45 KD CALCIUM-BINDING PROTEIN PRECURSOR (STROMAL CELL-
DERIVED FACTOR 4) (SDF-4).//3.3e-61:150:76//MUS MUSCULUS (MOUSE).//Q61112

55 F-HEMBA1001303

F-HEMBA1001310//HYPOTHETICAL PROTEIN KIAA0161.//2.7e-10:170:27//HOMO SAPIENS

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(HUMAN).//P50876

F-HEMBA1001319

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F-HEMBA1001323

10 F-HEMBA1001326//HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION.//1.1e-39:144:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43601

F-HEMBA1001327

15 F-HEMBA1001330

20 F-HEMBA1001351//VESICLE-ASSOCIATED MEMBRANE PROTEIN/SYNAPTOBREVIN BINDING PROTEIN (VAP-33).//1.9e-37:155:46//APLYSIA CALIFORNICA (CALIFORNIA SEA HARE).//Q16943

F-HEMBA1001361//RUBREDOXIN (RD).//0.95:44:29//ALCALIGENES EUTROPHUS.//P31912

25 F-HEMBA1001375//AEROLYSIN REGULATORY PROTEIN.//0.013:45:33//AEROMONAS SOBRIA.//P09165

30 F-HEMBA1001377//SPERM PROTAMINE P1.//1.0:22:40//PLANIGALE MACULATA SINUALIS (COMMON PLANIGALE).//O18746

35 F-HEMBA1001383//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.60:37:29//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z2/CDC-Z34 ISOLATE) (HIV-1).//P12506

F-HEMBA1001387//GTP-BINDING PROTEIN TC10.//6.6e-43:83:92//HOMO SAPIENS (HUMAN).//P17081

40 F-HEMBA1001388//HYPOTHETICAL PROTEIN KIAA0136 (FRAGMENT).//0.00088:46:45//HOMO SAPIENS (HUMAN).//Q14149

45 F-HEMBA1001391

F-HEMBA1001398//CLOACIN (EC 3.1.-.-) (RIBONUCLEASE).//1.0:59:37//ESCHERICHIA COLI.//P00645

50 F-HEMBA1001405//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.25:41:34//HOMO SAPIENS (HUMAN).//P22531

55 F-HEMBA1001407//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//4.0e-09:129:40//HOMO SAPIENS (HUMAN).//P04280

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F-HEMBA1001411//HYPOTHETICAL 34.9 KD PROTEIN IN CYSJ-ENO INTERGENIC REGION
(O313)//0.95:88:31//ESCHERICHIA COLI//P55140

5 F-HEMBA1001413//SOX-12 PROTEIN (FRAGMENT)//0.95:46:32//MUS MUSCULUS (MOUSE)
//Q04890

F-HEMBA1001415//HISTONE H5//0.43:95:29//GALLUS GALLUS (CHICKEN)//P02259

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F-HEMBA1001432//LANTIBIOTIC NISIN A PRECURSOR//0.77:46:32//LACTOCOCCUS
LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS)//P13068

15 F-HEMBA1001433//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//4.8e-09:132:
31//NYCTICEBUS COUCANG (SLOW LORIS)//P08548

20 F-HEMBA1001435//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.2e-31:84:77//HOMO
SAPIENS (HUMAN)//P39189

F-HEMBA1001442

25 F-HEMBA1001446//ANTIFREEZE PEPTIDE 4 PRECURSOR//0.71:41:
39//PSEUDOPLEURONECTA AMERICANUS (WINTER FLOUNDER)//P02734

30 F-HEMBA1001450//PROLINE-RICH PROTEIN LAS17//0.13:127:27//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST)//Q12446

35 F-HEMBA1001454//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.57:38:
47//HANSENULA WINGEI (YEAST)//P48882

F-HEMBA1001455//CHEMOTAXIS PROTEIN CHEA (EC 2.7.3.-)//0.98:124:25//BORRELIA
BURGDORFERI (LYME DISEASE SPIROCHETE)//Q44737

40 F-HEMBA1001463//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.8e-32:62:67//HOMO
SAPIENS (HUMAN)//P39194

45 F-HEMBA1001476//NUCLEOPORIN NUP159 (NUCLEAR PORE PROTEIN NUP159)//6.8e-
09:252:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40477

F-HEMBA1001478

50 F-HEMBA1001497//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.2e-33:105:72//HOMO
SAPIENS (HUMAN)//P39194

55 F-HEMBA1001510//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/8.3e-37:54:81//HOMO
SAPIENS (HUMAN)//P39189

F-HEMBA1001515//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//2.0e-63:223:57//HOMO

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SAPIENS (HUMAN).//P08547

F-HEMBA1001517

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F-HEMBA1001522//TROPOMYOSIN ALPHA CHAIN, SMOOTH MUSCLE.//0.78:150:22//COTURNIX COTURNIX JAPONICA (JAPANESE QUAIL).//P49437

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F-HEMBA1001526//PERIPLASMIC [FE] HYDROGENASE 1 (EC 1.18.99.1).//1.6e-06:130:29//CLOSTRIDIUM PASTEURIANUM.//P29166

15

F-HEMBA1001533//PROBABLE E5A PROTEIN.//0.73:35:37//HUMAN PAPILLOMAVIRUS TYPE 6A.//Q84296

20

F-HEMBA1001557//HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3'REGION.//1.5e-07:99:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38898

F-HEMBA1001566//HYPOTHETICAL PROTEIN BB0692.//0.91:27:44//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//O51635

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F-HEMBA1001569//SYNAPTOSOMAL VESICLE ASSOCIATED MEMBRANE PROTEIN 2 (VAMP-2).//2.2e-50:110:95//HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE).//P19065

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F-HEMBA1001570//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//3.3e-33:107:72//HOMO SAPIENS (HUMAN).//P39195

35

F-HEMBA1001579//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-14:111:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-HEMBA1001581

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F-HEMBA1001585

F-HEMBA1001589//PROBABLE DNA-BINDING PROTEIN (AGNOPROTEIN).//0.98:51:33//HUMAN ADENOVIRUS TYPE 2.//P03263

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F-HEMBA1001595//SEPTIN 2 HOMOLOG (FRAGMENT).//3.0e-124:274:85//HOMO SAPIENS (HUMAN).//Q14141

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F-HEMBA1001608//RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER).//0.99:28:39//ORYCTOLAGUS CUNICULUS (RABBIT).//Q28615

55

F-HEMBA1001620//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//4.3e-45:222:46//SPIRODELA POLYRRHIZA.//P42803

F-HEMBA1001635//FIBRILLARIN.//0.10:72:38//CAENORHABDITIS ELEGANS.//Q22053

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F-HEMBA1001636//PAIRED BOX PROTEIN PAX-8, ISOFORMS 8C/8D.//0.75:38:47//HOMO
 SAPIENS (HUMAN).//Q09155
 5
 F-HEMBA1001640///// ALU SUBFAMILY J WARNING ENTRY !!!!!14.7e-06:80:41//HOMO
 SAPIENS (HUMAN).//P39188
 10
 F-HEMBA1001647//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-
 135) (TAFII135) (TAFII-130) (TAFII130).//0.075:165:32//HOMO SAPIENS (HUMAN).//O00268
 F-HEMBA1001651//GOLGIN-95.//6.8e-05:141:24//HOMO-SAPIENS (HUMAN).//Q08379
 15
 F-HEMBA1001655//PROLINE-RICH PROTEIN LAS17.//0.19:97:30//SACCHAROMYCES
 CEREVISIAE (BAKER'S YEAST).//Q12446
 20
 F-HEMBA1001658//TETRAHYDROMETHANOPTERIN S-METHYLTRANSFERASE 12 KD
 SUBUNIT (EC 2.1.1.86) (N5-METHYLTETRAHYDROMETHANOPTERIN-COENZYME M
 METHYLTRANSFERASE 12 KD SUBUNIT).//1.0:29:44//METHANOBACTERIUM
 THERMOAUTOTROPHICUM (STRAIN MARBURG / DSM 2133).//Q50773
 25
 F-HEMBA1001661//CELLULOSE COMPLEMENTING PROTEIN.//0.35:87:33//ACETOBACTER
 XYLINUM (ACETOBACTER PASTEURIANUS).//P37697
 30
 F-HEMBA1001672//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//2.7e-10:216:
 35//PLASMODIUM CYNOMOLGI (STRAIN BEROK).//P08672
 F-HEMBA1001675//NODULIN 20 PRECURSOR (N-20).//0.98:36:44//GLYCINE MAX
 35 (SOYBEAN).//P08960
 F-HEMBA1001678///// ALU SUBFAMILY SX WARNING ENTRY !!!!!8.2e-13:62:64//HOMO
 SAPIENS (HUMAN).//P39195
 40
 F-HEMBA1001681//HYPOTHETICAL 41.5 KD PROTEIN IN P6.5-VP48 INTERGENIC REGION
 (P40) (ORF3) (ORF102).//1.0:51:39//ORGYIA PSEUDOTSUGATA MULTICAPSID
 45 POLYHEDROSIS VIRUS (OPMNPV).//P24653
 F-HEMBA1001702//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.017:54:
 37//TRYPANOSOMA BRUCEI BRUCEI.//P24499
 50
 F-HEMBA1001709//HYPOTHETICAL 21.2 KD PROTEIN IN TOR2-MNN4 INTERGENIC
 REGION.//0.59:109:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36042
 F-HEMBA1001711
 55
 F-HEMBA1001712//HYPOTHETICAL 6.9 KD PROTEIN IN 100 KD PROTEIN REGION.//0.54:
 44:34//HUMAN ADENOVIRUS TYPE 41.//P23690

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- 5 F-HEMBA1001714//ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR.//1.2e-19:60:75//RATTUS NORVEGICUS (RAT).//Q03344
- 10 F-HEMBA1001718//HYPOTHETICAL PROTEIN UL63.//1.0:54:37//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16820
- 15 F-HEMBA1001723//HYPOTHETICAL 34.0 KD TRP-ASP REPEATS CONTAINING PROTEIN IN SIS1-MRPL2 INTERGENIC REGION.//5.1e-26:90:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41318
- 20 F-HEMBA1001731//HYPOTHETICAL 16.6 KD PROTEIN.//0.71:49:32//AVIAN INFECTIOUS BURSAL DISEASE VIRUS (STRAIN 52/70) (IBDV).//P25221
- 25 F-HEMBA1001734
- 30 F-HEMBA1001744//SCY1 PROTEIN.//2.1e-11:182:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53009
- 35 F-HEMBA1001745//HYPOTHETICAL 11.6 KD PROTEIN IN NUT1-ARO2 INTERGENIC REGION PRECURSOR.//1.0:36:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53116
- 40 F-HEMBA1001746//PROTEIN-EXPORT MEMBRANE PROTEIN SECG HOMOLOG.//0.94:48:35//MYCOBACTERIUM LEPRAE.//P38388
- 45 F-HEMBA1001761
- 50 F-HEMBA1001781//ZINC FINGER PROTEIN 19 (ZINC FINGER PROTEIN KOX12) (FRAGMENT).//0.028:47:40//HOMO SAPIENS (HUMAN).//P17023
- 55 F-HEMBA1001784//HYPOTHETICAL 6.1 KD PROTEIN C03B1.10 IN CHROMOSOME X.//0.00068:32:46//CAENORHABDITIS ELEGANS .//Q11116
- F-HEMBA1001791//METALLOTHIONEIN (MT).//1.0:34:35//PLEURONECTES PLATESSA (PLAICE).//P07216
- F-HEMBA1001800//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//1.5e-14:60:48//MUS MUSCULUS (MOUSE).//P16372
- F-HEMBA1001803
- F-HEMBA1001804//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1 PRECURSOR.//9.3e-17:56:57//ORYZA SATIVA (RICE).//P25074
- F-HEMBA1001808//PARANEOPLASTIC ENCEPHALOMYELITIS ANTIGEN HUD HOMOLOG

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(HU-ANTIGEN D).//0.75:97:31//RATTUS NORVEGICUS (RAT).//O09032

5 F-HEMBA1001809//IMMEDIATE-EARLY PROTEIN IE180.//4.5e-11:206:36//PSEUDORABIES
VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675

10 F-HEMBA1001815//60S RIBOSOMAL PROTEIN L37-B (YL27) (FRAGMENT).//0.34:30:
30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P05733

F-HEMBA1001819//ZINC FINGER PROTEIN 135.//2.6e-102:262:66//HOMO SAPIENS
(HUMAN).//P52742

15 F-HEMBA1001820

F-HEMBA1001822//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE
20 15 (PROTEIN EPS15).//1.2e-18:251:33//MUS MUSCULUS (MOUSE).//P42567

F-HEMBA1001824//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN)
//4.7e-11:124:37//OVIS ARIES (SHEEP).//P26372

25 F-HEMBA1001835

F-HEMBA1001844/////ALU SUBFAMILY SX WARNING ENTRY !!!!!//4.3e-14:36:63//HOMO
30 SAPIENS (HUMAN).//P39195

F-HEMBA1001847//ZINC FINGER PROTEIN 29 (ZFP-29).//2.7e-36:135:51//MUS MUSCULUS
(MOUSE).//Q07230

35 F-HEMBA1001861

F-HEMBA1001864//HEAT-STABLE ENTEROTOXIN A3/A4 PRECURSOR (STA3/STA4) (ST-IB)
40 (ST-H).//1.0:31:38//ESCHERICHIA COLI.//P07965

F-HEMBA1001866//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE
PRECURSOR (EC 2.4.1.-) (DUGT).//9.7e-42:234:41//DROSOPHILA MELANOGASTER (FRUIT
45 FLY).//Q09332

F-HEMBA1001869//HYPOTHETICAL 94.9 KD PROTEIN C22E12.11C IN CHROMOSOME
I.//5.3e-13:65.47//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10362

50 F-HEMBA1001888//HYPOTHETICAL 11.4 KD PROTEIN (ORF1).//0.85:62:
37//STREPTOMYCES FRADIAE.//P26800

F-HEMBA1001896//DIMETHYLGLYCINE DEHYDROGENASE PRECURSOR (EC 1.5.99.2)
55 (ME2GLYDH).//9.8e-20:250:29//RATTUS NORVEGICUS (RAT).//Q63342

F-HEMBA1001910//EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E) (EIF4E)

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(MRNA CAP-BINDING PROTEIN) (EIF-4F 25 KD SUBUNIT).//0.94:44:38//CAENORHABDITIS ELEGANS.//O61955

5 F-HEMBA1001912//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//8.7e-07:53:62//HOMO SAPIENS (HUMAN).//P39188

10 F-HEMBA1001913//GCN20 PROTEIN.//1.8e-21:68:60//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43535

15 F-HEMBA1001915//KLEE PROTEIN (KCRB3 PROTEIN).//0.94:64:21//ESCHERICHIA COLI.//Q52280

F-HEMBA1001918

20 F-HEMBA1001921

F-HEMBA1001939//CHLOROPLAST 50S RIBOSOMAL PROTEIN L24.//1.0:47:31//ODONTELLA SINENSIS.//P49560

25 F-HEMBA1001940//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.0017:31:77//HOMO SAPIENS (HUMAN).//P39188

30 F-HEMBA1001942//HIBERNATION-ASSOCIATED PLASMA PROTEIN HP-27 PRECURSOR (HIBERNATOR- SPECIFIC BLOOD COMPLEX, 27 KD SUBUNIT).//1.0:77:28//TAMIAS ASIATICUS (CHIPMUNK).//Q06577

35 F-HEMBA1001945//HYPOTHETICAL 4.6 KD PROTEIN IN GP47-AGT INTERGENIC REGION (ORF E).//1.0:35:37//BACTERIOPHAGE T4.//P32269

40 F-HEMBA1001950//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.43:18:44//DROSOPHILA YAKUBA (FRUIT FLY).//P03933

F-HEMBA1001960//HOMEODOMAIN PROTEIN HOX-C5 (HOX-3D) (CP11).//0.17:12:66//HOMO SAPIENS (HUMAN).//Q00444

45 F-HEMBA1001962//HYPOTHETICAL 9.0 KD PROTEIN IN ADH4 5'REGION.//1.0:30:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53056

50 F-HEMBA1001964

F-HEMBA1001967//HYPOTHETICAL PROTEIN UL61.//0.027:111:36//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16818

55 F-HEMBA1001979

F-HEMBA1001987//HYPOTHETICAL 11.2 KD PROTEIN (ORF117).//1.0:83:32//ORGANIA

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PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10356

5 F-HEMBA1001991//NEUROTOXIN 1 (TOXIN ATX-I).//0.99:31:45//ANEMONIA SULCATA
(SNAKE-LOCKS SEA ANEMONE).//P01533

10 F-HEMBA1002003//GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, TESTIS-
SPECIFIC (EC 1.2.1.12) (GAPDH).//5.5e-07:109:32//MUS MUSCULUS (MOUSE).//Q64467

F-HEMBA1002008

15 F-HEMBA1002018//EC PROTEIN HOMOLOG 2 (FRAGMENT).//0.83:66:33//ARABIDOPSIS
THALIANA (MOUSE-EAR CRESS).//Q42377

F-HEMBA1002022//INSULIN.//1.0:59:32//SQUALUS ACANTHIAS (SPINY DOGFISH).//P12704

20 F-HEMBA1002035//MONOCYTIC LEUKEMIA ZINC FINGER PROTEIN.//8.3e-15:64:40//HOMO
SAPIENS (HUMAN).//Q92794

25 F-HEMBA1002039//HYPOTHETICAL PROLINE-RICH PROTEIN KIAA0269.//0.0070:70:
40//HOMO SAPIENS (HUMAN).//Q92558

30 F-HEMBA1002049//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.5e-07:37:75//HOMO
SAPIENS (HUMAN).//P39188

F-HEMBA1002084

35 F-HEMBA1002092//SPT23 PROTEIN.//0.12:208:26//SACCHAROMYCES CEREVISIAE
(BAKER'S YEAST).//P35210

F-HEMBA1002100

40 F-HEMBA1002102//ANKYRIN.//1.4e-12:106:35//MUS MUSCULUS (MOUSE).//Q02357

45 F-HEMBA1002113//EARLY NODULIN 20 PRECURSOR (N-20).//0.073:155:32//MEDICAGO
TRUNCATULA (BARREL MEDIC).//P93329

F-HEMBA1002119//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.85:22:36//DROSOPHILA
MELANOGASTER (FRUIT FLY).//Q01643

50 F-HEMBA1002125//GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12,
P30].//0.35:111:33//FELINE SARCOMA VIRUS (STRAIN SNYDER-THEILEN).//P03338

55 F-HEMBA1002139//HYPOTHETICAL 12.4 KD PROTEIN IN SEC17-QCR1 INTERGENIC
REGION.//0.88:72:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38192

F-HEMBA1002144

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- F-HEMBA1002150//THROMBOMODULIN (FETOMODULIN) (TM) (FRAGMENT).//4.8e-10:65:
46//BOS TAURUS (BOVINE).//P06579
- 5 F-HEMBA1002151//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.24:146:
28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323
- 10 F-HEMBA1002153//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.93:
58:25//APIS MELLIFERA (HONEYBEE).//P34859
- 15 F-HEMBA1002160//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//5.1e-21:94:65//HOMO
SAPIENS (HUMAN).//P39193
- F-HEMBA1002161//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//1.4e-51:
180:56//SUS SCROFA (PIG).//P79293
- 20 F-HEMBA1002162//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//4.1e-40:102:75//HOMO
SAPIENS (HUMAN).//P39193
- 25 F-HEMBA1002166//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.8e-13:133:45//HOMO
SAPIENS (HUMAN).//P39188
- 30 F-HEMBA1002177//ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654).//0.0014:153:
26//HOMO SAPIENS (HUMAN).//P52746
- F-HEMBA1002185
- 35 F-HEMBA1002189//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//0.86:46:45//HOMO
SAPIENS (HUMAN).//P39194
- 40 F-HEMBA1002191//MALE SPECIFIC SPERM PROTEIN MST84DC.//0.037:14:
57//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01644
- F-HEMBA1002199
- 45 F-HEMBA1002204
- F-HEMBA1002212//DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE
- 50 KINASE DSOR1 (EC 2.7.1.-) (DOWNSTREAM OF RAF) (MAPKK).//3.2e-13:201:
30//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24324
- 55 F-HEMBA1002215//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//1.1e-62:147:84//MUS
MUSCULUS (MOUSE).//P47226
- F-HEMBA1002226//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.6e-26:168:44//HOMO

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SAPIENS (HUMAN).//P39188

5 F-HEMBA1002229//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!!/6.8e-18:68:72//HOMO
SAPIENS (HUMAN).//P39190

10 F-HEMBA1002237//EAMZP30-47 PROTEIN (FRAGMENT).//0.96:21:61//EIMERIA
ACERVULINA.//P21959

F-HEMBA1002241//METALLOTHIONEIN (MT).//0.95:25:48//PARACENTROTUS LIVIDUS
(COMMON SEA URCHIN).//P80367

15 F-HEMBA1002253//METALLOTHIONEIN-II (MT-II).//0.97:27:48//MESOCRICETUS AURATUS
(GOLDEN HAMSTER).//P17808

F-HEMBA1002257

20 F-HEMBA1002265//MALE SPECIFIC SPERM PROTEIN MST84DC.//0.95:24:50//DROSOPHILA
MELANOGASTER (FRUIT FLY).//Q01644

25 F-HEMBA1002267//NEURONAL PROTEIN 3.1 (P311 PROTEIN).//0.94:33:33//GALLUS
GALLUS (CHICKEN).//Q90667

F-HEMBA1002270

30 F-HEMBA1002321//HYPOTHETICAL IMMUNITY REGION PROTEIN 14.//0.99:22:
40//BACTERIOPHAGE PHI-105.//P10437

35 F-HEMBA1002328

F-HEMBA1002337

40 F-HEMBA1002341//P53-BINDING PROTEIN 53BP2 (FRAGMENT).//3.7e-55:109:96//MUS
MUSCULUS (MOUSE).//Q62415

45 F-HEMBA1002348//PROBABLE E5 PROTEIN.//0.43:30:50//HUMAN PAPILLOMAVIRUS TYPE
35.//P27226

F-HEMBA1002349

50 F-HEMBA1002363//CHROMOSOME ASSEMBLY PROTEIN XCAP-E.//5.7e-105:278:
71//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P50533

55 F-HEMBA1002381//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.3e-24:69:73//HOMO
SAPIENS (HUMAN).//P39188

F-HEMBA1002389//EARLY NODULIN 20 PRECURSOR (N-20).//0.16:110:31//MEDICAGO

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TRUNCATULA (BARREL MEDIC).//P93329

5 F-HEMBA1002417//TIGHT JUNCTION PROTEIN ZO-1 (TIGHT JUNCTION PROTEIN 1).//2.6e-51:187:56//MUS MUSCULUS (MOUSE).//P39447

10 F-HEMBA1002419//PROLINE-RICH PEPTIDE P-B.//1.0:18:61//HOMO SAPIENS (HUMAN).//P02814

F-HEMBA1002430//HYPOTHETICAL 12.3 KD PROTEIN IN GAP1-NAP1 INTERGENIC REGION.//0.042:41:46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36140

15 F-HEMBA1002439//CHLOROPLAST 50S RIBOSOMAL PROTEIN L27 (FRAGMENT).//0.99:47:29//CALYPTROSPHAERA SPHAEROIDEA.//P41548

20 F-HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74.//4.1e-24:109:55//HOMO SAPIENS (HUMAN).//Q00994

F-HEMBA1002460

25 F-HEMBA1002462//SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT).//0.00025:80:30//HOMO SAPIENS (HUMAN).//P81489

30 F-HEMBA1002469//PUTATIVE TUMOR SUPPRESSOR LUCA15.//0.0012:110:33//HOMO SAPIENS (HUMAN).//P52756

35 F-HEMBA1002475//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.37:106:33//MUS MUSCULUS (MOUSE).//P05143

F-HEMBA1002477//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.3e-34:96:71//HOMO SAPIENS (HUMAN).//P39194

40 F-HEMBA1002486

45 F-HEMBA1002495//LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1.//2.9e-31:110:39//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P48732

F-HEMBA1002498//SFT2 PROTEIN.//1.0:54:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38166

50 F-HEMBA1002503//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.0e-06:49:63//HOMO SAPIENS (HUMAN).//P39188

55 F-HEMBA1002508//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.6e-22:169:44//HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1002513//HYPOTHETICAL 89.8 KD PROTEIN F41H10.6 IN CHROMOSOME

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IV./0.00017:79:35//CAENORHABDITIS ELEGANS./Q20296

F-HEMBA1002515

5

F-HEMBA1002538//ATP SYNTHASE E CHAIN, MITOCHONDRIAL (EC 3.6.1.34)//1.0:53:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P81449

10

F-HEMBA1002542//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.7e-32:96:75//HOMO SAPIENS (HUMAN)//P39188

15

F-HEMBA1002547//AGRIN PRECURSOR./2.5e-100:218:80//RATTUS NORVEGICUS (RAT) .//P25304

20

F-HEMBA1002552//HEP27 PROTEIN (PROTEIN D)./9.5e-12:29:82//HOMO SAPIENS (HUMAN)//Q13268

F-HEMBA1002555//COLLAGEN ALPHA 1(III) CHAIN./2.4e-15:207:36//BOS TAURUS (BOVINE)//P04258

25

F-HEMBA1002558//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.0:34:50//HOMO SAPIENS (HUMAN)//P39193

30

F-HEMBA1002561//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG./1.5e-05:49:46//NYCTICEBUS COUCANG (SLOW LORIS)//P08548

35

F-HEMBA1002569//SINGLE-STRANDED DNA-BINDING PROTEIN P12./0.97:60:33//BACTERIOPHAGE PRD1./P17637

F-HEMBA1002583

40

F-HEMBA1002590//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.6e-15:54:55//HOMO SAPIENS (HUMAN)//P39188

45

F-HEMBA1002592//HISTIDINE-RICH PROTEIN./0.99:39:28//PLASMODIUM FALCIPARUM (ISOLATE FCM17 / SENEGAL)//P14586

F-HEMBA1002609//SSM4 PROTEIN./1.9e-12:135:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40318

50

F-HEMBA1002621//CYTOCHROME B6-F COMPLEX 3.5 KD SUBUNIT (CYTOCHROME B6-F COMPLEX SUBUNIT 6)./1.0:20:55//ZEA MAYS (MAIZE)//P19445

55

F-HEMBA1002624//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)./0.0035:124:33//NICOTIANA TABACUM (COMMON TOBACCO)//P13983

F-HEMBA1002628

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5 F-HEMBA1002629//IMMEDIATE-EARLY PROTEIN IE180.//0.84:80:36//PSEUDORABIES
VIRUS (STRAIN KAPLAN) (PRV).//P33479

10 F-HEMBA1002645//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.8e-16:57:68//HOMO
SAPIENS (HUMAN).//P39193

15 F-HEMBA1002651

F-HEMBA1002659//CUTICLE COLLAGEN 2.//0.0077:77:38//CAENORHABDITIS
ELEGANS.//P17656

20 F-HEMBA1002661//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.3e-89:116:72//HOMO
SAPIENS (HUMAN).//P08547

25 F-HEMBA1002666//BETA CRYSTALLIN A4.//0.18:58:44//GALLUS GALLUS (CHICKEN)
.//P49152

F-HEMBA1002678

30 F-HEMBA1002679//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//5.7e-06:219:
27//PLASMODIUM FALCIPARUM (ISOLATE FC27 / PAPUA NEW GUINEA).//P13816

35 F-HEMBA1002688//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//1.1e-07:198:
32//NEPHILA CLAVIPES (ORB SPIDER).//P46804

F-HEMBA1002696//COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN
COLLAGEN) (LC COLLAGEN).//0.16:158:33//HOMO SAPIENS (HUMAN).//Q02388

40 F-HEMBA1002703//HYPOTHETICAL BHLF1 PROTEIN.//0.78:147:29//EPSTEIN-BARR VIRUS
(STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181

F-HEMBA1002712//11.2 KD PROTEIN (ORF 103).//0.029:75:34//BACTERIOPHAGE
PF1.//P25133

45 F-HEMBA1002716//50S RIBOSOMAL PROTEIN L28.//1.0:44:27//BACILLUS
SUBTILIS.//P37807

50 F-HEMBA1002728//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/5.4e-18:56:75//HOMO
SAPIENS (HUMAN).//P39195

55 F-HEMBA1002730//HYPOTHETICAL PROTEIN MJ0316.//0.097:84:35//METHANOCOCCUS
JANNASCHII.//Q57764

F-HEMBA1002742//APOLIPOPROTEIN C-III PRECURSOR (APO-CIII).//0.97:26:50//SUS
SCROFA (PIG).//P27917

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- 5 F-HEMBA1002746//CALPHOTIN.//0.35:65:35//DROSOPHILA MELANOGASTER (FRUIT FLY)
//Q02910
- 5 F-HEMBA1002748//PLATELET GLYCOPROTEIN IB BETA CHAIN PRECURSOR (GP-IB BETA)
(GPIBB).//1.0:74:32//MUS MUSCULUS (MOUSE).//P56400
- 10 F-HEMBA1002750/////ALU SUBFAMILY J WARNING ENTRY !!!!!//7.0e-15:49:75//HOMO
SAPIENS (HUMAN).//P39188
- 15 F-HEMBA1002768//HYPOTHETICAL 72.2 KD PROTEIN C12C2.05C IN CHROMOSOME
II.//0.00036:197:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09746
- 20 F-HEMBA1002770//UTEROGLOBIN PRECURSOR (BLASTOKININ).//023:88:
27//ORYCTOLAGUS CUNICULUS (RABBIT).//P02779
- 25 F-HEMBA1002777//HOMEBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3).//0.00018:67:43//MUS
MUSCULUS (MOUSE).//P06798
- 25 F-HEMBA1002779//HYPOTHETICAL 17.6 KD PROTEIN IN NPR1-RPS3 INTERGENIC
REGION.//0.70:30:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53880
- 30 F-HEMBA1002780//OLFACTORY RECEPTOR 3 (K10) (FRAGMENT).//1.0:31:45//MUS
MUSCULUS (MOUSE).//Q60879
- 35 F-HEMBA1002794//HMG-Y RELATED PROTEIN B (SB16B PROTEIN) (FRAGMENT).//0.0044:
66:37//GLYCINE MAX (SOYBEAN).//Q10370
- F-HEMBA1002801
- 40 F-HEMBA1002810//HYPOTHETICAL 25.9 KD PROTEIN AH6.3 IN CHROMOSOME II.//0.0033:
116:31//CAENORHABDITIS ELEGANS.//Q09202
- 45 F-HEMBA1002816//HYPOTHETICAL 47.1 KD PROTEIN C9G1.13C IN CHROMOSOME
I.//1.0e-17:68:48//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14308
- F-HEMBA1002818//FIBULIN-2 PRECURSOR.//2.1e-27:92:44//MUS MUSCULUS (MOUSE)
//P37889
- 50 F-HEMBA1002826//DNA-BINDING PROTEIN 65 (PROTEIN GP65).//0.28:46:
34//BACTERIOPHAGE T4.//P16012
- 55 F-HEMBA1002833
- F-HEMBA1002850//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:27:37//METRIDIDIUM
SENILE (BROWN SEA ANEMONE) (FRILLED SEA ANEMONE).//O47493

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5 F-HEMBA1002863//PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV (PHOTOSYSTEM I
8.1 KD PROTEIN) (P30 PROTEIN) (PSI-E)//0.84:37:43//SYNECHOCYSTIS SP. (STRAIN PCC
6803)//P12975

10 F-HEMBA1002876//OCTAPEPTIDE-REPEAT PROTEIN T2//0.74:58:34//MUS MUSCULUS
(MOUSE)//Q06666

F-HEMBA1002886

15 F-HEMBA1002896//HOMEODOMAIN PROTEIN HOX-B3 (HOX-2G) (HOX-2.7)//4.7e-05:84:
35//HOMO SAPIENS (HUMAN)//P14651

20 F-HEMBA1002921//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN)//0.21:42:
42//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RF/HAT ISOLATE) (HIV-1)//P05908

F-HEMBA1002924//EC PROTEIN HOMOLOG 2 (FRAGMENT)//0.85:75:22//ARABIDOPSIS
THALIANA (MOUSE-EAR CRESS)//Q42377

25 F-HEMBA1002934//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.4e-31:92:72//HOMO
SAPIENS (HUMAN)//P39188

30 F-HEMBA1002935//GASTRULA ZINC FINGER PROTEIN XLCGF58.1 (FRAGMENT)//7.7e-06:
187:29//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P18730

F-HEMBA1002937//SUPPRESSOR PROTEIN SRP40//0.00031:150:24//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST)//P32583

35 F-HEMBA1002939//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN)//5.2e-
25:225:33//HOMO SAPIENS (HUMAN)//P16157

40 F-HEMBA1002944

F-HEMBA1002951//TRICHOHYALIN//0.0011:220:24//HOMO SAPIENS (HUMAN)//Q07283

45 F-HEMBA1002954//PROBABLE E8 PROTEIN//0.98:49:32//BOVINE PAPILLOMAVIRUS TYPE
4//P08352

50 F-HEMBA1002968//ACCESSORY GLAND PEPTIDE PRECURSOR (PARAGONIAL PEPTIDE
B)//0.93:41:34//DROSOPHILA SECHELLIA (FRUIT FLY)//O18417

55 F-HEMBA1002970//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/0.00010:35:62//HOMO
SAPIENS (HUMAN)//P39193

F-HEMBA1002971//INSULIN//1.0:31:35//HYDROLAGUS COLLIEI (SPOTTED RATFISH)
(PACIFIC RATFISH), AND CHIMAERA MONSTROSA (RABBIT FISH)//P09536 F-

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HEMBA1002973//CAMP-DEPENDENT 3',5'-CYCLIC PHOSPHODIESTERASE 4B (EC 3.1.4.17)
(DPDE4).//3.0e-29:63:100//RATTUS NORVEGICUS (RAT).//P14646

5 F-HEMBA1002997//HYPOTHETICAL 106.5 KD PROTEIN IN CTT1-PRP31 INTERGENIC
REGION.//1.0e-08:211:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53253

10 F-HEMBA1002999//SUPPRESSOR PROTEIN SRP40.//0.026:175:23//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST).//P32583

15 F-HEMBA1003021//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.3e-36:102:70//HOMO
SAPIENS (HUMAN).//P39194

F-HEMBA1003033//HYPOTHETICAL 23.1 KD PROTEIN CY277.20C.//0.029:75:
29//MYCOBACTERIUM TUBERCULOSIS.//P71779

20 F-HEMBA1003034//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//6.3e-23:144:46//HOMO
SAPIENS (HUMAN).//P39192

25 F-HEMBA1003035//HYPOTHETICAL 13.3 KD PROTEIN IN AROD-COMER INTERGENIC
REGION.//0.99:55:30//BACILLUS SUBTILIS.//P54457

30 F-HEMBA1003037//DNA-BINDING PROTEIN INHIBITOR ID-4.//0.17:42:40//HOMO SAPIENS
(HUMAN).//P47928

F-HEMBA1003041//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)
.//0.69:28:46//HOMO SAPIENS (HUMAN).//P30808

35 F-HEMBA1003046//MITOCHONDRIAL PROCESSING PROTEASE BETA SUBUNIT
PRECURSOR (EC 3.4.24.64) (BETA-MPP) (P-52).//7.9e-124:253:96//HOMO SAPIENS
(HUMAN).//O75439

40 F-HEMBA1003064//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3).//0.25:
263:22//TRYPANOSOMA BRUCEI BRUCEI.//P04540

45 F-HEMBA1003067//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC
REGION.//4.1e-05:189:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214

50 F-HEMBA1003071//CUTICLE COLLAGEN 40.//6.0e-07:126:38//CAENORHABDITIS
ELEGANS.//P34804

F-HEMBA1003077//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD
PROTEIN).//2.4e-12:139:34//HOMO SAPIENS (HUMAN).//Q06828

55 F-HEMBA1003078//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE
TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//7.2e-05:60:40//MUS MUSCULUS
(MOUSE).//P11369

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F-HEMBA1003079//PROTEIN Q300.//0.0012:16:87//MUS MUSCULUS (MOUSE).//Q02722

5 F-HEMBA1003083//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//3.3e-32:95:75//HOMO SAPIENS (HUMAN).//P39189

F-HEMBA1003086

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F-HEMBA1003096//PROTAMINE IA (IRIDINE IA).//0.36:20:40//SALMO IRIDEUS (RAINBOW TROUT).//P02328

15 F-HEMBA1003098//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.4e-09:43:72//HOMO SAPIENS (HUMAN).//P39188

20 F-HEMBA1003117//PUTATIVE CUTICLE COLLAGEN C09G5.5.//1.0:88:38//CAENORHABDITIS ELEGANS.//Q09456

F-HEMBA1003129//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.61:63:25//APIS MELLIFERA (HONEYBEE).//P34859

25

F-HEMBA1003133//COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGEN) (FRAGMENT).//0.48:79:37//HOMO SAPIENS (HUMAN).//P25067

30 F-HEMBA1003136//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//3.6e-25:190:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41940

35

F-HEMBA1003142

40 F-HEMBA1003148//HYPOTHETICAL 56.4 KD PROTEIN IN RPL30-CWH41 INTERGENIC REGION PRECURSOR.//0.068:171:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53189

45 F-HEMBA1003166//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.8e-13:54:66//HOMO SAPIENS (HUMAN).//P39192

F-HEMBA1003175//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.015:147:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214

50

F-HEMBA1003179//PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANSFERASE (EC 2.1.1.61).//2.6e-51:164:47//BACILLUS SUBTILIS.//O35020

55

F-HEMBA1003197

F-HEMBA1003199//HOMEBOX PROTEIN HOX-A4 (HOX-1D) (HOX-1.4).//0.00049:83:

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38//HOMO SAPIENS (HUMAN).//Q00056

5 F-HEMBA1003202//SPERM PROTAMINE P1.//0.98:53:28//PLANIGALE GILESI (FLAT-SKULLED MARSUPIAL MOUSE).//O18747

10 F-HEMBA1003204//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//5.2e-22:42:80//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1003212//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.6e-18:74:71//HOMO SAPIENS (HUMAN).//P39193

15 F-HEMBA1003220//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.3e-18:56:78//HOMO SAPIENS (HUMAN).//P39194

20 F-HEMBA1003222//HYPOTHETICAL 37.5 KD PROTEIN IN GNTR-HTPG INTERGENIC REGION.//0.0018:159:27//BACILLUS SUBTILIS.//P46327

25 F-HEMBA1003229//DIHYDRODIPICOLINATE SYNTHASE 1 PRECURSOR (EC 4.2.1.52) (DHDPS).//1.0:85:28//TRITICUM AESTIVUM (WHEAT).//P24846

F-HEMBA1003235//TROPOMYOSIN.//8.3e-07:109:33//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q02088

30 F-HEMBA1003250

F-HEMBA1003257//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//1.5e-07:27:74//OWENIA FUSIFORMIS.//P21260

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F-HEMBA1003273

F-HEMBA1003276

40

F-HEMBA1003278

45 F-HEMBA1003281//HOMEBOX PROTEIN HOX-A4 (CHOX-1.4).//0.0053:116:36//GALLUS GALLUS (CHICKEN).//P17277

50 F-HEMBA1003286//DNA-DIRECTED RNA POLYMERASE SUBUNIT N (EC 2.7.7.6).//0.96:37:35//SULFOLOBUS ACIDOCALDARIUS.//P39472

F-HEMBA1003291//5'-AMP-ACTIVATED PROTEIN KINASE, CATALYTIC ALPHA-2 CHAIN (EC 2.7.1.-) (AMPK ALPHA-2 CHAIN) (FRAGMENT).//3.3e-15:68:39//SUS SCROFA (PIG).//Q28948

55 F-HEMBA1003296//PULMONARY SURFACTANT-ASSOCIATED PROTEIN B (SP-B) (6 KD PROTEIN) (PULMONARY SURFACTANT-ASSOCIATED PROTEOLIPID SPL(PHE)).//0.98:49:28//BOS TAURUS (BOVINE).//P15781

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5 F-HEMBA1003304//MITOCHONDRIAL RIBOSOMAL PROTEIN S19.//0.99:36:
30//PROTOHECA WICKERHAMII.//P46750

10 F-HEMBA1003309//HYPOTHETICAL 7.9 KD PROTEIN.//0.69:54:37//VACCINIA VIRUS
(STRAIN WR), AND VACCINIA VIRUS (STRAIN COPENHAGEN).//P04306

15 F-HEMBA1003314//MIXED LINEAGE KINASE 2 (EC 2.7.1.-) (FRAGMENT).//2.3e-06:143:
22//HOMO SAPIENS (HUMAN).//Q02779

15 F-HEMBA1003322//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!1.5e-30:53:77//HOMO
SAPIENS (HUMAN).//P39194

F-HEMBA1003327

20 F-HEMBA1003328//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN)
(FRAGMENT).//0.53:21:42//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BH5 ISOLATE) (HIV-
1).//P04612

25 F-HEMBA1003330//LONG NEUROTOXIN 3 (TOXIN VN2).//1.0:26:34//DENDROASPIS
POLYLEPIS POLYLEPIS (BLACK MAMBA).//P25667

30 F-HEMBA1003348//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!6.5e-09:56:66//HOMO
SAPIENS (HUMAN).//P39194

35 F-HEMBA1003369//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG
PRECURSOR.//0.0042:97:36//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P40602

40 F-HEMBA1003370//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!7.0e-18:99:53//HOMO
SAPIENS (HUMAN).//P39188

45 F-HEMBA1003373

45 F-HEMBA1003376//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!4.7e-16:60:75//HOMO
SAPIENS (HUMAN).//P39189

50 F-HEMBA1003380//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!2.8e-10:50:68//HOMO
SAPIENS (HUMAN).//P39188

55 F-HEMBA1003384

F-HEMBA1003395//PROBABLE E5 PROTEIN.//0.62:64:29//HUMAN PAPILLOMAVIRUS TYPE
16.//P06927

F-HEMBA1003402//HYPOTHETICAL 12.0 KD PROTEIN IN TUB1-CPR3 INTERGENIC
REGION PRECURSOR.//0.89:74:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)

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./Q04521

- 5 F-HEMBA1003403//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25)
(FRAGMENT).//0.0010:69:33//RATTUS NORVEGICUS (RAT).//P10164
- 10 F-HEMBA1003408//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31).//4.8e-06:93:
25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38968
- 15 F-HEMBA1003417//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS:
CHONDROCALCIN].//0.0021:140:34//MUS MUSCULUS (MOUSE).//P28481
- 20 F-HEMBA1003418//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING
FACTOR SRP75).//1.7e-14:188:33//HOMO SAPIENS (HUMAN).//Q08170
- 25 F-HEMBA1003433//DNA REPAIR PROTEIN XRS2.//1.0:88:35//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST).//P33301
- 30 F-HEMBA1003447//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25)
(FRAGMENT).//0.0061:69:33//RATTUS NORVEGICUS (RAT).//P10164
- 35 F-HEMBA1003461//SPIDROIN 1 (DRAGLINE SILK FIBROIN 1) (FRAGMENT).//2.3e-09:239:
33//NEPHILA CLAVIPES (ORB SPIDER).//P19837
- 40 F-HEMBA1003463//METALLOTHIONEIN-A (MTA) (FRAGMENT).//1.0:40:
35//SPHAERECHINUS GRANULARIS (PURPLE SEA URCHIN).//Q26497
- 45 F-HEMBA1003480//FUSARIC ACID RESISTANCE PROTEIN FUSB.//0.0043:96:
32//BURKHOLDERIA CEPACIA (PSEUDOMONAS CEPACIA).//P24127.
- 50 F-HEMBA1003528//36.4 KD PROLINE-RICH PROTEIN.//6.4e-15:167:33//LYCOPERSICON
ESCULENTUM (TOMATO).//Q00451
- 55 F-HEMBA1003531//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.2e-18:56:78//HOMO
SAPIENS (HUMAN).//P39189
- F-HEMBA1003538//COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41).//2.5e-
28:136:47//HOMO SAPIENS (HUMAN).//P00736
- F-HEMBA1003545//INSULIN GENE ENHANCER PROTEIN ISL-2 (ISLET-2).//9.2e-105:217:
85//RATTUS NORVEGICUS (RAT).//P50480
- F-HEMBA1003548
- F-HEMBA1003555//HYPOTHETICAL 31.9 KD PROTEIN IN BET1-PAN1 INTERGENIC
REGION.//8.7e-57:180:55//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40558

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F-HEMBA1003556//HYPOTHETICAL 19.2 KD PROTEIN IN COX-REP INTERGENIC REGION (ORF5) (ORF21).//0.53:97:25//BACTERIOPHAGE HP1.//P51706

5 F-HEMBA1003560//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-2 SUBUNIT (G GAMMA-I).//1.8e-32:71:100//BOS TAURUS (BOVINE).//P16874

10 F-HEMBA1003568//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN).//4.1e-19:126:31//HOMO SAPIENS (HUMAN).//P14373

15 F-HEMBA1003569//METASTASIS-ASSOCIATED PROTEIN MTA1.//3.9e-83:143:74//HOMO SAPIENS (HUMAN).//Q13330

F-HEMBA1003571//HYPOTHETICAL 8.7 KD PROTEIN (READING FRAME D).//1.0:64:25//STAPHYLOCOCCUS AUREUS.//P03860

20 F-HEMBA1003579//CYTOTOXIN 1 (CYTOTOXIN V-II-1) (TOXIN V(II)1).//1.0:41:29//NAJA MELANOLEUCA (FOREST COBRA) (BLACK-LIPPED COBRA).//P01448

25 F-HEMBA1003581//TALIN.//3.7e-36:52:98//MUS MUSCULUS (MOUSE).//P26039

F-HEMBA1003591//CHLOROPLAST 28 KD RIBONUCLEOPROTEIN PRECURSOR (28RNP).//1.6e-05:91:31//NICOTIANA SYLVESTRIS (WOOD TOBACCO).//P19682

30 F-HEMBA1003595//HYPOTHETICAL 12.0 KD PROTEIN IN DST1-HEM2 INTERGENIC REGION.//1.0:55:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53182

35 F-HEMBA1003597

F-HEMBA1003598//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).//4.9e-10:85:41//ORYCTOLAGUS CUNICULUS (RABBIT).//P06333

40 F-HEMBA1003615//PUTATIVE MINOR COAT PROTEIN (ORF43).//0.086:10:70//BACTERIOPHAGE PHI-LF.//Q07482

45 F-HEMBA1003617//HYPOTHETICAL 36.8 KD PROTEIN C26A3.16 IN CHROMOSOME I.//4.4e-13:58:48//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10169

50 F-HEMBA1003621//LONG NEUROTOXIN 1 (NEUROTOXIN A).//0.096:40:37//OPHIOPHAGUS HANNAH (KING COBRA) (NAJA HANNAH).//P01387

F-HEMBA1003622

55 F-HEMBA1003630

F-HEMBA1003637//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.4e-13:47:74//HOMO SAPIENS (HUMAN).//P39188

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5 F-HEMBA1003640!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/0.87:25:64//HOMO
SAPIENS (HUMAN).//P39193

10 F-HEMBA1003645//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN
C14B1.4 IN CHROMOSOME III.//1.8e-10:157:26//CAENORHABDITIS ELEGANS.//Q17963

15 F-HEMBA1003646//SERINE-ARGININE PROTEIN 55 (SRP55) (ENHANCER OF DEFORMED)
(52-KD BRACKETING PROTEIN) (B52 PROTEIN).//4.9e-05:207:27//DROSOPHILA
MELANOGASTER (FRUIT FLY).//P26686

20 F-HEMBA1003656

25 F-HEMBA1003662//PROLINE-RICH PEPTIDE P-B.//0.57:17:52//HOMO SAPIENS (HUMAN)
./P02814

30 F-HEMBA1003667!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/6.0e-16:43:72//HOMO
SAPIENS (HUMAN).//P39194

35 F-HEMBA1003679

40 F-HEMBA1003680//PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III (EC 3.4.11.-)
./3.9e-08:137:27//CAENORHABDITIS ELEGANS.//P34629

45 F-HEMBA1003684//ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR
PROMOTER BINDING PROTEIN) (LP-1) (ZINC FINGER PROTEIN Z13).//2.1e-20:127:40//MUS
MUSCULUS (MOUSE).//Q60821

50 F-HEMBA1003690//HYPOTHETICAL PROTEIN KIAA0288 (HA6116).//3.0e-85:201:78//HOMO
SAPIENS (HUMAN).//P56524

55 F-HEMBA1003692//CELL DIVISION CONTROL PROTEIN 1.//0.13:69:30//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST).//P40986

F-HEMBA1003711//CARCINOEMBRYONIC ANTIGEN PRECURSOR (CEA) (MECONIUM
ANTIGEN 100) (CD66E ANTIGEN).//0.021:153:26//HOMO SAPIENS (HUMAN).//P06731

F-HEMBA1003714//ABAECIN.//0.99:34:32//BOMBUS PASCUORUM.//P81463

50 F-HEMBA1003715

55 F-HEMBA1003720//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.4e-34:155:56//HOMO
SAPIENS (HUMAN).//P08547

F-HEMBA1003725//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.3e-27:181:41//HOMO
SAPIENS (HUMAN).//P08547

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- F-HEMBA1003729//PTB-ASSOCIATED SPLICING FACTOR (PSF)//0.0037:103:33//HOMO
SAPIENS (HUMAN)//P23246
- 5 F-HEMBA1003733//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//5.0e-54:210:58//HOMO
SAPIENS (HUMAN)//P08547
- 10 F-HEMBA1003742//MALE SPECIFIC SPERM PROTEIN MST84DB//0.066:72:
33//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01643
- F-HEMBA1003758
- 15 F-HEMBA1003760//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT
INTERACTING PROTEIN)//1.5e-51:220:52//MUS MUSCULUS (MOUSE)//Q61221
- 20 F-HEMBA1003773
- F-HEMBA1003783
- 25 F-HEMBA1003784
- F-HEMBA1003799//SHORT NEUROTOXIN 1 (TOXIN AA C)//0.95:27:37//ACANTHOPHIS
ANTARCTICUS (COMMON DEATH ADDER)//P01434
- 30 F-HEMBA1003803//GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12,
P30]//0.46:96:34//FELINE SARCOMA VIRUS (STRAIN SNYDER-THEILEN)//P03338
- 35 F-HEMBA1003804//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)
//0.019:30:50//HOMO SAPIENS (HUMAN)//P30808
- F-HEMBA1003805//HYPOTHETICAL 75.0 KD PROTEIN B0280.11 IN CHROMOSOME
40 III//1.8e-20:109:47//CAENORHABDITIS ELEGANS//P42083
- F-HEMBA1003807
- 45 F-HEMBA1003827//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT)//2.1e-09:23:
78//OWENIA FUSIFORMIS//P21260
- F-HEMBA1003836//MOB1 PROTEIN (MPS1 BINDER 1)//2.0e-31:134:52//SACCHAROMYCES
50 CEREVISIAE (BAKER'S YEAST)//P40484
- F-HEMBA1003838//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.9e-22:39:76//HOMO
SAPIENS (HUMAN)//P39192
- 55 F-HEMBA1003856

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F-HEMBA1003864//HYPOTHETICAL 39.4 KD PROTEIN IN MET1-SIS2 INTERGENIC REGION.//1.5e-15:194:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36151

5 F-HEMBA1003866//PROTEIN A39.//0.0027:72:33//VACCINIA VIRUS (STRAIN COPENHAGEN).//P21062

10 F-HEMBA1003879//80 KD NUCLEAR CAP BINDING PROTEIN (NCBP 80 KD SUBUNIT) (CBP80).//2.9e-16:22:100//HOMO SAPIENS (HUMAN).//Q09161

15 F-HEMBA1003880//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.99:39:38//FELIS SILVESTRIUS CATUS (CAT).//P48896

F-HEMBA1003885//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//3.5e-28:47:76//HOMO SAPIENS (HUMAN).//P39193

20 F-HEMBA1003893//HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//1.7e-57:215:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53215

25 F-HEMBA1003902

F-HEMBA1003908

30 F-HEMBA1003926//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.3e-10:60:63//HOMO SAPIENS (HUMAN).//P39188

35 F-HEMBA1003937//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//8.1e-29:68:64//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1003939//PROTEIN Q300.//0.0025:24:62//MUS MUSCULUS (MOUSE).//Q02722

40 F-HEMBA1003942//EXCITATORY INSECT TOXIN BJXTR-IT PRECURSOR (BJ-XTRIT).//0.084:67:31//BUTHOTUS JUDAICUS (SCORPION) (HOTTENTOTTA JUDAICA).//P56637

45 F-HEMBA1003950//HYPOTHETICAL 8.1 KD PROTEIN IN SPEA-METK INTERGENIC REGION (O71).//0.95:26:34//ESCHERICHIA COLI.//P46878

F-HEMBA1003953//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//2.5e-17:89:46//MUS MUSCULUS (MOUSE).//P16372

50 F-HEMBA1003958//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.2e-23:43:76//HOMO SAPIENS (HUMAN).//P08547

55 F-HEMBA1003959

F-HEMBA1003976//HYPOTHETICAL PROTEIN KIAA0076 (HA0936).//0.99:88:28//HOMO SAPIENS (HUMAN).//Q14999

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- 5 F-HEMBA1003978//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)//0.98:19:57//HOMO SAPIENS (HUMAN)//P22531
- 5 F-HEMBA1003985//LYSYL-TRNA SYNTHETASE (EC 6.1.1.6) (LYSINE-TRNA LIGASE) (LYSRS) (FRAGMENT)//1.0:40:32//MYCOBACTERIUM LEPRAE//P46861
- 10 F-HEMBA1003987//HYPOTHETICAL PROTEIN UL66//0.27:65:33//HUMAN CYTOMEGALOVIRUS (STRAIN AD169)//P16822
- 15 F-HEMBA1003989//MALE SPECIFIC SPERM PROTEIN MST84DB//5.2e-05:64:40//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01643
- F-HEMBA1004000//PROTEIN Q300//0.00042:17:82//MUS MUSCULUS (MOUSE)//Q02722
- 20 F-HEMBA1004011//ALPHA-TYPE CALCITONIN GENE-RELATED PEPTIDE PRECURSOR (CGRP-1)//0.47:106:32//HOMO SAPIENS (HUMAN)//P06881
- 25 F-HEMBA1004012//ATP SYNTHASE PROTEIN 9, MITOCHONDRIAL (EC 3.6.1.34) (LIPID-BINDING PROTEIN)//0.96:36:33//PARAMECIUM TETRAURELIA//P16001
- 30 F-HEMBA1004015//HYPOTHETICAL 29.3 KD PROTEIN B0280.6 IN CHROMOSOME III//0.00018:90:34//CAENORHABDITIS ELEGANS//P41997
- F-HEMBA1004024//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/5.1e-34:75:80//HOMO SAPIENS (HUMAN)//P39194
- 35 F-HEMBA1004038
- F-HEMBA1004042
- 40 F-HEMBA1004045//40S RIBOSOMAL PROTEIN S27A//1.0:20:55//ASPARAGUS OFFICINALIS (GARDEN ASPARAGUS)//P31753
- 45 F-HEMBA1004048//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//1.3e-06:158:35//MUS MUSCULUS (MOUSE)//P05143
- 50 F-HEMBA1004049//32 KD HEAT SHOCK PROTEIN (4-1 PROTEIN)//0.098:106:32//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)//P54658
- F-HEMBA1004055//HYPOTHETICAL PROTEIN HI0258/259//0.87:133:23//HAEMOPHILUS INFLUENZAE//P43974
- 55 F-HEMBA1004056//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/3.3e-25:39:64//HOMO SAPIENS (HUMAN)//P39191

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F-HEMBA1004074//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/9.9e-08:35:68//HOMO SAPIENS (HUMAN).//P39188

5 F-HEMBA1004086

F-HEMBA1004097//IMMEDIATE-EARLY PROTEIN IE4 (IE68) (FRAGMENT)//0.71:95:35//HERPES SIMPLEX VIRUS (TYPE 2).//P14379

10

F-HEMBA1004111//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.7e-26:84:64//HOMO SAPIENS (HUMAN).//P39188

15 F-HEMBA1004131//SEPTIN 2 HOMOLOG (FRAGMENT).//2.8e-34:108:63//HOMO SAPIENS (HUMAN).//Q14141

20 F-HEMBA1004132//HYPOTHETICAL PROTEIN HI1736.//1.0:44:34//HAEMOPHILUS INFLUENZAE.//P44300

25 F-HEMBA1004133//HYPOTHETICAL 8.5 KD PROTEIN CY274.40C.//0.89:21:57//MYCOBACTERIUM TUBERCULOSIS.//Q10826

F-HEMBA1004138//EARLY NODULIN 75 (N-75) (NGM-75) (FRAGMENT).//0.016:39:41//MEDICAGO SATIVA (ALFALFA).//P11728

30 F-HEMBA1004143//CYTOCHROME C OXIDASE POLYPEPTIDE VIII PRECURSOR (EC 1.9.3.1).//0.93:34:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P04039

35 F-HEMBA1004146//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.63:52:36//HOMO SAPIENS (HUMAN).//P02811

40 F-HEMBA1004150//METALLOTHIONEIN-II (MT-II).//1.0:20:45//MUS MUSCULUS (MOUSE).//P02798

F-HEMBA1004164//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/3.0e-13:57:71//HOMO SAPIENS (HUMAN).//P39195

45 F-HEMBA1004168//V-TYPE SODIUM ATP SYNTHASE SUBUNIT F (EC 3.6.1.34) (NA(+)-TRANSLOCATING ATPASE SUBUNIT F).//0.00035:90:34//ENTEROCOCCUS HIRAE.//P43437

50 F-HEMBA1004199//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III.//5.1e-14:115:31//CAENORHABDITIS ELEGANS.//P34529

F-HEMBA1004200

55 F-HEMBA1004202//YPT1-RELATED PROTEIN 1.//2.5e-24:96:52//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P11620

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F-HEMBA1004203//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/2.2e-09:48:64//HOMO SAPIENS (HUMAN)//P39193

5 F-HEMBA1004207//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGENIC REGION (ORF70)//0.98:51:33//ASTASIA LONGA (EUGLENOPHYCEAN ALGA)//P34779

10 F-HEMBA1004225//METALLOTHIONEIN-II//1.0:30:33//CANDIDA GLABRATA (YEAST) (TORULOPSIS GLABRATA)//P15114

15 F-HEMBA1004227//PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015)//5.9e-06:109:33//HOMO SAPIENS (HUMAN)//P49593

F-HEMBA1004238//VERY HYPOTHETICAL XYLU PROTEIN//0.98:39:38//ESCHERICHIA COLI//P05056

20 F-HEMBA1004241//SOX-13 PROTEIN (FRAGMENT)//0.66:36:38//MUS MUSCULUS (MOUSE) //Q04891

25 F-HEMBA1004246

F-HEMBA1004248//INSULIN-INDUCED GROWTH RESPONSE PROTEIN CL-6 (IMMEDIATE-EARLY PROTEIN CL-6)//1.0e-43:98:84//RATTUS NORVEGICUS (RAT)//Q08755

30 F-HEMBA1004264//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT)//0.014:160:28//NEPHILA CLAVIPES (ORB SPIDER)//P46804

35 F-HEMBA1004267//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.8e-52:56:83//HOMO SAPIENS (HUMAN)//P39189

F-HEMBA1004272

40 F-HEMBA1004274//HYPOTHETICAL 13.0 KD PROTEIN F59B2.10 IN CHROMOSOME III//0.00084:33:54//CAENORHABDITIS ELEGANS//P34485

45 F-HEMBA1004275//HYPOTHETICAL 56.5 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION//9.3e-06:125:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40034

50 F-HEMBA1004276//BETA-ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105A)//3.7e-30:239:32//HOMO SAPIENS (HUMAN)//Q10567

55 F-HEMBA1004286//CUTICLE COLLAGEN 34//0.0027:71:38//CAENORHABDITIS ELEGANS//P34687

F-HEMBA1004289//PTR3 PROTEIN (SSY3 PROTEIN)//1.0:76:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P43606

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- 5 F-HEMBA1004295//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)
./0.075:58:39//HOMO SAPIENS (HUMAN).//P30808
- F-HEMBA1004306//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.020:132:30//ORGYIA
PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10341
- 10 F-HEMBA1004312//EARLY PROTEIN I73R.//0.99:65:32//AFRICAN SWINE FEVER VIRUS
(STRAIN BA71V) (ASFV).//P27946
- 15 F-HEMBA1004321//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10)
./4.3e-43:133:44//MUS MUSCULUS (MOUSE).//Q61967
- F-HEMBA1004323
- 20 F-HEMBA1004327//SMALL PROLINE-RICH PROTEIN 2-1.//0.027:48:43//HOMO SAPIENS
(HUMAN).//P35326
- 25 F-HEMBA1004330//HOMEBOX PROTEIN ENGRAILED-1 (HU-EN-1).//0.46:70:34//HOMO
SAPIENS (HUMAN).//Q05925
- F-HEMBA1004334//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.7e-05:83:34//HOMO
30 SAPIENS (HUMAN).//P08547
- F-HEMBA1004335//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.0e-24:41:80//HOMO
SAPIENS (HUMAN).//P39195
- 35 F-HEMBA1004341//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//2.8e-06:148:35//MUS
MUSCULUS (MOUSE).//P05143
- 40 F-HEMBA1004353//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.2e-29:57:80//HOMO
SAPIENS (HUMAN).//P39195
- 45 F-HEMBA1004354//CHL1 PROTEIN.//0.017:40:40//SACCHAROMYCES CEREVISIAE
(BAKER'S YEAST).//P22516
- F-HEMBA1004356
- 50 F-HEMBA1004366//LINE-1. REVERSE TRANSCRIPTASE HOMOLOG.//0.00045:49:46//HOMO
SAPIENS (HUMAN).//P08547
- 55 F-HEMBA1004372//VERY HYPOTHETICAL 20.6 KD PROTEIN C56F8.15 IN CHROMOSOME
I.//1.0:125:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10263
- F-HEMBA1004389//HYPOTHETICAL 113.1 KD PROTEIN IN PRE5-FET4 INTERGENIC
REGION.//0.76:170:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04893

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- F-HEMBA1004394
- 5 F-HEMBA1004396//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.2e-10:72:51//HOMO SAPIENS (HUMAN).//P08547
- F-HEMBA1004405
- 10 F-HEMBA1004408//PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN-10).//2.7e-29:146:48//CAENORHABDITIS ELEGANS.//P52017
- 15 F-HEMBA1004429!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/0.0019:47:59//HOMO SAPIENS (HUMAN).//P39191
- 20 F-HEMBA1004433!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.1e-20:47:68//HOMO SAPIENS (HUMAN).//P39192
- F-HEMBA1004460!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/6.2e-64:134:69//HOMO SAPIENS (HUMAN).//P39193
- 25 F-HEMBA1004461//METALLOTHIONEIN-LIKE PROTEIN 1.//1.0:39:35//PISUM SATIVUM (GARDEN PEA).//P20830
- 30 F-HEMBA1004479//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN).//9.7e-43:101:48//MUS MUSCULUS (MOUSE).//Q61221
- 35 F-HEMBA1004482//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34).//1.0:41:36//CANDIDA GLABRATA (YEAST) (TORULOPSIS GLABRATA).//P05040
- F-HEMBA1004499//TUBULIN BETA CHAIN.//0.00021:55:36//CAENORHABDITIS ELEGANS.//P52275
- 40 F-HEMBA1004502
- 45 F-HEMBA1004506//HYPOTHETICAL PROTEIN ORF-1137.//5.3-11:119:35//MUS MUSCULUS (MOUSE).//P11260
- 50 F-HEMBA1004507//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//0.00072:90:37//HOMO SAPIENS (HUMAN).//Q15428
- F-HEMBA1004509//HYPOTHETICAL 52.2 KD PROTEIN IN MPR1-GCN20 INTERGENIC REGION.//6.3e-28:169:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43589
- 55 F-HEMBA1004534//ENDOTHELIAL ACTIN-BINDING PROTEIN (ABP-280) (NONMUSCLE FILAMIN) (FILAMIN 1).//1.3e-80:226:66//HOMO SAPIENS (HUMAN).//P21333

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F-HEMBA1004538//HYPOTHETICAL PROTEIN MJ0764.//0.96:28:35//METHANOCOCCUS JANNASCHII.//Q58174

5 F-HEMBA1004542//METALLOTHIONEIN (MT).//0.78:36:41//GADUS MORHUA (ATLANTIC COD).//P51902

F-HEMBA1004554

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F-HEMBA1004560//HYPOTHETICAL PROTEIN KIAA0281 (HA6725).//4.2e-15:56:69//HOMO SAPIENS (HUMAN).//Q92556

15 F-HEMBA1004573//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//0.65:31:58//PLASMODIUM BERGHEI.//P06915

20 F-HEMBA1004577//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/3.9e-08:35:80//HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1004586//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/6.6e-08:64:54//HOMO SAPIENS (HUMAN).//P39194

25

F-HEMBA1004596//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN C (HNRNP C) (HNRNP CORE PROTEIN C) (FRAGMENT).//0.00057:88:31//RATTUS NORVEGICUS (RAT).//P17132

30

F-HEMBA1004604//COLLAGEN ALPHA 2(XI) CHAIN PRECURSOR (FRAGMENT).//0.045:37:45//MUS MUSCULUS (MOUSE).//Q64739

35 F-HEMBA1004610//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.3e-11:73:54//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1004617

40

F-HEMBA1004629

45 F-HEMBA1004631//HYPOTHETICAL 7.8 KD PROTEIN IN WAPA-LICT INTERGENIC REGION.//1.0:36:38//BACILLUS SUBTILIS.//P42303

50 F-HEMBA1004632//PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING 8.0 KD POLYPEPTIDE).//0.86:48:35//SYNECHOCOCCUS ELONGATUS NAEGELI.//P20453

55 F-HEMBA1004637//HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III.//1.7e-32:159:42//CAENORHABDITIS ELEGANS.//P34535

F-HEMBA1004638//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//2.8e-06:50:46//OWENIA FUSIFORMIS.//P21260

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F-HEMBA1004666//TOXIN S6C4.//1.0:36:30//DENDROASPIS JAMESONI KAIMOSAE
 (EASTERN JAMESON'S MAMBA).//P25682
 5
 F-HEMBA1004669//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING
 FACTOR SRP75).//1.6e-12:105:42//HOMO SAPIENS (HUMAN).//Q08170
 10
 F-HEMBA1004670//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//2.5e-06:62:45//HOMO
 SAPIENS (HUMAN).//P02452
 15
 F-HEMBA1004672//HYPOTHETICAL PROTEIN MJ0437.//0.95:37:29//METHANOCOCCUS
 JANNASCHII.//Q57879
 F-HEMBA1004693//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN
 HEAVY CHAIN, TYPE B) (NMMHC-B).//0.00035:217:23//HOMO SAPIENS (HUMAN).//P35580
 20
 F-HEMBA1004697//IMMUNOGLOBULIN G BINDING PROTEIN H PRECURSOR (PROTEIN H)
 .//0.058:118:30//STREPTOCOCCUS PYOGENES.//P50470
 25
 F-HEMBA1004705///// ALU SUBFAMILY J WARNING ENTRY !!!!!/6.8e-09:43:72//HOMO
 SAPIENS (HUMAN).//P39188
 30
 F-HEMBA1004709///// ALU SUBFAMILY SB WARNING ENTRY !!!!!/8.8e-18:50:84//HOMO
 SAPIENS (HUMAN).//P39189
 F-HEMBA1004711//ETS-RELATED PROTEIN 71 (ETS TRANSLOCATION VARIANT 2)
 .//0.0027:148:30//HOMO SAPIENS (HUMAN).//000321
 35
 F-HEMBA1004725//CUTICLE COLLAGEN 2.//0.0051:41:41//CAENORHABDITIS
 ELEGANS.//P17656
 40
 F-HEMBA1004730//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.4e-22:210:37//HOMO
 SAPIENS (HUMAN).//P08547
 45
 F-HEMBA1004733///// ALU SUBFAMILY J WARNING ENTRY !!!!!/4.7e-07:50:62//HOMO
 SAPIENS (HUMAN).//P39188
 F-HEMBA1004734//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19)
 (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.9e-39:143:
 50
 52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P42743
 F-HEMBA1004736//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.1e-60:210:61//HOMO
 SAPIENS (HUMAN).//P08547
 55
 F-HEMBA1004748

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F-HEMBA1004751!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.8e-20:88:63//HOMO
SAPIENS (HUMAN).//P39188

5 F-HEMBA1004752//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
./0.0043:126:34//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437

10 F-HEMBA1004753!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/7.8e-28:47:78//HOMO
SAPIENS (HUMAN).//P39193

15 F-HEMBA1004756//HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC
REGION./0.22:77:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39981

F-HEMBA1004758

20 F-HEMBA1004763//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//1.1e-06:58:
43//OWENIA FUSIFORMIS.//P21260

25 F-HEMBA1004768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.7e-65:298:53//HOMO
SAPIENS (HUMAN).//P08547

F-HEMBA1004770

30 F-HEMBA1004771

F-HEMBA1004776//GRANULIN 1./0.78:28:42//CYPRINUS CARPIO (COMMON CARP)
./P81013

35 F-HEMBA1004778

40 F-HEMBA1004795//CDC4-LIKE PROTEIN (FRAGMENT).//6.9e-20:74:63//HOMO SAPIENS
(HUMAN).//P50851

F-HEMBA1004803//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.4e-22:58:86//HOMO
SAPIENS (HUMAN).//P08547

45 F-HEMBA1004806//HYPOTHETICAL 24.3 KD PROTEIN IN PSBH-RPL11 INTERGENIC
REGION (ORF182).//0.72:75:33//CYANOPHORA PARADOXA.//P48324

50 F-HEMBA1004807

F-HEMBA1004816

55 F-HEMBA1004820//HEMOLYMPH TRYPSIN INHIBITOR A (BPI-TYPE) (FRAGMENT).//1.0:50:
38//MANDUCA SEXTA (TOBACCO HAWKMOTH) (TOBACCO HORNWORM).//P26226

F-HEMBA1004847//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//3.0e-76:

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171:91//CANIS FAMILIARIS (DOG).//Q00004

5 F-HEMBA1004850//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//3.0e-05:64:43//BOS TAURUS (BOVINE).//P25508

10 F-HEMBA1004863//TOXIN C13S1C1 PRECURSOR.//0.38:52:30//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA).//P18329

15 F-HEMBA1004864//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).//0.89:24:50//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BH5 ISOLATE) (HIV-1).//P04612

F-HEMBA1004865

20 F-HEMBA1004880

F-HEMBA1004889//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.66:23:47//HOMO SAPIENS (HUMAN).//P22532

25 F-HEMBA1004900

F-HEMBA1004909

30 F-HEMBA1004918//CHLOROPLAST 30S RIBOSOMAL PROTEIN S8 (FRAGMENT).//0.56:37:32//SPINACIA OLERACEA (SPINACH).//P09597

35 F-HEMBA1004923//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//3,5e-24:44:68//HOMO SAPIENS (HUMAN).//P39188

40 F-HEMBA1004929//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.97:39:38//STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN).//P15997

F-HEMBA1004930//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.6e-15:64:59//HOMO SAPIENS (HUMAN).//P08547

45 F-HEMBA1004933//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//0.34:58:41//HOMO SAPIENS (HUMAN).//P50552

50 F-HEMBA1004934

F-HEMBA1004944

55 F-HEMBA1004954//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3).//0.58:78:30//PARAMECIUM TETRAURELIA.//P15579

F-HEMBA1004956//HYPOTHETICAL 18.8 KD PROTEIN (ORF4).//0.98:57:31//PARAMECIUM

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TETRAURELIA.//P15605

5 F-HEMBA1004960//HYPOTHETICAL 12.6 KD PROTEIN-(ORFJ) (RETRON EC67).//1.0:58:27//ESCHERICHIA COLI.//P21324

F-HEMBA1004972

10 F-HEMBA1004973//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.90:55:30//HOMO SAPIENS (HUMAN).//P22531

F-HEMBA1004977

15

F-HEMBA1004978

20 F-HEMBA1004980//MOTILIN PRECURSOR.//0.088:79:31//MACACA MULATTA (RHESUS MACAQUE).//018811

25 F-HEMBA1004983//10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES).//0.87:51:31//BUCHNERA APHIDICOLA.//Q59176

30 F-HEMBA1004995//MYOCYTE-SPECIFIC ENHANCER FACTOR 2B (SERUM RESPONSE FACTOR-LIKE PROTEIN 2) (XMEF2) (RSRFR2).//0.17:52:40//HOMO SAPIENS (HUMAN).//Q02080

F-HEMBA1005008//METALLOTHIONEIN (MT).//1.0:52:32//CRASSOSTREA VIRGINICA (EASTERN OYSTER).//P23038

35 F-HEMBA1005009//ACTIN.//3.5e-27:171:38//CANDIDA ALBICANS (YEAST).//P14235

40 F-HEMBA1005019//HYPOTHETICAL PROTEIN HI1222.//0.13:58:31//HAEMOPHILUS INFLUENZAE.//P44129

F-HEMBA1005029//P2Y PURINOCEPTOR 5 (P2Y5) (PURINERGIC RECEPTOR 5) (6H1).//0.76:72:31//GALLUS GALLUS (CHICKEN).//P32250

45 F-HEMBA1005035//HOMEBOX PROTEIN HB9.//0.0086:60:40//HOMO SAPIENS (HUMAN).//P50219

50 F-HEMBA1005039//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.47:49:32//HOMO SAPIENS (HUMAN).//P22532

55 F-HEMBA1005047//RAS-RELATED PROTEIN RAB-24 (RAB-16).//1.5e-19:39:100//MUS MUSCULUS (MOUSE).//P35290

F-HEMBA1005050//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.074:34:44//BOS TAURUS (BOVINE).//P25508

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F-HEMBA1005062

5 F-HEMBA1005066//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.1e-44:126:65//HOMO
SAPIENS (HUMAN).//P08547

10 F-HEMBA1005075//SUPPRESSOR PROTEIN SRP40.//0.35:96:31//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST).//P32583

15 F-HEMBA1005079//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//3.6e-20:75:64//HOMO
SAPIENS (HUMAN).//P39191

F-HEMBA1005083//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.00015:72:34//BOS
TAURUS (BOVINE).//P25508

20 F-HEMBA1005101//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN 27C (HNRNP
48) (HRP48.1).//4.8e-10:176:25//DROSOPHILA MELANOGASTER (FRUIT FLY).//P48809

25 F-HEMBA1005113

F-HEMBA1005123//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.6e-24:99:60//HOMO
SAPIENS (HUMAN).//P39194

30 F-HEMBA1005133//HYPOTHETICAL 13.5 KD PROTEIN IN MOB1-SGA1 INTERGENIC
REGION.//0.11:22:54//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40490

35 F-HEMBA1005149//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.7e-16:59:71//HOMO
SAPIENS (HUMAN).//P39188

40 F-HEMBA1005152//GENOME POLYPROTEIN 2 [CONTAINS: HELPER COMPONENT
PROTEINASE (EC 3.4.22.-) (HC-PRO); 70 KD PROTEIN].//1.0:77:27//BARLEY YELLOW
MOSAIC VIRUS (JAPANESE STRAIN II-1) (BAYMV).//Q01207

45 F-HEMBA1005159//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.40:
53:33//APIS MELLIFERA (HONEYBEE).//P34859

F-HEMBA1005185//MYOSIN IB HEAVY CHAIN.//0.011:58:48//DICTYOSTELIUM DISCOIDEUM
(SLIME MOLD).//P34092

50 F-HEMBA1005201//HYPOTHETICAL 56.6 KD PROTEIN C16C9.03 IN CHROMOSOME I.//3.9e-
67:241:53//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09817

55 F-HEMBA1005202//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//3.8e-124:
257:95//CANIS FAMILIARIS (DOG).//Q00004

F-HEMBA1005206//CUTICLE COLLAGEN 1.//0.010:118:33//CAENORHABDITIS

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ELEGANS.//P08124

- 5 F-HEMBA1005219//PTB-ASSOCIATED SPLICING FACTOR (PSF).//0.99:85:40//HOMO SAPIENS (HUMAN).//P23246
- 10 F-HEMBA1005223//HYPOTHETICAL GENE 1.05 PROTEIN.//0.31:75:28//BACTERIOPHAGE T3.//P07715
- 15 F-HEMBA1005232//HYPOTHETICAL 7.8 KD PROTEIN.//0.99:48:29//VACCINIA VIRUS (STRAIN WR), AND VACCINIA VIRUS (STRAIN COPENHAGEN).//P20544
- 20 F-HEMBA1005244//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.014:39:41//HOMO SAPIENS (HUMAN).//P22531
- 25 F-HEMBA1005251//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.55:15:46//DICENTRARCHUS LABRAX (EUROPEAN SEA BASS).//Q36362
- 30 F-HEMBA1005252//EC PROTEIN HOMOLOG (ZINC-METALLOTHIONEIN CLASS II).//0.088:33:42//ZEA MAYS (MAIZE).//P43401
- 35 F-HEMBA1005274
- 40 F-HEMBA1005275//ALU SUBFAMILY J WARNING ENTRY !!!!!//0.96:42:45//HOMO SAPIENS (HUMAN).//P39188
- 45 F-HEMBA1005293//PROBABLE COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP).//0.55:98:30//CAENORHABDITIS ELEGANS.//Q20168
- 50 F-HEMBA1005296//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//0.095:75:34//HOMO SAPIENS (HUMAN).//Q02817
- 55 F-HEMBA1005304//ALU SUBFAMILY SB WARNING ENTRY !!!!!//5.4e-33:103:74//HOMO SAPIENS (HUMAN).//P39189
- 60 F-HEMBA1005311//PERIOD CLOCK PROTEIN (FRAGMENT).//0.99:45:31//DROSOPHILA SALTANS (FRUIT FLY).//Q04536
- 65 F-HEMBA1005314//HYPOTHETICAL 6.3 KD PROTEIN T19C3.3 IN CHROMOSOME III.//0.98:30:30//CAENORHABDITIS ELEGANS.//Q10009
- 70 F-HEMBA1005315//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.1e-05:35:51//HOMO SAPIENS (HUMAN).//P08547

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- F-HEMBA1005318//OLFACTORY RECEPTOR-LIKE PROTEIN COR8 (FRAGMENT).//0.57:44:
38//GALLUS GALLUS (CHICKEN).//Q98913
- 5 F-HEMBA1005331//IMMEDIATE-EARLY PROTEIN IE180.//0.57:106:33//PSEUDORABIES
VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675
- 10 F-HEMBA1005338//CARTIAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).//1.8e-55:199:
59//GALLUS GALLUS (CHICKEN).//P05099
- 15 F-HEMBA1005353//CHLOROPLAST 30S RIBOSOMAL PROTEIN S17.//0.88:33:
36//PORPHYRA PURPUREA.//P51305
- F-HEMBA1005359//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.1e-68:
255:48//HOMO SAPIENS (HUMAN).//P51522
- 20 F-HEMBA1005367//ALPHA-AMYLASE INHIBITOR AAI.//1.0:25:40//AMARANTHUS
HYPOCHONDRIACUS (PRINCE'S FEATHER).//P80403
- 25 F-HEMBA1005372
- F-HEMBA1005374//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.0e-34:92:75//HOMO
SAPIENS (HUMAN).//P39194
- 30 F-HEMBA1005382//APOLIPOPROTEIN C-II (APO-CII).//0.99:39:33//BOS TAURUS (BOVINE)
//P19034
- 35 F-HEMBA1005389//HYPOTHETICAL 70.0 KD PROTEIN IN DNAK 3'REGION (ORF4).//0.82:
164:31//LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS).//P42377
- 40 F-HEMBA1005394//HYPOTHETICAL 8.9 KD PROTEIN IN IE0-IE1 INTERGENIC
REGION.//0.98:44:38//AUTOGRAPHIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS
(ACMNPV).//P41703
- 45 F-HEMBA1005403//SPERM HISTONE P2 PRECURSOR (PROTAMINE MP2).//0.066:64:
29//MUS MUSCULUS (MOUSE).//P07978
- F-HEMBA1005408//50S RIBOSOMAL PROTEIN L33.//0.77:32:25//BACILLUS
SUBTILIS.//Q06798
- 50 F-HEMBA1005410//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE
TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE]//0.0065:38:52//MUS MUSCULUS
(MOUSE).//P11369
- 55 F-HEMBA1005411//TOXIN S4C8.//0.16:46:28//DENDROASPIS JAMESONI KAIMOSAE
(EASTERN JAMESON'S MAMBA).//P25683

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F-HEMBA1005423//CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT KINASE 4 INHIBITOR C) (P18-INK4C).//4.3e-09:29:96//HOMO SAPIENS (HUMAN).//P42773

5 F-HEMBA1005426//TOXIN C10S2C2.//0.99:49:34//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA).//P25684

10 F-HEMBA1005443//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.9e-16:78:60//HOMO SAPIENS (HUMAN).//P39188

15 F-HEMBA1005447//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.99:57:31//DASYPUS NOVEBORACENSIS (NINE-BANDED ARMADILLO).//O21329

20 F-HEMBA1005468//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3) (FRAGMENTS).//0.68:41:31//ARTEMIA SALINA (BRINE SHRIMP).//P19040

25 F-HEMBA1005469

F-HEMBA1005472//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.5e-39:142:70//HOMO SAPIENS (HUMAN).//P08547

30 F-HEMBA1005474//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//5.8e-10:44:68//HOMO SAPIENS (HUMAN).//P39194

35 F-HEMBA1005475//U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD (U1 SNRNP 70 KD) (SNRNP70).//9.2e-14:179:33//HOMO SAPIENS (HUMAN).//P08621

40 F-HEMBA1005497

F-HEMBA1005500//60S RIBOSOMAL PROTEIN L37.//0.11:53:33//SCHISTOSOMA MANSONI (BLOOD FLUKE).//O44125

45 F-HEMBA1005506

F-HEMBA1005508

50 F-HEMBA1005511//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.5e-30:92:73//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1005513//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//2.0e-39:95:61//DROSOPHILA MELANOGASTER (FRUIT FLY).//O02193

55 F-HEMBA1005517//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//2.1e-06:56:44//MUS MUSCULUS (MOUSE).//P05142

F-HEMBA1005518//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//5.8e-05:192:33//BOS

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TAURUS (BOVINE).//P02453

5 F-HEMBA1005520///// ALU SUBFAMILY J WARNING ENTRY !!!!/2.0e-18:87:57//HOMO
SAPIENS (HUMAN).//P39188

10 F-HEMBA1005526///// ALU SUBFAMILY SB2 WARNING ENTRY !!!!/5.1e-22:77:54//HOMO
SAPIENS (HUMAN).//P39191

F-HEMBA1005528//CCR4-ASSOCIATED FACTOR 1 (CAF1).//1.2e-81:157:98//MUS
MUSCULUS (MOUSE).//Q60809

15 F-HEMBA1005530//POLLEN ALLERGEN AMB P 5-A PRECURSOR (AMB P V-A).//0.98:19:
47//AMBROSIA PSILOSTACHYA (WESTERN RAGWEED).//P43174

20 F-HEMBA1005548//TRANSCRIPTION FACTOR MAF1.//1.4e-72:137:97//RATTUS
NORVEGICUS (RAT).//P54842

25 F-HEMBA1005552///// ALU SUBFAMILY SP WARNING ENTRY !!!!/1.7e-29:47:78//HOMO
SAPIENS (HUMAN).//P39193

F-HEMBA1005558//HYPOTHETICAL 25.6 KD PROTEIN IN ABF2-CHL12 INTERGENIC
REGION.//1.6e-20:202:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04272

30 F-HEMBA1005568

35 F-HEMBA1005570//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 6 (EC 1.6.5.3).//1.0:80:
31//CAENORHABDITIS ELEGANS.//P24885

F-HEMBA1005576//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//8.5e-58:152:
75//HOMO SAPIENS (HUMAN).//P51805

40 F-HEMBA1005577//KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A.//0.98:57:36//OVIS
ARIES (SHEEP).//P02438

45 F-HEMBA1005581//SLIT PROTEIN PRECURSOR.//1.1e-62:254:41//DROSOPHILA
MELANOGASTER (FRUIT FLY).//P24014

50 F-HEMBA1005582//DYNACTIN, 150 KD ISOFORM (150 KD DYNEIN-ASSOCIATED
POLYPEPTIDE) (DP-150) (DAP-150) (P150-GLUED).//0.0091:189:29//RATTUS NORVEGICUS
(RAT).//P28023

55 F-HEMBA1005583//HYPOTHETICAL 41.2 KD PROTEIN IN CPS REGION (ORF7).//0.83:119:
23//KLEBSIELLA PNEUMONIAE.//Q48453

F-HEMBA1005588///// ALU SUBFAMILY J WARNING ENTRY !!!!/1.9e-17:108:53//HOMO
SAPIENS (HUMAN).//P39188

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F-HEMBA1005593//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N)//0.23:24:
54//HOMO SAPIENS (HUMAN)//P22532

5 F-HEMBA1005595//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC)//2.7e-39:257:
39//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)//P34036

10 F-HEMBA1005606

F-HEMBA1005609//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.2e-20:27:96//HOMO
SAPIENS (HUMAN)//P39192

15 F-HEMBA1005616//LATE CONTROL GENE B PROTEIN (GPB)//0.48:51:
33//BACTERIOPHAGE 186//P08711

20 F-HEMBA1005621//MITOTIC MAD2 PROTEIN//1.2e-06:137:32//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST)//P40958

25 F-HEMBA1005627//HYPOTHETICAL 17.1 KD PROTEIN IN PUBS 3'REGION//0.18:100:
32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38898

F-HEMBA1005631

30 F-HEMBA1005632//HYPOTHETICAL 7.4 KD PROTEIN//0.32:59:32//VACCINIA VIRUS
(STRAIN WR)//P04309

35 F-HEMBA1005634//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.6e-14:93:58//HOMO
SAPIENS (HUMAN)//P39188

F-HEMBA1005666//HYPOTHETICAL PROTEIN KIAA0129//2.1e-05:126:25//HOMO SAPIENS
(HUMAN)//Q14142

40 F-HEMBA1005670

45 F-HEMBA1005679//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//2.2e-08:40:72//HOMO
SAPIENS (HUMAN)//P08547

50 F-HEMBA1005680//SMALL PROLINE-RICH PROTEIN 2-1//0.015:19:47//HOMO SAPIENS
(HUMAN)//P35326

F-HEMBA1005685

55 F-HEMBA1005699//EPHRIN-B3 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE
KINASE LIGAND 8) (LERK-8) (EPH-RELATED RECEPTOR TRANSMEMBRANE LIGAND ELK-
L3)//4.2e-38:98:81//HOMO SAPIENS (HUMAN)//Q15768

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F-HEMBA1005705//PROTEIN Q300.//0.11:23:56//MUS MUSCULUS (MOUSE).//Q02722

F-HEMBA1005717

5

F-HEMBA1005732//BACTENECIN 7 PRECURSOR (BAC7).//0.22:55:41//OVIS ARIES (SHEEP)
./P50415

10

F-HEMBA1005737//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B
REGULATORY SUBUNIT).//4.5e-18:167:34//SACCHAROMYCES CEREVISIAE (BAKER'S
YEAST).//P25296

15

F-HEMBA1005746

F-HEMBA1005755//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.4e-30:69:65//HOMO
SAPIENS (HUMAN).//P08547

20

F-HEMBA1005765//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.8e-19:60:63//HOMO
SAPIENS (HUMAN).//P39194

25

F-HEMBA1005780//METALLOTHIONEIN-I (MT-1).//1.0:31:38//COLUMBA LIVIA (DOMESTIC
PIGEON).//P15786

F-HEMBA1005813

30

F-HEMBA1005815//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-
ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU/M-TYPE).//1.0e-23:200:31//GALLUS
GALLUS (CHICKEN).//P00789

35

F-HEMBA1005822//PROTEIN Q300.//0.0016:21:80//MUS MUSCULUS (MOUSE).//Q02722 F-
HEMBA1005829//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/9.6e-33:96:73//HOMO
SAPIENS (HUMAN).//P39194

40

F-HEMBA1005834//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.6e-22:103:
46//NYCTICEBUS COUCANG (SLOW LORIS).//P08548

45

F-HEMBA1005852//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//8.8e-06:95:35//MUS
MUSCULUS (MOUSE).//P05143

F-HEMBA1005853//HYPOTHETICAL PROTEIN

50

MJ0647.//0.39:28:39//METHANOCOCCUS JANNASCHII.//Q58063

F-HEMBA1005884

55

F-HEMBA1005891//HYPOTHETICAL PROTEIN MTH137.//0.95:51:27//METHANOBACTERIUM
THERMOAUTOTROPHICUM.//O26240

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F-HEMBA1005894//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.6e-29:81:71//HOMO
 SAPIENS (HUMAN)//P39195
 5
 F-HEMBA1005909//HYPOTHETICAL 8.2 KD PROTEIN B0353.1 IN CHROMOSOME III./0.98:
 19:52//CAENORHABDITIS ELEGANS./Q10958
 10
 F-HEMBA1005911//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.9e-27:86:70//HOMO
 SAPIENS (HUMAN)//P39188
 F-HEMBA1005921//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.3e-38:99:81//HOMO
 15
 SAPIENS (HUMAN)//P39194
 F-HEMBA1005931//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1)/2.3e-17:76:
 51//HOMO SAPIENS (HUMAN)//P51522
 20
 F-HEMBA1005934//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/0.024:54:40//HOMO
 SAPIENS (HUMAN)//P39189
 25
 F-HEMBA1005962
 F-HEMBA1005963//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP)
 ./1.7e-32:89:79//BOS TAURUS (BOVINE)//P53620
 30
 F-HEMBA1005990//HYPOTHETICAL BHLF1 PROTEIN./3.0e-09:180:36//EPSTEIN-BARR
 VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4)//P03181
 35
 F-HEMBA1005991//HYPOTHETICAL PROTEIN KIAA0032./3.0e-17:107:43//HOMO SAPIENS
 (HUMAN)//Q15034
 F-HEMBA1005999
 40
 F-HEMBA1006002
 F-HEMBA1006005//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B)
 45
 ./0.0017:45:44//MUS MUSCULUS (MOUSE)//Q62267
 F-HEMBA1006031//BASIC PROLINE-RICH PEPTIDE IB-1./0.00016:84:39//HOMO SAPIENS
 (HUMAN)//P04281
 50
 F-HEMBA1006035//DNAK PROTEIN 1 (HEAT SHOCK PROTEIN 70) (HSP70)/0.43:100:
 27//SYNECHOCYSTIS SP. (STRAIN PCC 6803)//Q55154
 55
 F-HEMBA1006036//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/6.2e-64:150:74//HOMO
 SAPIENS (HUMAN)//P39194

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F-HEMBA1006042

5 F-HEMBA1006067//METALLOTHIONEIN A (MT-A)//0.86:34:41//THERMARCES
CERBERUS//P52721

F-HEMBA1006081

10 F-HEMBA1006090//SODIUM/GLUCOSE COTRANSPORTER 3 (NA+)/GLUCOSE
COTRANSPORTER 3) (LOW AFFINITY SODIUM-GLUCOSE COTRANSPORTER)//0.87:35:
54//SUS SCROFA (PIG)//P31636

15 F-HEMBA1006091//EARLY NODULIN 20 PRECURSOR (N-20)//0.027:87:32//MEDICAGO
TRUNCATULA (BARREL MEDIC)//P93329

20 F-HEMBA1006100/////ALU SUBFAMILY SX WARNING ENTRY !!!!!/8.1e-09:58:60//HOMO
SAPIENS (HUMAN)//P39195

25 F-HEMBA1006108//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC
REGION//5.6e-16:88:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53867

F-HEMBA1006121//HOMEBOX PROTEIN CDX-1 (CAUDAL-TYPE HOMEBOX PROTEIN 1)
./3.4e-05:106:37//HOMO SAPIENS (HUMAN)//P47902

30 F-HEMBA1006124//50S RIBOSOMAL PROTEIN L33//1.0:12:83//BACILLUS
STEARTHERMOPHILUS//P23375

35 F-HEMBA1006130//SEL-10 PROTEIN//7.7e-05:129:28//CAENORHABDITIS
ELEGANS//Q93794

40 F-HEMBA1006138/////ALU SUBFAMILY SQ WARNING ENTRY !!!!!/7.8e-13:41:73//HOMO
SAPIENS (HUMAN)//P39194

F-HEMBA1006142/////ALU SUBFAMILY SC WARNING ENTRY !!!!!/2.3e-39:101:77//HOMO
SAPIENS (HUMAN)//P39192

45 F-HEMBA1006155//GENE 33 POLYPEPTIDE//0.21:70:31//RATTUS NORVEGICUS (RAT)
./P05432

50 F-HEMBA1006158

55 F-HEMBA1006173//PROTEIN-TYROSINE PHOSPHATASE STRIATUM-ENRICHED (EC
3.1.3.48) (STEP) (NEURAL-SPECIFIC PROTEIN-TYROSINE PHOSPHATASE) (FRAGMENT)
./0.017:20:95//HOMO SAPIENS (HUMAN)//P54829

F-HEMBA1006182/////ALU SUBFAMILY J WARNING ENTRY !!!!!/0.37:31:61//HOMO SAPIENS
(HUMAN)//P39188

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F-HEMBA1006198//HOMEBOX PROTEIN HOX-B3 (HOX-2.7) (MH-23)//0.85:61:29//MUS
 MUSCULUS (MOUSE)//P09026
 5
 F-HEMBA1006235//50S RIBOSOMAL PROTEIN L33//1.0:26:38//AQUIFEX
 AEOLICUS//O67756
 10
 F-HEMBA1006248//MALE SPECIFIC SPERM PROTEIN MST84DB//0.0041:64:
 37//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01643
 15
 F-HEMBA1006252//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR DE-3//1.0:22:
 40//DOLICHOS AXILLARIS (MACROTYLOMA AXILLARE)//P01057
 20
 F-HEMBA1006253//DISINTEGRIN ERISTICOPHIN (PLATELET AGGREGATION ACTIVATION
 INHIBITOR)//0.95:19:47//ERISTOCOPHIS MACMAHONI (LEAF-NOSED VIPER)//P22826
 25
 F-HEMBA1006259
 F-HEMBA1006268//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//7.0e-05:32:65//HOMO
 SAPIENS (HUMAN)//P39192
 30
 F-HEMBA1006272//RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 2)//4.8e-112:
 248:78//HOMO SAPIENS (HUMAN)//P10264
 35
 F-HEMBA1006278//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE
 ADENYLYLTRANSFERASE) (FRAGMENT)//2.5e-71:164:75//HOMO SAPIENS (HUMAN)
 //P51003
 40
 F-HEMBA1006283//50S RIBOSOMAL PROTEIN L32//0.81:27:44//THERMUS AQUATICUS
 (SUBSP. THERMOPHILUS)//P80339
 45
 F-HEMBA1006284//CUTICLE COLLAGEN 2//0.36:42:40//CAENORHABDITIS
 ELEGANS//P17656
 50
 F-HEMBA1006291//HYPOTHETICAL 43.3 KD PROTEIN IN EVGS-GLK INTERGENIC
 REGION//2.4e-37:143:31//ESCHERICHIA COLI//P76518
 55
 F-HEMBA1006293//MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR//0.20:
 134:29//RATTUS NORVEGICUS (RAT)//Q63345 F-HEMBA1006309//HYPOTHETICAL 54.2 KD
 PROTEIN IN ERP5-ORC6 INTERGENIC REGION//2.1e-43:187:48//SACCHAROMYCES
 CEREVISIAE (BAKER'S YEAST)//P38821
 F-HEMBA1006310//SIGNAL TRANSDUCER CD24 PRECURSOR (HEAT STABLE ANTIGEN)
 (HSA) (NECTADRIN)//0.71:46:39//RATTUS NORVEGICUS (RAT)//Q07490
 F-HEMBA1006328//RNA POLYMERASE ALPHA SUBUNIT (EC 2.7.7.48) (NUCLEOCAPSID

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PHOSPHOPROTEIN).//0.44:141:24//HUMAN PARAINFLUENZA 1 VIRUS (STRAIN CI-5/73)
//P32531

5 F-HEMBA1006334//HYPOTHETICAL TRANSCRIPTIONAL REGULATOR AF1627.//0.98:26:
46//ARCHAEOGLOBUS FULGIDUS.//028646

F-HEMBA1006344//EZRIN (P81) (CYTOVILLIN) (VILLIN-2).//8.8e-08:91:36//MUS MUSCULUS
10 (MOUSE).//P26040

F-HEMBA1006347//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//9.1e-48:149:
50//DROSOPHILA MELANOGASTER (FRUIT FLY).//02193

15 F-HEMBA1006349//METALLOTHIONEIN-LIKE PROTEIN 1.//0.015:59:33//CASUARINA
GLAUCA (SWAMP OAK).//Q39511

20 F-HEMBA1006359//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//6.8e-96:261:
66//HOMO SAPIENS (HUMAN).//P28160

F-HEMBA1006364//PUTATIVE ENDONUCLEASE C1F12.06C (EC 3.1.-.-).//0.97:60:
25 35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10348

F-HEMBA1006377//EARLY NODULIN 20 PRECURSOR (N-20).//0.00023:110:35//MEDICAGO
TRUNCATULA (BARREL MEDIC).//P93329

30 F-HEMBA1006380

F-HEMBA1006381//METALLOTHIONEIN-II.//1.0:26:38//CANDIDA GLABRATA (YEAST)
35 (TORULOPSIS GLABRATA).//P15114

F-HEMBA1006398//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.3e-26:123:52//HOMO
SAPIENS (HUMAN).//P08547

40 F-HEMBA1006416

F-HEMBA1006419//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.2e-24:102:50//HOMO
45 SAPIENS (HUMAN).//P39189

F-HEMBA1006421//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.1e-21:101:57//HOMO
SAPIENS (HUMAN).//P39188

50 F-HEMBA1006424//HYPOTHETICAL PROTEIN IORF1.//0.85:55:30//BOVINE CORONAVIRUS
(STRAIN MEBUS), AND BOVINE CORONAVIRUS (STRAIN QUEBEC).//P22053

55 F-HEMBA1006426//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.8e-36:78:74//HOMO
SAPIENS (HUMAN).//P39195

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F-HEMBA1006438//HYPOTHETICAL 8.1 KD PROTEIN (ORF65).//1.0:38:36//GUILLARDIA THETA (CRYPTOMONAS PHI).//O78421

5 F-HEMBA1006445//RAS-LIKE PROTEIN 3.//1.9e-06:40:47//RHIZOMUCOR RACEMOSUS (MUCOR CIRCINELLOIDES F. LUSITANICUS).//P22280

F-HEMBA1006446

10

F-HEMBA1006461//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/4.1e-18:68:67//HOMO SAPIENS (HUMAN).//P39192

15 F-HEMBA1006467

F-HEMBA1006471

20 F-HEMBA1006474//40 KD PROTEIN.//1.1e-37:231:38//BORNA DISEASE VIRUS (BDV).//Q01552

25 F-HEMBA1006483//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/6.1e-38:77:74//HOMO SAPIENS (HUMAN).//P39192

30 F-HEMBA1006485//HYPOTHETICAL 9.3 KD PROTEIN IN NAD3-NAD7 INTERGENIC REGION (ORF 79).//0.91:30:40//MARCHANTIA POLYMORPHA (LIVERWORT).//P38465

F-HEMBA1006486//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.1e-12:78:51//HOMO SAPIENS (HUMAN).//P08547

35 F-HEMBA1006489//FUN34 PROTEIN.//0.94:58:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32907

40 F-HEMBA1006492//NADH-UBIQUINONE OXIDOREDUCTASE MWFE SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-MWFE) (CI-MWFE).//0.87:44:36//HOMO SAPIENS (HUMAN).//O15239

45 F-HEMBA1006494//FERREDOXIN-LIKE PROTEIN IN NIF REGION.//0.11:46:26//RHIZOBIUM LEGUMINOSARUM (BIOVAR TRIFOLII).//P42711

F-HEMBA1006497

50 F-HEMBA1006502//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.15:26:73//HOMO SAPIENS (HUMAN).//P39188

55 F-HEMBA1006507//DIAPHANOUS PROTEIN.//0.0055:129:28//DROSOPHILA MELANOGASTER (FRUIT FLY).//P48608

F-HEMBA1006521//3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) (3-

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KETOACYL- ACYL CARRIER PROTEIN REDUCTASE).//1.1e-32:177:41//ESCHERICHIA COLI.//P25716

5 F-HEMBA1006530//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.052:84:26//LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE) .//P15583

10 F-HEMBA1006535//INHIBITOR OF APOPTOSIS PROTEIN 1 (MIAP1) (MIAP-1).//6.6e-05:53:39//MUS MUSCULUS (MOUSE).//O08863

15 F-HEMBA1006540//PRESYNAPTIC PROTEIN SAP97 (SYNAPSE-ASSOCIATED PROTEIN 97) (DISCS, LARGE HOMOLOG 1).//2.1e-07:206:23//RATTUS NORVEGICUS (RAT).//Q62696

F-HEMBA1006546//PROBABLE E5 PROTEIN.//0.11:70:32//HUMAN PAPILLOMAVIRUS TYPE 51.//P26553

20 F-HEMBA1006559//SUPPRESSOR PROTEIN SRP40.//0.015:221:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583

25 F-HEMBA1006562//SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR (ALLELE S) .//1.5e-07:122:33//HOMO SAPIENS (HUMAN).//P10163

30 F-HEMBA1006566//CELL DIVISION PROTEIN KINASE 2 (EC 2.7.1.-) (CDC2 HOMOLOG EG1 PROTEIN KINASE).//0.63:53:37//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P23437

F-HEMBA1006569//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT).//4.4e-06:88:39//BOS TAURUS (BOVINE).//P02465

35 F-HEMBA1006579

40 F-HEMBA1006583//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.011:61:40//MUS MUSCULUS (MOUSE).//P05142

45 F-HEMBA1006595//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//5.6e-34:93:77//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1006597//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.9e-26:75:74//HOMO SAPIENS (HUMAN).//P39195

50 F-HEMBA1006612//SUPPRESSOR PROTEIN SRP40.//0.026:221:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583

55 F-HEMBA1006617//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//6.6e-20:73:63//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1006624//HYPOTHETICAL 41.9 KD PROTEIN IN SDS3-THS1 INTERGENIC

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REGION.//2.6e-31:209:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40506

5 F-HEMBA1006631//HYPOTHETICAL 62.8 KD PROTEIN IN TAF145-YOR1 INTERGENIC
REGION.//1.5e-15:131:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53331

F-HEMBA1006635

10 F-HEMBA1006639//POLYADENYLATE-BINDING PROTEIN 1 (POLY(A) BINDING PROTEIN 1)
(PABP 1).//2.2e-11:48:75//MUS MUSCULUS (MOUSE).//P29341

15 F-HEMBA1006643//LONG NEUROTOXIN CR1 PRECURSOR (KAPPA NEUROTOXIN).//0.28:
48:27//BUNGARUS MULTICINCTUS (MANY-BANDED KRAIT).//P15817

20 F-HEMBA1006648//ZINC FINGER PROTEIN 12 (ZINC FINGER PROTEIN KOX3)
(FRAGMENT).//0.26:17:47//HOMO SAPIENS (HUMAN).//P17014

F-HEMBA1006652//60S RIBOSOMAL PROTEIN L7.//2.4e-44:206:47//MUS MUSCULUS
(MOUSE).//P14148

25 F-HEMBA1006653

F-HEMBA1006659

30 F-HEMBA1006665//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.018:43:58//HOMO
SAPIENS (HUMAN).//P08547

35 F-HEMBA1006674//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-
135) (TAFII135) (TAFII-130) (TAFII130).//2.9e-05:154:33//HOMO SAPIENS (HUMAN).//O00268

40 F-HEMBA1006676//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//3.6e-09:52:
51//OWENIA FUSIFORMIS.//P21260

F-HEMBA1006682

45 F-HEMBA1006695//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.1e-06:35:65//HOMO
SAPIENS (HUMAN).//P39188

F-HEMBA1006696

50 F-HEMBA1006708//HYPOTHETICAL 46.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN
PMC1-TFG2 INTERGENIC REGION.//3.4e-19:104:45//SACCHAROMYCES CEREVISIAE
(BAKER'S YEAST).//P53196

55 F-HEMBA1006709//RETINOIC ACID RECEPTOR RXR-BETA.//0.24:111:36//HOMO SAPIENS
(HUMAN).//P28702

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F-HEMBA1006717

5 F-HEMBA1006737//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID)
(FRAGMENT).//5.8e-09:111:40//HOMO SAPIENS (HUMAN).//Q01485

10 F-HEMBA1006744//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//1.8e-32:84:78//HOMO
SAPIENS (HUMAN).//P39191

F-HEMBA1006754//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.3e-75:220:62//HOMO
SAPIENS (HUMAN).//P08547

15 F-HEMBA1006758//VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VECADHERIN)
(CADHERIN-5) (7B4 ANTIGEN) (CD144 ANTIGEN).//0.024:110:29//HOMO SAPIENS (HUMAN)
//P33151

20 F-HEMBA1006767

F-HEMBA1006779//MITOCHONDRIAL RIBOSOMAL PROTEIN S12.//0.67:19:42//LEISHMANIA
TARENTOLAE (SAUROLEISHMANIA TARENTOLAE).//Q34940

25 F-HEMBA1006780

30 F-HEMBA1006789//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.056:98:30//MUS
MUSCULUS (MOUSE).//P05143

F-HEMBA1006795//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.9e-11:143:
30//NYCTICEBUS COUCANG (SLOW LORIS).//P08548

35 F-HEMBA1006796//WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).//0.16:38:
42//MUS MUSCULUS (MOUSE).//P70315

40 F-HEMBA1006807//HYPOTHETICAL 46.4 KD PROTEIN T16H12.5 IN CHROMOSOME
III.//4.4e-75:184:77//CAENORHABDITIS ELEGANS.//P34568

45 F-HEMBA1006821//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//0.011:20:85//HOMO
SAPIENS (HUMAN).//P39194

F-HEMBA1006824//PROTEIN B11.//0.44:27:44//VACCINIA VIRUS (STRAIN WR).//Q01229

50 F-HEMBA1006832//HYPOTHETICAL 34.6 KD PROTEIN C13G5.2 IN CHROMOSOME III.//1.0:
46:36//CAENORHABDITIS ELEGANS.//P34327

55 F-HEMBA1006849

F-HEMBA1006865//ACROSIN INHIBITORS IIA AND IIB (BUSI-II).//1.0:41:31//BOS TAURUS
(BOVINE).//P01001

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- F-HEMBA1006877//OXYSTEROL-BINDING PROTEIN.//3.7e-26:239:36//ORYCTOLAGUS CUNICULUS (RABBIT).//P16258
- 5 F-HEMBA1006885//HYPOTHETICAL 27.2 KD PROTEIN F09E5.8 IN CHROMOSOME II.//4.5e-38:185:43//CAENORHABDITIS ELEGANS.//P52057
- 10 F-HEMBA1006900
- F-HEMBA1006914//UBIQUITIN-ACTIVATING ENZYME E1-LIKE (POLYMERASE-INTERACTING PROTEIN 2).//5.2e-27:269:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P52488
- 15 F-HEMBA1006921//CYTOTOXIN 3 (COMPONENT 3.20).//0.99:32:37//NAJA MELANOLEUCA (FOREST COBRA) (BLACK-LIPPED COBRA).//P01473
- 20 F-HEMBA1006926//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN).//0.0024:148:33//RATTUS NORVEGICUS (RAT).//P54258
- 25 F-HEMBA1006929//HYPOTHETICAL PROTEIN MJ0525.//0.95:35:20//METHANOCOCCUS JANNASCHII.//Q57945
- F-HEMBA1006936//SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1 / PRP-3) (PRP-2 / PRP-4) (PIF-F / PIF-S) (PROTEIN A / PROTEIN C) [CONTAINS: PEPTIDE P-C].//0.074:116:31//HOMO SAPIENS (HUMAN).//P02810
- 30 F-HEMBA1006938
- 35 F-HEMBA1006941//THIOREDOXIN H-TYPE 1 (TRX-H1).//2.1e-13:90:33//NICOTIANA TABACUM (COMMON TOBACCO).//P29449
- 40 F-HEMBA1006949
- F-HEMBA1006973//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.75:29:55//BOS TAURUS (BOVINE).//P25508
- 45 F-HEMBA1006976//CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (EC 2.4.99.-) (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALIII) (ALPHA 2,3-ST) (GAL-NAC6S) (STZ) (SIAT4-C) (SAT-3) (ST-4).//3.9e-108:117:95//HOMO SAPIENS (HUMAN).//Q11206
- 50 F-HEMBA1006993
- 55 F-HEMBA1006996//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGENIC REGION (ORF70).//0.12:51:33//ASTASIA LONGA (EUGLENOPHYCEAN ALGA).//P34779

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F-HEMBA1007002//PLATELET GLYCOPROTEIN IX PRECURSOR (GPIX) (CD42A).//0.00096:
60:33//HOMO SAPIENS (HUMAN).//P14770

5 F-HEMBA1007017//HYPOTHETICAL 7.2 KD PROTEIN IN CYAY-DAPF INTERGENIC
REGION.//1.0:25:56//ESCHERICHIA COLI.//P39166

10 F-HEMBA1007018//DYNEIN LIGHT INTERMEDIATE CHAIN 1, CYTOSOLIC (LIC57/59)
(DYNEIN LIGHT CHAIN A) (DLC-A).//8.5e-120:278:80//GALLUS GALLUS (CHICKEN).//Q90828

F-HEMBA1007045//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
15 .//2.1e-12:158:29//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437

F-HEMBA1007051

20 F-HEMBA1007052//60S RIBOSOMAL PROTEIN L37-B (L35) (YP55).//0.94:37:
35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P51402

F-HEMBA1007062//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.93:55:
25 29//RHINOCEROS UNICORNIS (GREATER INDIAN RHINOCEROS).//Q96063

F-HEMBA1007066//ECLOSION HORMONE PRECURSOR (ECDYSIS ACTIVATOR) (EH)
//0.58:49:38//BOMBYX MORI (SILK MOTH).//P25331

30 F-HEMBA1007073//PUTATTVE SMALL MEMBRANE PROTEIN (ORF 4).//0.86:46:34//CANINE
ENTERIC CORONAVIRUS (STRAIN INSAVC-1) (CCV).//P36696

35 F-HEMBA1007078//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//8.6e-29:56:67//HOMO
SAPIENS (HUMAN).//P39193

F-HEMBA1007080//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
40 .//0.028:122:30//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437

F-HEMBA1007085//RTOA PROTEIN (RATIO-A).//7.4e-11:221:31//DICTYOSTELIUM
DISCOIDEUM (SLIME MOLD).//P54681

45 F-HEMBA1007087//HYPOTHETICAL PROTEIN MJ0162.//3.3e-29:173:36//METHANOCOCCUS
JANNASCHII.//Q57626

50 F-HEMBA1007112

F-HEMBA1007113

55 F-HEMBA1007121//INOSITOL POLYPHOSPHATE 1-PHOSPHATASE (EC 3.1.3.57) (IPP)
//5.4e-07:90:28//HOMO SAPIENS (HUMAN).//P49441

F-HEMBA1007129//HIRUSTASIN.//0.88:37:32//HIRUDO MEDICINALIS (MEDICINAL LEECH)

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./P80302

5 F-HEMBA1007147//HYPOTHETICAL 12.0 KD PROTEIN IN DST1-HEM2 INTERGENIC
REGION.//0.92:23:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53182

10 F-HEMBA1007149//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17).//0.0078:17:
70//ESCHERICHIA COLI.//P05834

15 F-HEMBA1007151//WDNM1 PROTEIN PRECURSOR.//0.25:45:37//MUS MUSCULUS
(MOUSE).//Q62477

20 F-HEMBA1007174//HYPOTHETICAL 45.1 KD PROTEIN IN RPS5-ZMS1 INTERGENIC
REGION.//6.9e-18:97:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47160

25 F-HEMBA1007178//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!/9.8e-06:38:65//HOMO
SAPIENS (HUMAN).//P39195

30 F-HEMBA1007194//GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHOLOROPLAST
ISOFORM PRECURSOR (EC 1.1.1.49) (G6PD).//1.0:80:32//NICOTIANA TABACUM (COMMON
TOBACCO).//Q43793

35 F-HEMBA1007203//PROTEIN A22.//1.0:115:26//VARIOLA VIRUS.//P33845

40 F-HEMBA1007206

45 F-HEMBA1007224//HYPOTHETICAL 35.7 KD PROTEIN C41C4.6 IN CHROMOSOME II.//2.4e-
05:92:30//CAENORHABDITIS ELEGANS.//Q09275

50 F-HEMBA1007243//HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC
2.4.2.8) (HGPRT) (HGPRTASE) (HPRT B).//3.1e-74:205:67//MUS MUSCULUS (MOUSE)
./P00493

55 F-HEMBA1007251//VITELLINE MEMBRANE PROTEIN VM26AB PRECURSOR (PROTEIN TU-
4) (PROTEIN SV23).//0.52:108:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//P13238

60 F-HEMBA1007256

65 F-HEMBA1007267//CALICIN (FRAGMENT).//0.060:88:31//HOMO SAPIENS (HUMAN).//Q13939

70 F-HEMBA1007273//HYPOTHETICAL 8.1 KD PROTEIN (ORF65).//0.95:40:37//GUILLARDIA
THETA (CRYPTOMONAS PHI).//O78421

75 F-HEMBA1007279//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.6e-24:98:64//HOMO
SAPIENS (HUMAN).//P39188

F-HEMBA1007281

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F-HEMBA1007288//HYPOTHETICAL 13.5 KD PROTEIN IN ZMS1-MNS1 INTERGENIC
 REGION.//0.88:11:54//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47162
 5
 F-HEMBA1007300//CGMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE (EC 3.1.4.17)
 (CGB-PDE).//2.7e-43:220:41//BOS TAURUS (BOVINE).//Q28156
 10 F-HEMBA1007301//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.//3.3e-22:115:
 33//HOMO SAPIENS (HUMAN).//P02461
 F-HEMBA1007319
 15 F-HEMBA1007320//HYPOTHETICAL 28.0 KD PROTEIN IN GLOB-RNHA INTERGENIC
 REGION.//1.0:48:37//ESCHERICHIA COLI.//P75672
 20 F-HEMBA1007322//THREONINE DEHYDRATASE OPERON ACTIVATOR PROTEIN.//1.0:59:
 33//ESCHERICHIA COLI.//P11866
 F-HEMBA1007327
 25 F-HEMBA1007341//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/9.1e-12:37:62//HOMO
 SAPIENS (HUMAN).//P39188
 30 F-HEMBA1007342//PROBABLE E5 PROTEIN.//0.89:96:29//PYGMY CHIMPANZEE
 PAPILLOMAVIRUS TYPE 1.//Q02268
 F-HEMBA1007347//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECURSOR
 35 (IGFBP-2) (IBP-2) (IGF-BINDING PROTEIN 2).//0.92:62:43//OVIS ARIES (SHEEP).//Q29400
 F-HEMBA1000005//WEAK NEUROTOXIN 5.//0.98:30:33//NAJA NAJA (INDIAN COBRA)
 .//P29179
 40 F-HEMBA1000008//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.7e-35:73:84//HOMO
 SAPIENS (HUMAN).//P39195
 45 F-HEMBA1000018//HYPOTHETICAL BHLF1 PROTEIN.//0.39:90:37//EPSTEIN-BARR VIRUS
 (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
 F-HEMBA1000024//VIRE LOCUS 9 KD VIRULENCE PROTEIN.//0.66:36:
 50 41//AGROBACTERIUM TUMEFACIENS.//P08061
 F-HEMBA1000025//MUSCARINIC TOXIN ALPHA (MT-ALPHA).//0.46:32:40//DENDROASPIS
 POLYLEPIS POLYLEPIS (BLACK MAMBA).//P80494
 55 F-HEMBA1000030//SUPPRESSOR PROTEIN SRP40.//6.7e-07:50:52//SACCHAROMYCES
 CEREVISIAE (BAKER'S YEAST).//P32583

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- 5 F-HEMBB1000036//HYPOTHETICAL 43.2 KD PROTEIN C34E10.1 IN CHROMOSOME III.//2.5e-07:120:29//CAENORHABDITIS ELEGANS.//P46576
- F-HEMBB1000037//HYPOTHETICAL 59.9 KD PROTEIN-IN SGA1-KTR7 INTERGENIC REGION.//1.7e-05:71:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40492
- 10 F-HEMBB1000039//VERY HYPOTHETICAL 11.9 KD PROTEIN C4H3.12C IN CHROMOSOME I.//1.0:61:21//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10219
- F-HEMBB1000044
- 15 F-HEMBB1000048//HYPOTHETICAL 15.7 KD PROTEIN IN IDH-DEOR INTERGENIC REGION.//1.0:63:31//BACILLUS SUBTILIS.//P54942
- 20 F-HEMBB1000050//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/9.0e-14:34:79//HOMO SAPIENS (HUMAN).//P39194
- F-HEMBB1000054//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/5.9e-31:45:73//HOMO SAPIENS (HUMAN).//P39193
- 25 F-HEMBB1000055//MUSCARINIC TOXIN ALPHA (MT-ALPHA).//1.0:14:57//DENDROASPIS POLYLEPIS POLYLEPIS (BLACK MAMBA).//P80494
- 30 F-HEMBB1000059//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.0e-21:82:59//HOMO SAPIENS (HUMAN).//P39195
- 35 F-HEMBB1000083//CHROMOGRANIN A PRECURSOR (CGA) [CONTAINS: PANCREASTATIN; BETA-GRANIN; WE-14].//0.87:172:28//RATTUS NORVEGICUS (RAT) .//P10354
- 40 F-HEMBB1000089//HYPOTHETICAL 9.5 KD PROTEIN IN SPEA-METK INTERGENIC REGION (F83).//1.0:42:33//ESCHERICHIA COLI.//P46879
- F-HEMBB1000099//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/7.7e-08:31:87//HOMO SAPIENS (HUMAN).//P39189
- 45 F-HEMBB1000103//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.4e-38:136:58//HOMO SAPIENS (HUMAN).//P08547
- 50 F-HEMBB1000113//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.9e-13:57:64//HOMO SAPIENS (HUMAN).//P39188
- 55 F-HEMBB1000119//MAF PROTEIN.//3.6e-32:195:43//BACILLUS SUBTILIS.//Q02169
- F-HEMBB1000136//HYPOTHETICAL 12.7 KD PROTEIN IN PCS60-ABD1 INTERGENIC

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REGION.//0.65:71:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38327

5 F-HEMBB1000141//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.00014:34:
64//HOMO SAPIENS (HUMAN).//P20931

F-HEMBB1000144//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//2.0e-26:81:69//HOMO
10 SAPIENS (HUMAN).//P39191

F-HEMBB1000173//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//9.2e-29:91:71//HOMO
SAPIENS (HUMAN).//P39188

15 F-HEMBB1000175//ANTIMICROBIAL PEPTIDE ENAP-1 (FRAGMENT).//0.97:41:36//EQUUS
CABALLUS (HORSE).//P80930

F-HEMBB1000198//HYPOTHETICAL 7.7 KD PROTEIN YCF33 (ORF67).//0.91:21:
20 52//PORPHYRA PURPUREA.//P51329

F-HEMBB1000215//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//3.4e-08:39:76//HOMO
25 SAPIENS (HUMAN).//P39192

F-HEMBB1000217//DNA DAMAGE TOLERANCE PROTEIN RHC31 (RAD31 HOMOLOG)
.//2.9e-32:174:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06624

30 F-HEMBB1000218//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.73:31:38//MICROTUS
PENNSYLVANICUS (MEADOW VOLE).//P24949

F-HEMBB1000226//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II.//6.5e-
35 26:191:34//CAENORHABDITIS ELEGANS.//Q09217

F-HEMBB1000240

40 F-HEMBB1000244//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.9e-05:44:61//HOMO
SAPIENS (HUMAN).//P39188

45 F-HEMBB1000250

F-HEMBB1000258

50 F-HEMBB1000264//CUTICLE COLLAGEN SQT-1.//0.15:89:33//CAENORHABDITIS
ELEGANS.//P12114

F-HEMBB1000266//TRANSLATION INITIATION FACTOR IF-2.//2.7e-06:167:
55 22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39730

F-HEMBB1000272//CYTOCHROME C OXIDASE POLYPEPTIDE VIB (EC 1.9.3.1) (AED).//0.75:
30:43//BOS TAURUS (BOVINE).//P00429

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5 F-HEMBB1000274//CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) (SPRP)//1.0:38:36//SUS SCROFA (PIG) //P35323

10 F-HEMBB1000284//CALTRIN (CALCIUM TRANSPORT INHIBITOR)//1.0:56:30//MUS MUSCULUS (MOUSE)//Q09098

F-HEMBB1000307

15 F-HEMBB1000312

F-HEMBB1000317//THROMBOSPONDIN 1 PRECURSOR//3.2e-32:135:43//HOMO SAPIENS (HUMAN)//P07996

20 F-HEMBB1000318//PUTATIVE SMALL MEMBRANE PROTEIN (NONSTRUCTURAL PROTEIN NS3) (NONSTRUCTURAL 9.5 KD PROTEIN)//0.41:51:31//HUMAN CORONAVIRUS (STRAIN OC43)//Q04854

25 F-HEMBB1000335//ZINC FINGER PROTEIN 13 (ZFP-13) (KROX-8 PROTEIN) (FRAGMENT) //0.82:33:45//MUS MUSCULUS (MOUSE)//P10754

30 F-HEMBB1000336//ALDEHYDE OXIDASE (EC 1.2.3.1) (FRAGMENTS)//0.80:44:40//ORYCTOLAGUS CUNICULUS (RABBIT)//P80456

F-HEMBB1000337//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75)//0.94:118:22//HOMO SAPIENS (HUMAN)//Q08170

35 F-HEMBB1000338//MALE SPECIFIC SPERM PROTEIN MST84DA//0.042:33:39//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01642

40 F-HEMBB1000339//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.2e-14:54:55//HOMO SAPIENS (HUMAN)//P39188

45 F-HEMBB1000341//GENE 74 PROTEIN (GP74)//1.0:39:33//MYCOBACTERIOPHAGE L5//Q05289

F-HEMBB1000343

50 F-HEMBB1000354//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-15:83:56//HOMO SAPIENS (HUMAN)//P39188

55 F-HEMBB1000369//PROTEIN Q300//0.99:27:40//MUS MUSCULUS (MOUSE)//Q02722

F-HEMBB1000374//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/4.7e-34:56:78//HOMO SAPIENS (HUMAN)//P39189

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F-HEMBB1000376

5 F-HEMBB1000391//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS)//0.0013:79:35//BOS
TAURUS (BOVINE)//P25508

10 F-HEMBB1000399//CHECKPOINT PROTEIN RAD17//2.8e-15:187:
31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//P50531

15 F-HEMBB1000402//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3)
(FRAGMENT)//0.027:60:38//LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE)
//P15583

20 F-HEMBB1000404//CYANELLE 50S RIBOSOMAL PROTEIN L28//0.94:29:27//CYANOPHORA
PARADOXA//P48129

F-HEMBB1000420//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53)//0.023:
97:35//HOMO SAPIENS (HUMAN)//Q15427

25 F-HEMBB1000434//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/4.8e-20:111:54//HOMO
SAPIENS (HUMAN)//P39194

30 F-HEMBB1000438//HYPOTHETICAL 7.9 KD PROTEIN IN GP55-NRDG INTERGENIC
REGION//0.93:24:50//BACTERIOPHAGE T4//P07076

35 F-HEMBB1000441//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.4e-23:85:70//HOMO
SAPIENS (HUMAN)//P39188

F-HEMBB1000449//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.88:27:51//HOMO
SAPIENS (HUMAN)//P39195

40 F-HEMBB1000455

F-HEMBB1000472

45 F-HEMBB1000480//PROTEIN STBC//1.0:52:30//ESCHERICHIA COLI//P11905

50 F-HEMBB1000487//SHORT NEUROTOXIN 1 (NEUROTOXIN ALPHA) (NEUROTOXIN II)//0.93:
29:34//NAJA OXIANA (CENTRAL ASIAN COBRA) (OXUS COBRA)//P01427

F-HEMBB1000490//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.3e-16:50:80//HOMO
SAPIENS (HUMAN)//P39195

55 F-HEMBB1000491

F-HEMBB1000493//3A PROTEIN//1.0:51:35//AVIAN INFECTIOUS BRONCHITIS VIRUS

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(STRAIN BEAUDETTE) (IBV).//P30237

- 5 F-HEMBB1000510//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.7e-27:132:45//HOMO SAPIENS (HUMAN).//P08547
- 10 F-HEMBB1000518//CYTOCHROME C OXIDASE POLYPEPTIDE III (EC 1.9.3.1).//0.021:47:40//LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE).//P14546
- 10 F-HEMBB1000523
- 15 F-HEMBB1000530//COLLAGEN ALPHA 1(XIV) CHAIN PRECURSOR (UNDULIN).//9.8e-14:43:83//GALLUS GALLUS (CHICKEN).//P32018
- 20 F-HEMBB1000550//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3).//0.19:97:30//TRYPANOSOMA BRUCEI BRUCEI.//P04540
- 25 F-HEMBB1000554//MATERNAL B9.10 PROTEIN (P30 B9.10).//0.94:82:25//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P40744
- 30 F-HEMBB1000556//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//0.043:201:29//HOMO SAPIENS (HUMAN).//000268
- 30 F-HEMBB1000564//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:5:2:34//METRIDIDIUM SENILE (BROWN SEA ANEMONE) (FRILLED SEA ANEMONE).//O47493
- 35 F-HEMBB1000573//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//2.3e-10:52:73//HOMO SAPIENS (HUMAN).//P39191
- 40 F-HEMBB1000575//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.8e-26:76:76//HOMO SAPIENS (HUMAN).//P39192
- 40 F-HEMBB1000586//NADH-UBIQUINONE OXIDOREDUCTASE MLRQ SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-MLRQ) (CI-MLRQ).//0.74:23:52//HOMO SAPIENS (HUMAN).//O00483
- 45 F-HEMBB1000589//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//2.9e-25:61:75//HOMO SAPIENS (HUMAN).//P39193
- 50 F-HEMBB1000591//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:34:35//PETROMYZON MARINUS (SEA LAMPREY).//Q35537
- 55 F-HEMBB1000592//SMALL PROLINE-RICH PROTEIN 2-1.//0.0016:49:42//HOMO SAPIENS (HUMAN).//P35326
- F-HEMBB1000593//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENTS).//0.0070:189:32//GALLUS GALLUS (CHICKEN).//P12105

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F-HEMBB1000598//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.7e-10:110:
 41//NYCTICEBUS COUCANG (SLOW LORIS).//P08548
 5
 F-HEMBB1000623//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME
 III.//0.0022:98:28//CAENORHABDITIS ELEGANS.//P34284
 10 F-HEMBB1000630
 F-HEMBB1000631//ALPHA-2C-1 ADRENERGIC RECEPTOR (ALPHA-2C-1
 ADRENOCEPTOR) (SUBTYPE C4).//8.8e-06:59:40//HOMO SAPIENS (HUMAN).//P18825
 15 F-HEMBB1000632//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//7.3e-13:173:
 28//MUS MUSCULUS (MOUSE).//P27671
 20 F-HEMBB1000637//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/4.6e-41:94:82//HOMO
 SAPIENS (HUMAN).//P39193
 F-HEMBB1000638//INVOLUCRIN.//1.9e-06:144:29//HOMO SAPIENS (HUMAN).//P07476
 25 F-HEMBB1000643//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/8.3e-30:77:76//HOMO
 SAPIENS (HUMAN).//P39195
 30 F-HEMBB1000649//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.5e-37:58:81//HOMO
 SAPIENS (HUMAN).//P39189
 F-HEMBB1000652//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/2.2e-37:61:77//HOMO
 35 SAPIENS (HUMAN).//P39193
 F-HEMBB1000665//HYPOTHETICAL PROTEIN BBD24.//0.83:38:36//BORRELIA
 BURGENDORFERI (LYME DISEASE SPIROCHETE).//P70845
 40 F-HEMBB1000671//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.8e-51:74:71//HOMO
 SAPIENS (HUMAN).//P08547
 45 F-HEMBB1000673//HEAT-STABLE ENTEROTOXIN A3/A4 PRECURSOR (STA3/STA4) (ST-IB)
 (ST-H).//0.012:37:37//ESCHERICHIA COLI.//P07965
 F-HEMBB1000684//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/3.1e-21:66:72//HOMO
 50 SAPIENS (HUMAN).//P39193
 F-HEMBB1000693//HUNTINGTIN ASSOCIATED PROTEIN 1 (HAP1).//5.2e-26:121:
 49//RATTUS NORVEGICUS (RAT).//P54256
 55 F-HEMBB1000705

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F-HEMBB1000706

5 F-HEMBB1000709//HYPOTHETICAL 5.8 KD PROTEIN.//1.0:29:44//CLOVER YELLOW
MOSAIC VIRUS (CYMV).//P16485

10 F-HEMBB1000725//RAS-RELATED PROTEIN RAB-8B.//7.4e-105:205:98//RATTUS
NORVEGICUS (RAT).//P70550

F-HEMBB1000726//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.4e-25:85:70//HOMO
SAPIENS (HUMAN).//P39194

15 F-HEMBB1000738//50S RIBOSOMAL PROTEIN L33.//1.0:41:31//THERMUS AQUATICUS
(SUBSP. THERMOPHILUS).//P35871

20 F-HEMBB1000749//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.3e-29:42:85//HOMO
SAPIENS (HUMAN).//P39194

F-HEMBB1000763//NIFU PROTEIN.//0.089:63:36//FRANKIA ALNI.//P46045

25 F-HEMBB1000770//CALTRIN-LIKE PROTEIN II.//0.98:13:69//CAVIA PORCELLUS (GUINEA
PIG).//P22075

30 F-HEMBB1000774//HIGH MOBILITY GROUP PROTEIN HMG-Y.//0.029:53:32//MUS
MUSCULUS (MOUSE).//P17095

35 F-HEMBB1000781//MAPK/ERK KINASE KINASE 2 (EC 2.7.1.-) (MEK KINASE 2) (MEKK 2)
.//3.5e-75:144:98//MUS MUSCULUS (MOUSE).//Q61083

F-HEMBB1000789//PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC
REGION.//2.6e-49:232:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39956

40 F-HEMBB1000790//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.9e-16:93:51//HOMO
SAPIENS (HUMAN).//P39188

45 F-HEMBB1000794

F-HEMBB1000807//MUSCARINIC ACETYLCHOLINE RECEPTOR M3.//0.54:111:27//GALLUS
GALLUS (CHICKEN).//P49578

50 F-HEMBB1000810

F-HEMBB1000821

55 F-HEMBB1000822//HYPOTHETICAL 10 KD PROTEIN (ORF 6).//0.10:50:34//NARCISSUS
MOSAIC VIRUS (NMV).//P15099

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- F-HEMBB1000826//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.00025:73:39//HOMO SAPIENS (HUMAN).//P20931
- 5 F-HEMBB1000827//HYPOTHETICAL 7.4 KD PROTEIN.//0.89:23:52//THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19302
- F-HEMBB1000831//MALE SPECIFIC SPERM PROTEIN MST87F.//0.98:35:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175
- 10 F-HEMBB1000835//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.8e-31:96:46//HOMO SAPIENS (HUMAN).//P08547
- 15 F-HEMBB1000840//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.00012:102:36//NYCTICEBUS COUCANG (SLOW LORIS).//P08548
- 20 F-HEMBB1000848//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.3e-97:239:70//HOMO SAPIENS (HUMAN).//P08547
- F-HEMBB1000852
- 25 F-HEMBB1000870
- F-HEMBB1000876//METALLOTHIONEIN (MT).//0.99:14:64//PERCA FLUVIATILIS (PERCH).//P52725
- 30 F-HEMBB1000883//HYPOTHETICAL 7.8 KD PROTEIN (ORF62).//0.34:60:33//GUILLARDIA THETA (CRYPTOMONAS PHI).//O78459
- 35 F-HEMBB1000887//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE.//1.0:26:42//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//Q48251
- 40 F-HEMBB1000888
- F-HEMBB1000890
- 45 F-HEMBB1000893
- F-HEMBB1000908//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.0074:45:51//HOMO SAPIENS (HUMAN).//P39188
- 50 F-HEMBB1000910//PROBABLE E5 PROTEIN.//1.0:49:36//HUMAN PAPILLOMAVIRUS TYPE 58.//P26552
- 55 F-HEMBB1000913//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.29:56:46//HOMO SAPIENS (HUMAN).//P39195

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- F-HEMBB1000915//CYTOCHROME B (EC 1.10.2.2)//2.5e-24:62:90//HOMO SAPIENS (HUMAN)//P00156
- 5 F-HEMBB1000917//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/5.9e-26:53:66//HOMO SAPIENS (HUMAN)//P39193
- 10 F-HEMBB1000927//NEURONAL CALCIUM SENSOR 1 (NCS-1) (FREQUENIN)//3.9e-44:182:45//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//Q91614
- 15 F-HEMBB1000947//SMALL PROLINE-RICH PROTEIN 2-1//0.24:69:27//HOMO SAPIENS (HUMAN)//P35326
- F-HEMBB1000959//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/3.0e-31:89:68//HOMO SAPIENS (HUMAN)//P39195
- 20 F-HEMBB1000973//CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR//0.96:66:36//BOS TAURUS (BOVINE)//018739
- 25 F-HEMBB1000975//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR (HISTIDINE-PROLINE RICH GLYCOPROTEIN) (HPRG)//0.00042:77:41//HOMO SAPIENS (HUMAN)//P04196
- F-HEMBB1000981
- 30 F-HEMBB1000985//MIPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN)//1.0e-18:178:30//MUS MUSCULUS (MOUSE)//P28575
- 35 F-HEMBB1000991
- F-HEMBB1000996//HYPOTHETICAL 10.1 KD PROTEIN IN RHSD-GCL INTERGENIC REGION (ORFD3)//0.58:34:35//ESCHERICHIA COLI//P33669
- 40 F-HEMBB1001004//PROBABLE E4 PROTEIN//0.24:110:35//HUMAN PAPILLOMAVIRUS TYPE 5B//P26550
- 45 F-HEMBB1001008
- F-HEMBB1001011//ZINC FINGER PROTEIN 7 (ZINC FINGER PROTEIN KOX4) (ZINC FINGER PROTEIN HF.16)//3.2e-17:104:47//HOMO SAPIENS (HUMAN)//P17097
- 50 F-HEMBB1001014//EOTAXIN PRECURSOR (EOSINOPHIL CHEMOTACTIC PROTEIN)//1.0:58:39//RATTUS NORVEGICUS (RAT)//P97545
- 55 F-HEMBB1001020//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.4e-07:36:75//HOMO SAPIENS (HUMAN)//P39189
- F-HEMBB1001024

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5 F-HEMBB1001037//FERREDOXIN.//1.0:52:25//MOORELLA THERMOACETICA
(CLOSTRIDIUM THERMOACETICUM).//P00203

F-HEMBB1001047

10 F-HEMBB1001051//PROTEIN FAN (FACTOR ASSOCIATED WITH N-SMASE ACTIVATION)
./3.4e-21:50:100//HOMO SAPIENS (HUMAN).//Q92636

15 F-HEMBB1001056//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.0099:115:35//ORGYIA
PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10341

F-HEMBB1001058//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.1e-33:95:76//HOMO
SAPIENS (HUMAN).//P39192

20 F-HEMBB1001060//HYPOTHETICAL 8.2 KD PROTEIN ZC21.7 IN CHROMOSOME III.//1.0:38:
36//CAENORHABDITIS ELEGANS.//P34591

25 F-HEMBB1001063

F-HEMBB1001068

30 F-HEMBB1001096//NOXIUSTOXIN (NTX) (TOXIN II.11).//0.99:36:38//CENTRUROIDES
NOXIUS (MEXICAN SCORPION).//P08815

35 F-HEMBB1001102//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//1.1e-
27:115:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09701

F-HEMBB1001105//CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN
PRECURSOR.//0.80:70:40//HOMO SAPIENS (HUMAN).//P28067

40 F-HEMBB1001112//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.1e-126:
287:85//RATTUS NORVEGICUS (RAT).//P38378

45 F-HEMBB1001114//HYPOTHETICAL 9.6 KD PROTEIN (ORF2).//0.84:62:
27//BACTERIOPHAGE L2.//P42537

F-HEMBB1001117

50 F-HEMBB1001119//COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR.//1.6e-21:50:98//HOMO
SAPIENS (HUMAN).//Q99715

55 F-HEMBB1001126//HYPOTHETICAL 55.9 KD PROTEIN EEED8.6 IN CHROMOSOME II.//1.7e-
50:184:53//CAENORHABDITIS ELEGANS.//Q09296

F-HEMBB1001133//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.4e-09:53:62//HOMO

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SAPIENS (HUMAN).//P39192

5 F-HEMBB1001137//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6)
(RPB1) (FRAGMENT).//2.0e-05:206:27//CRICETULUS GRISEUS (CHINESE HAMSTER)
./P11414

10 F-HEMBB1001142//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/4.1e-05:46:56//HOMO
SAPIENS (HUMAN).//P39193

15 F-HEMBB1001151//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME
I.//2.3e-23:109:44//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10149

20 F-HEMBB1001153//PROCOLLAGEN ALPHA 2(IV) CHAIN PRECURSOR.//0.75:76:
34//ASCARIS SUUM (PIG ROUNDWORM) (ASCARIS LUMBRICOIDES).//P27393

25 F-HEMBB1001169//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.4e-16:71:59//HOMO
SAPIENS (HUMAN).//P39195

30 F-HEMBB1001175//ANKYRIN.//3.2e-12:169:31//MUS MUSCULUS (MOUSE).//Q02357

35 F-HEMBB1001177//PERIODIC TRYPTOPHAN PROTEIN 2 HOMOLOG.//9.4e-07:148:
27//HOMO SAPIENS (HUMAN).//Q15269

40 F-HEMBB1001182//HYPOTHETICAL 36.0 KD PROTEIN.//1.3e-09:110:31//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST).//P54858

45 F-HEMBB1001199

50 F-HEMBB1001208//HYPOTHETICAL PROTEIN LAMBDA-SP5.//0.053:23:47//MUS MUSCULUS
(MOUSE).//P15974

55 F-HEMBB1001209

F-HEMBB1001210//HYPOTHETICAL PROTEIN LAMBDA-SP5.//0.14:40:37//MUS MUSCULUS
(MOUSE).//P15974

F-HEMBB1001218//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.4e-19:49:67//HOMO
SAPIENS (HUMAN).//P39194

F-HEMBB1001221//CYTOCHROME C OXIDASE POLYPEPTIDE VIIA-LIVER PRECURSOR
(EC 1.9.3.1).//0.11:44:38//HOMO SAPIENS (HUMAN).//P14406

F-HEMBB1001234//65 KD YES-ASSOCIATED PROTEIN (YAP65).//2.0e-45:192:53//MUS
MUSCULUS (MOUSE).//P46938

F-HEMBB1001242//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN

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C12G12.13C IN CHROMOSOME I.//5.5e-37:226:41//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09876

5 F-HEMBB1001249//OXALOACETATE DECARBOXYLASE GAMMA CHAIN (EC 4.1.1.3).//1.0:23:43//KLEBSIELLA PNEUMONIAE.//P13155

10 F-HEMBB1001253//METALLOTHIONEIN-IH (MT-1H) (METALLOTHIONEIN-0) (MT-0).//0.14:16:43//HOMO SAPIENS (HUMAN).//P80294

15 F-HEMBB1001254//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.4e-12:40:75//HOMO SAPIENS (HUMAN).//P39195

F-HEMBB1001267//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.0e-12:33:78//HOMO SAPIENS (HUMAN).//P39193

20 F-HEMBB1001271//HYPOTHETICAL 25.1 KD PROTEIN B0302.5 IN CHROMOSOME X.//1.0:58:37//CAENORHABDITIS ELEGANS.//Q10928

25 F-HEMBB1001282//ANKYRIN HOMOLOG PRECURSOR.//9.5e-13:206:31//CHROMATIUM VINOSUM.//Q06527

30 F-HEMBB1001288//COPPER HOMEOSTASIS PROTEIN CUTC.//4.6e-42:163:51//ESCHERICHIA COLI.//P46719

F-HEMBB1001289//HYPOTHETICAL PROTEIN ORF-1137.//1.0e-05:106:26//MUS MUSCULUS (MOUSE).//P11260

35 F-HEMBB1001294//GTP-BINDING PROTEIN TC10.//1.3e-34:58:94//HOMO SAPIENS (HUMAN).//P17081

40 F-HEMBB1001302//HOMEBOX PROTEIN CDX-2 (CAUDAL-TYPE HOMEBOX PROTEIN 2) (CDX-3).//0.24:49:46//HOMO SAPIENS (HUMAN).//Q99626

45 F-HEMBB1001304//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).//1.0:17:70//LYCOPERSICON ESCULENTUM (TOMATO).//Q01157

F-HEMBB1001314//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.21:104:27//DROSOPHILA ERECTA (FRUIT FLY).//P13730

50 F-HEMBB1001315//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.3e-24:53:71//HOMO SAPIENS (HUMAN).//P39195

55 F-HEMBB1001317//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.//0.24:90:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09782

F-HEMBB1001326//HYPOTHETICAL PROTEIN LAMBDA-SP5.//0.36:26:50//MUS MUSCULUS

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(MOUSE).//P15974

5 F-HEMBB1001331//HYPOTHETICAL BHLF1 PROTEIN.//1.0:127:33//EPSTEIN-BARR VIRUS
(STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181

10 F-HEMBB1001335//ESCARGOT/SNAIL PROTEIN HOMOLOG (FRAGMENT).//0.85:44:
29//SCIARA COPROPHILA (FUNGUS GNAT).//Q01799

F-HEMBB1001337//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/4.2e-20:62:62//HOMO
SAPIENS (HUMAN).//P39194

15 F-HEMBB1001339//HYPOTHETICAL 17.3 KD PROTEIN CY1A11.16C.//8.2e-07:123:
34//MYCOBACTERIUM TUBERCULOSIS.//Q50606

20 F-HEMBB1001346//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.2e-14:60:45//HOMO
SAPIENS (HUMAN).//P08547

F-HEMBB1001348//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.6e-14:61:62//HOMO
SAPIENS (HUMAN).//P39188

25 F-HEMBB1001356

30 F-HEMBB1001364

F-HEMBB1001366/HISTIDINE-RICH PROTEIN.//0.87:26:42//PLASMODIUM FALCIPARUM
(ISOLATE FCM17 / SENEGAL).//P14586

35 F-HEMBB1001367//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/8.6e-40:146:61//HOMO
SAPIENS (HUMAN).//P39192

40 F-HEMBB1001369

F-HEMBB1001380//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.9e-25:49:83//HOMO
SAPIENS (HUMAN).//P39193

45 F-HEMBB1001384//BH3 INTERACTING DOMAIN DEATH AGONIST (BID).//0.80:95:29//MUS
MUSCULUS (MOUSE).//P70444

50 F-HEMBB1001387//PEA2 PROTEIN (PPF2 PROTEIN).//0.022:117:34//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST).//P40091

55 F-HEMBB1001394//ALPHA-ADAPTIN A (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2
ALPHA-A LARGE CHAIN) (100 KD COATED VESICLE PROTEIN A) (PLASMA MEMBRANE
ADAPTOR HA2/AP2 ADAPTIN ALPHA A SUBUNIT).//0.38:85:31//MUS MUSCULUS (MOUSE)
./P17426

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F-HEMBB1001410

5 F-HEMBB1001424//PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN
PRECURSOR.//0.99:37:21//ORYZA SATIVA (RICE).//P12162

10 F-HEMBB1001426//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.0035:40:60//HOMO
SAPIENS (HUMAN).//P39195

15 F-HEMBB1001429//CYTOSOL AMINOPEPTIDASE (EC 3.4.11.1) (LEUCINE
AMINOPEPTIDASE) (LAP) (LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (EC
3.4.11.5) (PROLYL AMINOPEPTIDASE).//1.1e-99:21:86//BOS TAURUS (BOVINE).//P00727

20 F-HEMBB1001436//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//3.4e-30:57:78//HOMO
SAPIENS (HUMAN).//P39195

25 F-HEMBB1001443//[PYRUVATE DEHYDROGENASE (LIPOAMIDE)]-PHOSPHATASE
PRECURSOR (PDP) (EC 3.1.3.43) (PYRUVATE DEHYDROGENASE PHOSPHATASE,
CATALYTIC SUBUNIT (PDPC).//2.5e-79:155:97//BOS TAURUS (BOVINE).//P35816

30 F-HEMBB1001449

35 F-HEMBB1001454//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS:
PEPTIDE P-D] (FRAGMENT).//1.1e-05:196:31//HOMO SAPIENS (HUMAN).//P10161

40 F-HEMBB1001458//24 KD ANTIGEN (FRAGMENT).//0.94:18:50//PLASMODIUM
CHABAUDI.//P14592

45 F-HEMBB1001463

50 F-HEMBB1001464//PPF2L ANTIGEN (FRAGMENT).//1.0:45:28//PLASMODIUM FALCIPARUM
(ISOLATE PALO ALTO / UGANDA).//P07765

55 F-HEMBB1001482//GASTRULA ZINC FINGER PROTEIN XLCGF16.1 (FRAGMENT).//4.2e-10:
37:43//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P18712 F-HEMBB1001500

60 F-HEMBB1001521//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.4e-39:59:72//HOMO
SAPIENS (HUMAN).//P39188

65 F-HEMBB1001527//HOMEODOMAIN PROTEIN HOX-B5 (XLHBOX-4) (XHOX-1B) (FRAGMENT)
//0.21:131:25//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P09019

70 F-HEMBB1001531//GENE 32 PROTEIN (GP32).//0.88:95:30//MYCOBACTERIOPHAGE
L5.//Q05241

75 F-HEMBB1001535//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:31:38//LUMBRICUS
TERRESTRIS (COMMON EARTHWORM).//Q34942

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F-HEMBB1001536

5 F-HEMBB1001537//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/0.0063:52:50//HOMO
SAPIENS (HUMAN)//P39191

F-HEMBB1001555//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.9e-23:69:63//HOMO
10 SAPIENS (HUMAN)//P39188

F-HEMBB1001562//RABPHILIN-3A//0.087:147:27//RATTUS NORVEGICUS (RAT)//P47709

15 F-HEMBB1001564//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//5.9e-27:107:54//HOMO
SAPIENS (HUMAN)//P08547

F-HEMBB1001565//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.9e-12:51:54//HOMO
20 SAPIENS (HUMAN)//P39194

F-HEMBB1001585

25 F-HEMBB1001586

F-HEMBB1001588//HYPOTHETICAL 12.3 KD PROTEIN IN GAP1-NAP1 INTERGENIC
REGION//0.0031:31:48//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P36140
30

F-HEMBB1001603

F-HEMBB1001618//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE
35 TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE]//0.00076:47:44//MUS MUSCULUS
(MOUSE)//P11369

F-HEMBB1001619//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)//1.0:52:
40 32//HOMO SAPIENS (HUMAN)//P22531

F-HEMBB1001630

45 F-HEMBB1001635//METALLOTHIONEIN-LIKE PROTEIN TYPE 2 A//1.0:27:
44//LYCOPERSICON ESCULENTUM (TOMATO)//Q40157

F-HEMBB1001637//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.0042:26:73//HOMO
50 SAPIENS (HUMAN)//P39188

F-HEMBB1001641

55 F-HEMBB1001653//SURVIVAL MOTOR NEURON PROTEIN 1//0.51:36:47//CANIS FAMILIARIS
(DOG)//O02771

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F-HEMBB1001665//HOMEBOX PROTEIN ENGRAILED-1 (HU-EN-1)//0.0030:135:34//HOMO SAPIENS (HUMAN)//Q05925

5 F-HEMBB1001668//PROBABLE 60S RIBOSOMAL PROTEIN L39//0.99:25:44//CAENORHABDITIS ELEGANS//P52814

10 F-HEMBB1001673//HYPOTHETICAL 46.1 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION//0.0054:128:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38823.

15 F-HEMBB1001684//SUPPRESSOR PROTEIN SRP40//0.56:81:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32583

F-HEMBB1001685//CYTOCHROME C OXIDASE POLYPEPTIDE VIII-HEART PRECURSOR (EC 1.9.3.1) (VIII) (IX)//1.0:21:47//BOS TAURUS (BOVINE)//P10175

20 F-HEMBB1001695//MYOSIN IC HEAVY CHAIN//8.9e-05:86:40//ACANTHAMOEBA CASTELLANII (AMOEBA)//P10569

25 F-HEMBB1001704//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//9.0e-08:35:71//HOMO SAPIENS (HUMAN)//P39195

30 F-HEMBB1001706//CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) (SPRP)//0.91:39:41//SUS SCROFA (PIG)//P35323

35 F-HEMBB1001707//FERREDOXIN-LIKE PROTEIN IN NIF REGION//1.0:43:23//BRADYRHIZOBIUM JAPONICUM//P27394

F-HEMBB1001717//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3) (FRAGMENT)//1.0:71:25//LEMUR CATTI (RING-TAILED LEMUR)//Q34878

40 F-HEMBB1001735//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//9.0e-35:97:74//HOMO SAPIENS (HUMAN)//P39194

45 F-HEMBB1001736//EUKARYOTIC TRANSLATION INITIATION FACTOR 3 BETA SUBUNIT (EIF-3 BETA) (EIF3 P116) (EIF3 P110)//0.00069:180:28//HOMO SAPIENS (HUMAN)//P55884

F-HEMBB1001747

50 F-HEMBB1001749//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//1.8e-43:75:70//HOMO SAPIENS (HUMAN)//P39195

55 F-HEMBB1001753//PROTEIN Q300//0.00091:16:81//MUS MUSCULUS (MOUSE)//Q02722

F-HEMBB1001756//CYCLIN-DEPENDENT KINASES REGULATORY SUBUNIT 2 (XE-P9) //0.94:35:42//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//Q91879

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F-HEMBB1001760

5 F-HEMBB1001762//GENE 35 PROTEIN (GP35)//0.76:21:47//MYCOBACTERIOPHAGE
L5//Q05245

F-HEMBB1001785

10

F-HEMBB1001797//CHLOROPLAST 50S RIBOSOMAL PROTEIN L35//0.99:41:
31//PORPHYRA PURPUREA//P51270

15 F-HEMBB1001802

F-HEMBB1001812//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/2.2e-39:54:77//HOMO
SAPIENS (HUMAN)//P39193

20

F-HEMBB1001816//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.1e-19:97:57//HOMO
SAPIENS (HUMAN)//P39194

25 F-HEMBB1001831//HYPOTHETICAL 45.6 KD PROTEIN IN COX5A-ALG11 INTERGENIC
REGION//0.62:204:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53951

30 F-HEMBB1001834//GLYCINE-RICH RNA-BINDING PROTEIN 1 (FRAGMENT)//0.0014:40:
45//SORGHUM VULGARE (SORGHUM)//Q99069

F-HEMBB1001836//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/7.1e-14:85:61//HOMO
SAPIENS (HUMAN)//P39191

35

F-HEMBB1001839//PROBABLE E4 PROTEIN//0.61:49:34//HUMAN PAPILLOMAVIRUS TYPE
6C//P20969

40 F-HEMBB1001850

F-HEMBB1001863//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.7e-30:57:68//HOMO
SAPIENS (HUMAN)//P39194

45

F-HEMBB1001867

50 F-HEMBB1001868//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH
GLYCOPROTEIN)//0.00036:47:53//NICOTIANA TABACUM (COMMON TOBACCO)//P13983

F-HEMBB1001869//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/7.0e-11:95:45//HOMO
SAPIENS (HUMAN)//P39188

55

F-HEMBB1001872//HYPOTHETICAL 8.2 KD PROTEIN IN LEF8-FP INTERGENIC
REGION//1.0:34:38//AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS

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(ACMNPV).//P41459

5 F-HEMBB1001874

F-HEMBB1001875

F-HEMBB1001880

10 F-HEMBB1001899//GENE 11 PROTEIN.//1.0:45:31//SPIROPLASMA VIRUS SPV1-R8A2 B.//P15902

15 F-HEMBB1001905//HYPOTHETICAL 81.7 KD PROTEIN IN MOL1-NAT2 INTERGENIC REGION.//8.8e-54:216:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48234

F-HEMBB1001906

20 F-HEMBB1001908//MONOCYTIC LEUKEMIA ZINC FINGER PROTEIN.//6.3e-51:138:80//HOMO SAPIENS (HUMAN).//Q92794

25 F-HEMBB1001910

F-HEMBB1001911

30 F-HEMBB1001915//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E).//2.3e-27:71:70//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24574

35 F-HEMBB1001921//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.8e-13:75:53//HOMO SAPIENS (HUMAN).//P08547

40 F-HEMBB1001922

F-HEMBB1001925//EPITHELIAL MEMBRANE PROTEIN-1 (EMP-1) (TUMOR-ASSOCIATED MEMBRANE PROTEIN).//1.0:55:30//MUS MUSCULUS (MOUSE).//P47801

45 F-HEMBB1001930//HYPOTHETICAL 9.6 KD PROTEIN K10D2.7 IN CHROMOSOME III.//0.43:49:26//CAENORHABDITIS ELEGANS.//Q09412

50 F-HEMBB1001944//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//5.1e-34:63:85//HOMO SAPIENS (HUMAN).//P39189

55 F-HEMBB1001945//NONSPECIFIC LIPID-TRANSFER PROTEIN (LTP) (PHOSPHOLIPID TRANSFER PROTEIN) (PLTP).//0.28:45:40//AMARANTHUS CAUDATUS (LOVE-LIES-BLEEDING) (INCA-WHEAT).//P80450

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F-HEM BB1001947//PROTEIN UL24.//0.48:42:47//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).//P10208

5 F-HEM BB1001950//HYPOTHETICAL 42.6 KD PROTEIN IN GSHB-ANSB INTERGENIC REGION (O378).//1.6e-24:162:36//ESCHERICHIA COLI.//P52062

F-HEM BB1001952

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F-HEM BB1001953

15 F-HEM BB1001957//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.7e-11:51:60//HOMO SAPIENS (HUMAN).//P39188

F-HEM BB1001962//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/7.6e-24:163:42//HOMO SAPIENS (HUMAN).//P39188

20

F-HEM BB1001967//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.1e-35:55:80//HOMO SAPIENS (HUMAN).//P39189

25 F-HEM BB1001973//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/2.1e-37:108:75//HOMO SAPIENS (HUMAN).//P39192

30 F-HEM BB1001983//LYSIS PROTEIN (E PROTEIN) (GPE).//0.84:45:37//BACTERIOPHAGE ALPHA-3.//P31280

F-HEM BB1001988

35

F-HEM BB1001990

40 F-HEM BB1001996//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.4e-14:98:40//HOMO SAPIENS (HUMAN).//P08547

F-HEM BB1001997//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.1e-19:38:73//HOMO SAPIENS (HUMAN).//P39188

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F-HEM BB1002002//CYTOCHROME C BIOGENESIS PROTEIN CCSA.//1.0:150:25//PORPHYRA PURPUREA.//P51369

50 F-HEM BB1002005//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/7.6e-12:94:40//HOMO SAPIENS (HUMAN).//P39195

F-HEM BB1002009

55 F-HEM BB1002015//HYPOTHETICAL 7.7 KD PROTEIN IN MRR-TSR INTERGENIC REGION (F67).//1.0:17:47//ESCHERICHIA COLI.//P39395

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F-HEMBB1002042//CYTOCHROME P450 4C1 (EC 1.14.14.1) (CYP1VC1).//2.4e-50:139:55//BLABERUS DISCOIDALIS (TROPICAL COCKROACH).//P29981

5 F-HEMBB1002043//HYPOTHETICAL 9.5 KD PROTEIN IN DHFR 3'REGION (ORF3).//0.052:40:42//HERPESVIRUS SAIMIRI (SUBGROUP C / STRAIN 488).//P22577

10 F-HEMBB1002044//CELLULOSE COMPLEMENTING PROTEIN.//0.45:87:33//ACETOBACTER XYLINUM (ACETOBACTER PASTEURIANUS).//P37697

15 F-HEMBB1002045//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.78:18:55//HOMO SAPIENS (HUMAN).//P03928

F-HEMBB1002049

20 F-HEMBB1002050//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC PEPTIDE P-F] (FRAGMENT).//1.0e-06:188:27//HOMO SAPIENS (HUMAN).//P02812

25 F-HEMBB1002068//HOMEBOX PROTEIN HOX-A4 (CHOX-1.4).//0.0023:56:44//GALLUS GALLUS (CHICKEN).//P17277

30 F-HEMBB1002069//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//0.0074:134:33//NICOTIANA TABACUM (COMMON TOBACCO).//P13983

35 F-HEMBB1002092//ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: OUTER MEMBRANE PROTEIN GP70; TRANSMEMBRANE PROTEIN P20E].//2.4e-07:75:40//BABOON ENDOGENOUS VIRUS (STRAIN M7).//P10269

F-HEMBB1002094//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//1.9e-24:63:82//HOMO SAPIENS (HUMAN).//P39191

40 F-HEMBB1002115//EC PROTEIN HOMOLOG (ZINC-METALLOTHIONEIN CLASS II).//0.94:26:42//ZEA MAYS (MAIZE).//P43401

45 F-HEMBB1002134//ZINC-FINGER PROTEIN NEURO-D4.//4.6e-57:176:67//RATTUS NORVEGICUS (RAT).//P56163

50 F-HEMBB1002139//CHLOROPLAST 50S RIBOSOMAL PROTEIN L35.//1.0:17:52//PORPHYRA PURPUREA.//P51270

F-HEMBB1002142//EARLY NODULIN 20 PRECURSOR (N-20).//0.087:52:36//MEDICAGO TRUNCATULA (BARREL MEDIC).//P93329

55 F-HEMBB1002152//HYPOTHETICAL 12.3 KD PROTEIN IN RPL3-RPL33 INTERGENIC REGION (ORF102).//5.8e-05:61:37//CYANOPHORA PARADOXA.//P15811

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F-HEMBB1002189//HYPOTHETICAL PROTEIN UL125.//1.0:77:32//HUMAN
CYTOMEGALOVIRUS (STRAIN AD169).//P16835

5 F-HEMBB1002190

F-HEMBB1002193//TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR
(TYROSINE-PROTEIN KINASE RSE) (TYROSINE-PROTEIN KINASE SKY) (TYROSINE-
10 PROTEIN KINASE DTK).//1.2e-27:59:100//HOMO SAPIENS (HUMAN).//Q06418

F-HEMBB1002217//ZINC FINGER PROTEIN 184 (FRAGMENT).//6.6e-22:106:50//HOMO
15 SAPIENS (HUMAN).//Q99676

F-HEMBB1002218//PROTEIN Q300.//0.85:19:52//MUS MUSCULUS (MOUSE).//Q02722

F-HEMBB1002232//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//9.6e-21:56:71//HOMO
20 SAPIENS (HUMAN).//P39195

F-HEMBB1002247

25 F-HEMBB1002249//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//7.2e-29:93:69//HOMO
SAPIENS (HUMAN).//P39194

30 F-HEMBB002254//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.0e-29:101:67//HOMO
SAPIENS (HUMAN).//P39194

35 F-HEMBB1002255//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3).//1.0:73:
28//PARAMECIUM TETRAURELIA.//P15579

F-HEMBB1002266//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//0.0079:151:
26//PLASMODIUM FALCIPARUM (ISOLATE FC27 / PAPUA NEW GUINEA).//P13816

40 F-HEMBB1002280//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.2e-15:182:
36//NYCTICEBUS COUCANG (SLOW LORIS).//P08548

45 F-HEMBB1002300

F-HEMBB1002306//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.00011:26:84//HOMO
SAPIENS (HUMAN).//P39195

50 F-HEMBB1002327//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//4.1e-11:41:85//HOMO
SAPIENS (HUMAN).//P39189

55 F-HEMBB1002329//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC
REGION.//9.9e-17:232:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40032

F-HEMBB1002340

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- 5 F-HEMBB1002342//HYPOTHETICAL 32.5 KD PROTEIN IN MSH6-BMH2 INTERGENIC REGION.//3.6e-40:102:57//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q03835
- 10 F-HEMBB1002358//THYMIDYLATE KINASE (EC 2.7.4.9) (DTMP KINASE).//6.1e-30:63:96//HOMO SAPIENS (HUMAN).//P23919
- 15 F-HEMBB1002359//HYPOTHETICAL 7.1 KD PROTEIN C6G9.01C IN CHROMOSOME I.//0.97:28:46//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q92346
- 20 F-HEMBB1002364//RETROVIRUS-RELATED POL POLYPROTEIN (FRAGMENT).//0.47:119:25//HOMO SAPIENS (HUMAN).//P12895
- 25 F-HEMBB1002371//HYPOTHETICAL 15.5 KD PROTEIN C2F7.12 IN CHROMOSOME I PRECURSOR.//3.0e-05:111:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09703
- 30 F-HEMBB1002381//PUTATIVE CUTICLE COLLAGEN C09G5.4.//0.34:105:34//CAENORHABDITIS ELEGANS.//Q09455
- 35 F-HEMBB1002383//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.049:103:32//AQUIFEX AEOLICUS.//066566
- 40 F-HEMBB1002387//10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES) (HEAT SHOCK PROTEIN 11).//0.18:75:28//RICKETTSIA TSUTSUGAMUSHI.//P16626
- 45 F-HEMBB1002409//HIGH MOBILITY GROUP PROTEIN HMG-Y.//0.014:61:36//MUS MUSCULUS (MOUSE).//P17095
- 50 F-HEMBB1002415
- 55 F-HEMBB1002425//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.8e-18:55:70//HOMO SAPIENS (HUMAN).//P39194
- 60 F-HEMBB1002442//LIN-10 PROTEIN.//5.1e-15:121:31//CAENORHABDITIS ELEGANS.//P34692
- 65 F-HEMBB1002453//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.2e-32:54:75//HOMO SAPIENS (HUMAN).//P39189
- 70 F-HEMBB1002457//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.5e-07:31:64//HOMO SAPIENS (HUMAN).//P39188
- 75 F-HEMBB1002458//MALE SPECIFIC SPERM PROTEIN MST84DA.//0.92:28:53//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01642

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F-HEMBB1002477//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6)
(RPB1) (FRAGMENT).//0.0066:198:27//CRICETULUS GRISEUS (CHINESE HAMSTER)
//P11414

5 F-HEMBB1002489//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//0.030:
182:28//HOMO SAPIENS (HUMAN).//Q15427

10 F-HEMBB1002492

F-HEMBB1002495//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//2.1e-08:41:75//HOMO
SAPIENS (HUMAN).//P39192

15 F-HEMBB1002502//RETROVIRUS-RELATED POL POLYPROTEIN (FRAGMENT).//0.00030:
31:77//HOMO SAPIENS (HUMAN).//P12895

20 F-HEMBB1002509

F-HEMBB1002510

25 F-HEMBB1002520//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.8e-36:162:
50//NYCTICEBUS COUCANG (SLOW LORIS).//P08548

F-HEMBB1002522//7 KD PROTEIN (ORF 4).//0.77:32:40//CHRYSANthemUM VIRUS B (CVB)
30 .//P37990

F-HEMBB1002531

35 F-HEMBB1002534//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//3.1e-36:80:73//HOMO
SAPIENS (HUMAN).//P39195

F-HEMBB1002545

40 F-HEMBB1002550//HOMEBOX PROTEIN HOX-D11 (HOX-4.6) (HOX-5.5).//3.8e-05:83:
34//MUS MUSCULUS (MOUSE).//P23813

45 F-HEMBB1002556

F-HEMBB1002579//SPLICING FACTOR U2AF 35 KD SUBUNIT (U2 AUXILIARY FACTOR 35
KD SUBUNIT) (U2 SNRNP AUXILIARY FACTOR SMALL SUBUNIT) (FRAGMENT).//5.0e-06:27:
50 77//SUS SCROFA (PIG).//Q29350

F-HEMBB1002582//PROTEINASE INHIBITOR.//1.0:27:40//SOLANUM MELONGENA
(EGGPLANT) (AUBERGINE).//P01078

55 F-HEMBB1002590//HYPOTHETICAL PROTEIN IN MMSB 3'REGION (ORF1) (FRAGMENT)
//1.9e-20:90:54//PSEUDOMONAS AERUGINOSA.//P28812

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F-HEMBB1002596

5 F-HEMBB1002600//NOVEL ANTIGEN 2 (NAG-2)//1.9e-60:187:59//HOMO SAPIENS (HUMAN)
//O14817

10 F-HEMBB1002601//M PROTEIN, SEROTYPE 6 PRECURSOR//1.0:71:
35//STREPTOCOCCUS PYOGENES//P08089

F-HEMBB1002603

15 F-HEMBB1002607//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS:
PEPTIDE P-D] (FRAGMENT)//0.0032:142:33//HOMO SAPIENS (HUMAN)//P10162

20 F-HEMBB1002610//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//2.0e-11:79:49//HOMO
SAPIENS (HUMAN)//P08547

25 F-HEMBB1002613//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.9e-08:41:60//HOMO
SAPIENS (HUMAN)//P39188

F-HEMBB1002614//HYPOTHETICAL 9.5 KD PROTEIN//1.0:40:35//VACCINIA VIRUS (STRAIN
COPENHAGEN)//P20553

30 F-HEMBB1002617//INSECT TOXIN 1 (BOT IT1)//1.0:44:29//BUTHUS OCCITANUS
TUNETANUS (COMMON EUROPEAN SCORPION)//P55902

35 F-HEMBB1002623//HYPOTHETICAL 9.7 KD PROTEIN (ORF88) (PUTATIVE DNA-BINDING
PROTEIN)//0.42:31:54//BACTERIOPHAGE P4//P12552

40 F-HEMBB1002635//STRESS-ACTIVATED PROTEIN KINASE JNK3 (EC 2.7.1.-) (C-JUN N-
TERMINAL KINASE 3) (MAP KINASE P49 3F12)//6.2e-17:44:95//HOMO SAPIENS (HUMAN)
//P53779

45 F-HEMBB1002664//SMALL NUCLEAR RIBONUCLEOPROTEIN ASSOCIATED PROTEIN B
(SM-B) (SNRNP-B) (SM11) (FRAGMENT)//1.0:57:36//RATTUS NORVEGICUS (RAT)//P17136

F-HEMBB1002677//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//1.9e-06:194:
34//NYCTICEBUS COUCANG (SLOW LORIS)//P08548

50 F-HEMBB1002683//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3)
(FRAGMENT)//0.96:56:35//LEMUR CATTAL (RING-TAILED LEMUR)//Q34879

55 F-HEMBB1002684//SILLUCIN//1.0:16:50//RHIZOMUCOR PUSILLUS//P02885

F-HEMBB1002686

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F-HEMBB1002692

5 F-HEMBB1002697//HELIX-DESTABILIZING PROTEIN (SINGLE-STRANDED DNA BINDING
PROTEIN) (GPV).//0.57:36:38//BACTERIOPHAGE FD, BACTERIOPHAGE F1, AND
BACTERIOPHAGE M13.//P03669

10 F-HEMBB1002699

F-HEMBB1002702

15 F-HEMBB1002705//HYPOTHETICAL 34.8 KD PROTEIN C4H3.04C IN CHROMOSOME
I.//3.6e-40:180:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10212

F-HEMBB1002712

20 F-MAMMA1000009//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.2e-32:95:75//HOMO
SAPIENS (HUMAN).//P39189

25 F-MAMMA1000019

30 F-MAMMA1000020//DIMETHYLANILINE MONOOXYGENASE [N-OXIDE FORMING] 5 (EC
1.14.13.8) (HEPATIC FLAVIN-CONTAINING MONOOXYGENASE 5) (FMO 5)
(DIMETHYLANILINE OXIDASE 5).//5.2e-12:24:100//HOMO SAPIENS (HUMAN).//P49326

F-MAMMA1000025//BETA-2-MICROGLOBULIN PRECURSOR.//1.0:73:26//BRACHYDANIO
RERIO (ZEBRAFISH) (ZEBRA DANIO).//Q04475

35 F-MAMMA1000043//HYPOTHETICAL PXBL-I PROTEIN (FRAGMENT).//0.057:130:31//BOVINE
LEUKEMIA VIRUS (JAPANESE ISOLATE BLV-1) (BLV).//P03412

40 F-MAMMA1000045

F-MAMMA1000055//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//7.5e-44:138:55//MUS
MUSCULUS (MOUSE).//P47226

45 F-MAMMA1000057//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.2e-39:92:69//HOMO
SAPIENS (HUMAN).//P39194

50 F-MAMMA1000069//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.0044:96:34//ORGYIA
PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10341

55 F-MAMMA1000084//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//5.4e-28:94:73//HOMO
SAPIENS (HUMAN).//P39195

F-MAMMA1000085//PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C (EC 6.1.1.16)
(CYSTEINE- TRNA LIGASE) (CYSRS).//6.6e-38:90:51//SCHIZOSACCHAROMYCES POMBE

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(FISSION YEAST).//Q09860

- 5 F-MAMMA1000092//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/6.4e-30:43:86//HOMO SAPIENS (HUMAN).//P39192
- 10 F-MAMMA1000103//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.038:17:52//HOMO SAPIENS (HUMAN).//P22531
- F-MAMMA1000117//50S RIBOSOMAL PROTEIN L24E (HL21/HL22).//0.90:25:48//HALOARCUA MARISMORTUI (HALOBACTERIUM MARISMORTUI).//P14116
- 15 F-MAMMA1000129//HYPOTHETICAL BHLF1 PROTEIN.//0.0016:75:40//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
- 20 F-MAMMA1000133
- F-MAMMA1000134//HYPOTHETICAL PROTEIN MJ0647.//1.0:41:41//METHANOCOCCUS JANNASCHII.//Q58063
- 25 F-MAMMA1000139//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-3 SUBUNIT.//0.99:69:28//BOS TAURUS (BOVINE), AND MUS MUSCULUS (MOUSE).//P29798
- 30 F-MAMMA1000143//CALPAIN INHIBITOR (CALPASTATIN) (FRAGMENT).//0.023:111:27//MUS MUSCULUS (MOUSE).//P51125
- 35 F-MAMMA1000155//PUTATIVE CUTICLE COLLAGEN C09G5.5.//0.018:125:34//CAENORHABDITIS ELEGANS.//Q09456
- 40 F-MAMMA1000163//MERCURIC TRANSPORT PROTEIN PERIPLASMIC COMPONENT PRECURSOR (PERIPLASMIC MERCURY ION BINDING PROTEIN) (MERCURY SCAVENGER PROTEIN).//0.11:88:25//SHEWANELLA PUTREFACIENS (PSEUDOMONAS PUTREFACIENS).//Q54463
- F-MAMMA1000171
- 45 F-MAMMA1000173//DREBRIN E.//7.6e-41:197:43//HOMO SAPIENS (HUMAN).//Q16643
- 50 F-MAMMA1000175//GAMMA-THIONIN HOMOLOG PPT PRECURSOR.//0.92:39:38//PETUNIA INTEGRIFOLIA (VIOLET-FLOWERED PETUNIA) (PETUNIA INFLATA).//Q40901
- F-MAMMA1000183//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.4e-106:249:61//HOMO SAPIENS (HUMAN).//P51523
- 55 F-MAMMA1000198//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.0014:35:42//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645

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F-MAMMA1000221

5 F-MAMMA1000227//6.8 KD MITOCHONDRIAL PROTEOLIPID.//1.0:30:40//MUS MUSCULUS (MOUSE).//P56379

10 F-MAMMA1000241//PHOTOSYSTEM I REACTION CENTRE SUBUNIT X (PSI-K).//1.0:40:37//PORPHYRA PURPUREA.//P51370

15 F-MAMMA1000251//HYPOTHETICAL 6.8 KD PROTEIN IN FIC-PPIA INTERGENIC REGION.//0.99:29:48//SALMONELLA TYPHIMURIUM.//P37771

20 F-MAMMA1000254//HYPOTHETICAL 6.0 KD PROTEIN IN THI12 5'REGION.//1.0:20:50//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53820

25 F-MAMMA1000257//HYPOTHETICAL 50.0 KD PROTEIN IN HEML 3'REGION (ORF2).//0.22:50:44//PSEUDOMONAS AERUGINOSA.//Q51470

30 F-MAMMA1000264//GASTRIN-RELEASING PEPTIDE RECEPTOR (GRP-R) (GRP-PREFERRING BOMBESIN RECEPTOR).//0.80:39:43//HOMO SAPIENS (HUMAN).//P30550

F-MAMMA1000266

35 F-MAMMA1000270/////ALU SUBFAMILY SB WARNING ENTRY /////9.5e-42:95:84//HOMO SAPIENS (HUMAN).//P39189

40 F-MAMMA1000277//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN].//0.0062:90:34//MUS MUSCULUS (MOUSE).//P28481

45 F-MAMMA1000278//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT).//0.00096:59:33//HORDEUM VULGARE (BARLEY).//P17991

50 F-MAMMA1000279/////ALU SUBFAMILY SX WARNING ENTRY /////8.4e-17:56:76//HOMO SAPIENS (HUMAN).//P39195

55 F-MAMMA1000284//ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR 2 (ARNT PROTEIN 2).//0.017:146:30//MUS MUSCULUS (MOUSE).//Q61324

F-MAMMA1000287/////ALU SUBFAMILY SB WARNING ENTRY /////1.5e-32:84:58//HOMO SAPIENS (HUMAN).//P39189

F-MAMMA1000302//C-HORDEIN (CLONE PC-919) (FRAGMENT).//1.0:42:33//HORDEUM VULGARE (BARLEY).//P17992

F-MAMMA1000307//PROBABLE E4 PROTEIN.//0.21:71:30//RHESUS PAPILLOMAVIRUS TYPE 1 (RHPV 1).//P24832

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F-MAMMA1000309//COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN).//0.0026:141:36//HOMO SAPIENS (HUMAN).//P27658

5 F-MAMMA1000312

F-MAMMA1000313//DNA REPAIR PROTEIN RAD51 HOMOLOG (25 KD PROTEIN) (FRAGMENT).//0.76:52:32//STAPHYLOCOCCUS AUREUS.//P31337

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F-MAMMA1000331

F-MAMMA1000339//50S RIBOSOMAL PROTEIN L29P.//0.78:32:46//METHANOBACTERIUM THERMOAUTOTROPHICUM.//O26117

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F-MAMMA1000340//HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REGION.//1.0:29:58//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36039

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F-MAMMA1000348//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//7.5e-09:63:60//HOMO SAPIENS (HUMAN).//P39188

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F-MAMMA1000356//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.3e-05:42:52//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1000360

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F-MAMMA1000361//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//4.4e-33:84:72//HOMO SAPIENS (HUMAN).//P39189

35

F-MAMMA1000372//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//6.6e-21:53:71//HOMO SAPIENS (HUMAN).//P39193

F-MAMMA1000385

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F-MAMMA1000388//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).//0.40:72:36//HOMO SAPIENS (HUMAN).//P43489

45

F-MAMMA1000395//RABPHILIN-3A (FRAGMENT).//0.032:125:25//MUS MUSCULUS (MOUSE).//P47708

50

F-MAMMA1000402//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.1e-28:266:40//HOMO SAPIENS (HUMAN).//P08547

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F-MAMMA1000410//NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-B SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-13KD-B) (CI-13KD-B) (B13).//5.9e-06:32:68//HOMO SAPIENS (HUMAN).//Q16718

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F-MAMMA1000413//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//6.7e-05:93:31//MUS MUSCULUS (MOUSE).//P11369

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F-MAMMA1000414

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F-MAMMA1000416//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III.//4.1e-28:119:53//CAENORHABDITIS ELEGANS.//Q09232

15

F-MAMMA1000421//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.7e-23:68:76//HOMO SAPIENS (HUMAN).//P39194

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F-MAMMA1000422//METALLOTHIONEIN (MT).//0.037:42:42//GADUS MORHUA (ATLANTIC COD).//P51902

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F-MAMMA1000423

F-MAMMA1000424//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//0.048:23:73//HOMO SAPIENS (HUMAN).//P39189

30

F-MAMMA1000429//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS5.//2.7e-05:110:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q92331

35

F-MAMMA1000431//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//9.4e-15:85:58//HOMO SAPIENS (HUMAN).//P39194

40

F-MAMMA1000444//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//4.3e-25:65:76//HOMO SAPIENS (HUMAN).//P39194

45

F-MAMMA1000446//ZYNIN.//0.79:155:29//GALLUS GALLUS (CHICKEN).//Q04584

50

F-MAMMA1000458//HYPOTHETICAL 37.7 KD PROTEIN C18B11.06 IN CHROMOSOME I.//0.0048:46:43//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09713

F-MAMMA1000468//PERIOD CLOCK PROTEIN (FRAGMENT).//0.50:20:55//DROSOPHILA ROBUSTA (FRUIT FLY).//Q03296

55

F-MAMMA1000472//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.5e-17:106:55//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1000478//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//3.9e-35:80:68//HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1000483//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//2.8e-24:74:77//HOMO SAPIENS (HUMAN).//P39193

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F-MAMMA1000490//TYROSINE-PROTEIN KINASE TXK (EC 2.7.1.112) (PTK-RL-18)
(RESTING LYMPHOCYTE KINASE).//0.43:21:57//MUS MUSCULUS (MOUSE).//P42682

5 F-MAMMA1000500//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.61:33:
54//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z2/CDC-Z34 ISOLATE) (HIV-1).//P12506

10 F-MAMMA1000501//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.1e-32:43:83//HOMO
SAPIENS (HUMAN).//P39194

F-MAMMA1000516

15 F-MAMMA1000522//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.0015:113:32//HOMO
SAPIENS (HUMAN).//P08547

20 F-MAMMA1000524//HYPOTHETICAL HOST RANGE 8.5 KD PROTEIN.//1.0:63:31//VACCINIA
VIRUS (STRAIN WR).//P17359

25 F-MAMMA1000559//METALLOTHIONEIN-I (MT-I) (MT-IB/MT-IA).//0.31:16:50//CALLINECTES
SAPIDUS (BLUE CRAB).//P55949

F-MAMMA1000565//FERREDOXIN-TYPE PROTEIN NAPF.//0.98:37:35//ESCHERICHIA
COLI.//P33939

30 F-MAMMA1000567//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/5.5e-37:95:76//HOMO
SAPIENS (HUMAN).//P39195

35 F-MAMMA1000576//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/4.1e-07:34:64//HOMO
SAPIENS (HUMAN).//P39191

F-MAMMA1000583

40 F-MAMMA1000585//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.5e-28:89:75//HOMO
SAPIENS (HUMAN).//P39194

45 F-MAMMA1000594//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/4.8e-24:38:71//HOMO
SAPIENS (HUMAN).//P39195

50 F-MAMMA1000597//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.1e-25:74:77//HOMO
SAPIENS (HUMAN).//P39195

F-MAMMA1000605//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.1e-18:83:50//HOMO
SAPIENS (HUMAN).//P39195

55 F-MAMMA1000612//HYPOTHETICAL 34.0 KD TRP-ASP REPEATS CONTAINING PROTEIN IN
SIS1-MRPL2 INTERGENIC REGION.//4.0e-42:166:48//SACCHAROMYCES CEREVISIAE
(BAKER'S YEAST).//P41318

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F-MAMMA1000616

5 F-MAMMA1000621

F-MAMMA1000623//METALLOTHIONEIN-IK (MT-1K)//0.0045:25:48//HOMO SAPIENS (HUMAN)//P80296

10 F-MAMMA1000625//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//0.00078:79:35//MUS MUSCULUS (MOUSE)//P05143

15 F-MAMMA1000643//HYPOTHETICAL 9.3 KD PROTEIN//1.0:25:28//MAGUARI VIRUS//P16607

F-MAMMA1000664

20 F-MAMMA1000669//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//4.2e-05:186:30//HOMO SAPIENS (HUMAN)//P08547

F-MAMMA1000670//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//1.6e-06:195:30//MUS MUSCULUS (MOUSE)//P05143

25 F-MAMMA1000672//VITELLOGENIC CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.-)//3.8e-28:184:35//AEDES AEGYPTI (YELLOW FEVER MOSQUITO)//P42660

30 F-MAMMA1000684//DNA-BINDING PROTEIN (VMW21)//1.1e-07:55:56//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)//P04487

35 F-MAMMA1000696//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!1.2e-31:97:74//HOMO SAPIENS (HUMAN)//P39194

F-MAMMA1000707//METALLOTHIONEIN-II (MT-II) (MT-IIB/MT-IIA)//0.31:19:42//CALLINECTES SAPIDUS (BLUE CRAB)//P55950

40 F-MAMMA1000713//XYLULOSE KINASE (EC 2.7.1.17) (XYLUKINASE)//1.6e-05:88:35//LACTOBACILLUS PENTOSUS//P21939

45 F-MAMMA1000714//PROTEIN-LYSINE 6-OXIDASE PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE)//0.44:126:30//RATTUS NORVEGICUS (RAT)//P16636

50 F-MAMMA1000718//METALLOTHIONEIN-III (MT-2E)//1.0:51:31//ORYCTOLAGUS CUNICULUS (RABBIT)//P80292

F-MAMMA1000720//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!3.3e-28:60:71//HOMO SAPIENS (HUMAN)//P39193

55 F-MAMMA1000723//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//3.7e-14:63:53//HOMO

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SAPIENS (HUMAN).//P08547

5 F-MAMMA1000731//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2).//1.8e-43:258:43//HOMO SAPIENS (HUMAN).//O14647

10 F-MAMMA1000732//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//9.9e-12:76:55//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1000733

15 F-MAMMA1000734//NPL1 PROTEIN (SEC63 PROTEIN).//2.5e-18:181:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P14906

20 F-MAMMA1000738//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.//5.4e-52:196:58//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87115

F-MAMMA1000744//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!!//6.3e-36:144:47//HOMO SAPIENS (HUMAN).//P39190

25 F-MAMMA1000746

F-MAMMA1000752

30 F-MAMMA1000760//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//6.6e-29:75:72//HOMO SAPIENS (HUMAN).//P39195

35 F-MAMMA1000761//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.6e-09:59:64//HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1000775

40 F-MAMMA1000776//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//3.3e-35:99:74//HOMO SAPIENS (HUMAN).//P39193

45 F-MAMMA1000778//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.1e-19:65:70//HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1000782

50 F-MAMMA1000798//HYPOTHETICAL PROTEIN ORF-1137.//0.015:59:37//MUS MUSCULUS (MOUSE).//P11260

55 F-MAMMA1000802//MYOSIN IC HEAVY CHAIN.//0.35:94:41//ACANTHAMOEBA CASTELLANII (AMOEBIA).//P10569

F-MAMMA1000824//ACTIN 1.//0.046:60:31//ZEA MAYS (MAIZE).//P02582

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F-MAMMA1000831//PROBABLE NI/FE-HYDROGENASE 1 B-TYPE CYTOCHROME
 SUBUNIT.//1.0:30:46//ESCHERICHIA COLI.//P19929
 5
 F-MAMMA1000839//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-28:80:58//HOMO
 SAPIENS (HUMAN).//P39188
 10
 F-MAMMA1000841//PUTATIVE AMIDASE (EC 3.5.1.4).//1.5e-39:130:
 36//METHANOBACTERIUM THERMOAUTOTROPHICUM.//O27540
 15
 F-MAMMA1000842//C-HORDEIN (CLONE PC-919) (FRAGMENT).//0.064:43:41//HORDEUM
 VULGARE (BARLEY).//P17992
 F-MAMMA1000843
 20
 F-MAMMA1000845//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3).//0.43:58:
 34//DROSOPHILA YAKUBA (FRUIT FLY).//P03895
 25
 F-MAMMA1000851//CUTICLE COLLAGEN 34.//0.019:107:29//CAENORHABDITIS
 ELEGANS.//P34687
 F-MAMMA1000855//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//0.00098:
 149:32//HOMO SAPIENS (HUMAN).//Q15428
 30
 F-MAMMA1000856//METALLOTHIONEIN (MT).//0.63:39:41//POTAMON POTAMIOS.//P55952
 F-MAMMA1000859//GLYCOPROTEIN X PRECURSOR.//0.014:192:28//EQUINE
 35
 HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).//P28968
 F-MAMMA1000862//DISINTEGRIN KISTRIN (PLATELET AGGREGATION ACTIVATION
 INHIBITOR).//1.0:66:27//AGKISTRODON RHODOSTOMA (MALAYAN PIT VIPER)
 40
 (CALLOSELASMA RHODOSTOMA).//P17494
 F-MAMMA1000863//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.4e-16:41:68//HOMO
 SAPIENS (HUMAN).//P39188
 45
 F-MAMMA1000865//SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT).//0.030:100:
 32//HOMO SAPIENS (HUMAN).//P81489
 50
 F-MAMMA1000867//APTOTOXIN IX (PARALYTIC PEPTIDE IX) (PP IX).//0.98:43:
 32//APTOSTICHUS SCHLINGERI (TRAP-DOOR SPIDER).//P49272
 55
 F-MAMMA1000875//PROLINE-RICH PEPTIDE P-B.//0.18:21:47//HOMO SAPIENS (HUMAN)
 .//P02814
 F-MAMMA1000876//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.5e-22:85:71//HOMO

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SAPIENS (HUMAN).//P39189

5 F-MAMMA1000877//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.2e-38:62:74//HOMO
SAPIENS (HUMAN).//P39188

10 F-MAMMA1000880//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.49:79:32//BOS
TAURUS (BOVINE).//P25508

F-MAMMA1000883//HYPOTHETICAL 6.1 KD PROTEIN C03B1.10 IN CHROMOSOME X.//0.87:
15:60//CAENORHABDITIS ELEGANS.//Q11116

15 F-MAMMA1000897//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H4 PRECURSOR (ITI
HEAVY CHAIN H4) (INTER-ALPHA-TRYPSIN INHIBITOR FAMILY HEAVY CHAIN-RELATED
PROTEIN) (PLASMA KALLIKREIN SENSITIVE GLYCOPROTEIN 120) (PK-120).//5.3e-17:130:
40//HOMO SAPIENS (HUMAN).//Q14624

20 F-MAMMA1000905

25 F-MAMMA1000906

F-MAMMA1000908//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//8.0e-17:70:62//HOMO
SAPIENS (HUMAN).//P08547

30 F-MAMMA1000914//HYPOTHETICAL 6.2 KD PROTEIN.//0.97:36:36//THERMOPROTEUS
TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19299

35 F-MAMMA1000921

F-MAMMA1000931//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.6e-10:49:65//HOMO
SAPIENS (HUMAN).//P39188

40 F-MAMMA1000940//MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L32.//0.42:22:
54//RECLINOMONAS AMERICANA.//O21281

45 F-MAMMA1000941//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.3e-25:55:69//HOMO
SAPIENS (HUMAN).//P39188

F-MAMMA1000942//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.3e-08:36:75//HOMO
SAPIENS (HUMAN).//P39194

50 F-MAMMA1000943

55 F-MAMMA1000956//SMALL HISTIDINE-ALANINE-RICH PROTEIN PRECURSOR (SHARP)
(ANTIGEN 57).//0.041:122:25//PLASMODIUM FALCIPARUM (ISOLATE FC27 / PAPUA NEW
GUINEA).//P04930

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F-MAMMA1000957//HEAT-STABLE ENTEROTOXIN A2 PRECURSOR (STA2)//0.024:37:37//ESCHERICHIA COLI//Q47185

5 F-MAMMA1000962//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/6.0e-39:61:78//HOMO SAPIENS (HUMAN)//P39189

10 F-MAMMA1000968//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/0.0054:29:72//HOMO SAPIENS (HUMAN)//P39194

15 F-MAMMA1000975//CUTICLE COLLAGEN DPY-2 PRECURSOR//1.0:93:30//CAENORHABDITIS ELEGANS//P35799

F-MAMMA1000979//PROLINE-RICH PEPTIDE P-B//0.012:12:66//HOMO SAPIENS (HUMAN) //P02814

20 F-MAMMA1000987//HYPOTHETICAL PROTEIN LAMBDA-SP34//1.0:47:40//MUS MUSCULUS (MOUSE)//P15973

25 F-MAMMA1000998

F-MAMMA1001003//PROBABLE E5 PROTEIN//1.0:52:42//HUMAN PAPILLOMAVIRUS TYPE 33//P06426

30 F-MAMMA1001008//PROGASTRICSIN PRECURSOR (EC 3.4.23.3) (PEPSINOGEN C) (FRAGMENT)//3.2e-14:131:35//MACACA FUSCATA FUSCATA (JAPANESE MACAQUE) //P03955

35 F-MAMMA1001021//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556//0.016:61:42//STREPTOMYCES FRADIAE//P20186

40 F-MAMMA1001024

F-MAMMA1001030//LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR (LH/CG-R) (LSH-R) (LUTEINIZING HORMONE RECEPTOR) (FRAGMENT)//2.4e-20:234:29//GALLUS GALLUS (CHICKEN)//Q90674

45 F-MAMMA1001035//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.7e-15:52:78//HOMO SAPIENS (HUMAN)//P39193

50 F-MAMMA1001038//NEUROTOXIN II (TOXIN RP-II) (SODIUM CHANNEL TOXIN II)//0.53:25:48//RADIANTHUS PAUMOTENSIS (SEA ANEMONE) (HETERACTIS PAUMOTENSIS)//P01534

55 F-MAMMA1001041//SPECTRIN BETA CHAIN, ERYTHROCYTE//6.3e-18:112:43//MUS MUSCULUS (MOUSE)//P15508

F-MAMMA1001050

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F-MAMMA1001059//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//1.3e-34:187:
 47//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09747
 5
 F-MAMMA1001067//PROTEIN Q300.//0.36:12:75//MUS MUSCULUS (MOUSE).//Q02722
 F-MAMMA1001073//HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 1 (HFH-1)
 10 .//1.0:70:37//RATTUS NORVEGICUS (RAT).//Q63244
 F-MAMMA1001074//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.00067:163:32//HOMO
 SAPIENS (HUMAN).//P08547
 15
 F-MAMMA1001075//RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1).//0.53:72:34//HOMO
 SAPIENS (HUMAN).//P29374
 F-MAMMA1001078//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.0e-79:184:73//HOMO
 SAPIENS (HUMAN).//P08547
 20
 F-MAMMA1001080//IG HEAVY CHAIN PRECURSOR V-III REGION (VH26).//1.7e-27:82:
 25 71//HOMO SAPIENS (HUMAN).//P01764
 F-MAMMA1001082
 F-MAMMA1001091//HYPOTHETICAL BHLF1 PROTEIN.//3.1e-05:198:32//EPSTEIN-BARR
 VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
 30
 F-MAMMA1001092//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.1e-21:65:72//HOMO
 SAPIENS (HUMAN).//P08547
 35
 F-MAMMA1001105//OVO PROTEIN (SHAVEN BABY PROTEIN).//1.0e-18:68:48//DROSOPHILA
 MELANOGASTER (FRUIT FLY).//P51521
 40
 F-MAMMA1001110//PROCOLLAGEN ALPHA 1(IV) CHAIN PRECURSOR.//0.080:108:37//MUS
 MUSCULUS (MOUSE).//P02463
 F-MAMMA1001126//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.3e-07:66:45//HOMO
 SAPIENS (HUMAN).//P39189
 45
 F-MAMMA1001133//HYPOTHETICAL 13.2 KD PROTEIN IN RPS4A-BAT2 INTERGENIC
 REGION.//0.96:43:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47174
 50
 F-MAMMA1001139//HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II.//5.4e-42:
 81:62//CAENORHABDITIS ELEGANS.//Q09201
 55
 F-MAMMA1001143//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.00014:36:66//HOMO
 SAPIENS (HUMAN).//P39188

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F-MAMMA1001145

- 5 F-MAMMA1001154//CSBA PROTEIN.//1.0:39:38//BACILLUS SUBTILIS.//P37953
- F-MAMMA1001161//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.2e-23:53:64//HOMO SAPIENS (HUMAN).//P39188
- 10 F-MAMMA1001162//CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27).//0.69:86:31//MUS MUSCULUS (MOUSE).//P41272
- 15 F-MAMMA1001181//HYPOTHETICAL 81.0 KD PROTEIN C35D10.4 IN CHROMOSOME III.//0.00010:74:47//CAENORHABDITIS ELEGANS.//Q18486
- 20 F-MAMMA1001186//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/9.0e-32:44:86//HOMO SAPIENS (HUMAN).//P39194
- F-MAMMA1001191//OCTAMER-BINDING TRANSCRIPTION FACTOR 1 (OTF-1) (NF-A1) (FRAGMENT).//0.096:40:40//MACROPUS EUGENII (TAMMAR WALLABY).//Q28466
- 25 F-MAMMA1001198//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN).//2.5e-75:204:70//HOMO SAPIENS (HUMAN) .//P42566
- 30 F-MAMMA1001202//METALLOTHIONEIN-II (MT-II) (MT-IIB/MT-IIA).//0.52:46:32//CALLINECTES SAPIDUS (BLUE CRAB).//P55950
- 35 F-MAMMA1001203//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/7.3e-11:82:58//HOMO SAPIENS (HUMAN).//P39192
- 40 F-MAMMA1001206//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.9e-17:67:71//HOMO SAPIENS (HUMAN).//P39188
- F-MAMMA1001215//9 KD PROTEIN.//1.0:51:33//HOMO SAPIENS (HUMAN).//P13994
- 45 F-MAMMA1001220//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/3.4e-37:55:87//HOMO SAPIENS (HUMAN).//P39189
- 50 F-MAMMA1001222//HYPOTHETICAL 73.6 KD PROTEIN CY49.21.//3.7e-06:168:38//MYCOBACTERIUM TUBERCULOSIS.//Q10690
- F-MAMMA1001243
- 55 F-MAMMA1001244//TRP OPERON LEADER PEPTIDE.//1.0:18:55//SERRATIA MARCESCENS.//P03055

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F-MAMMA1001249//HYPOTHETICAL 7.2 KD PROTEIN IN RPS2 3'REGION (ORF57).//0.57:23:34//ASTASIA LONGA (EUGLENOPHYCEAN ALGA).//P34774

5 F-MAMMA1001256//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.3e-07:79:44//HOMO SAPIENS (HUMAN).//P39188

10 F-MAMMA1001259//PUTATIVE DNA HELICASE II HOMOLOG (EC 3.6.1.-).//0.046:86:32//MYCOPLASMA GENITALIUM.//P47486

15 F-MAMMA1001260//MYOSIN HEAVY CHAIN, PERINATAL SKELETAL MUSCLE.//2.7e-05:219:27//HOMO SAPIENS (HUMAN).//P13535

F-MAMMA1001268//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.7e-27:89:67//HOMO SAPIENS (HUMAN).//P08547

20 F-MAMMA1001271//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN).//4.0e-06:126:38//HOMO SAPIENS (HUMAN).//P54259

25 F-MAMMA1001274//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//7.4e-29:57:66//HOMO SAPIENS (HUMAN).//P39194

30 F-MAMMA1001280//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17).//0.27:24:54//ESCHERICHIA COLI.//P05834

F-MAMMA1001292//HYPOTHETICAL PROTEIN KIAA0176 (FRAGMENT).//1.3e-73:208:69//HOMO SAPIENS (HUMAN).//Q14681

35 F-MAMMA1001296//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//6.9e-22:41:80//HOMO SAPIENS (HUMAN).//P39193

40 F-MAMMA1001298//HYPOTHETICAL PROTEIN HI0371.//0.99:29:37//HAEMOPHILUS INFLUENZAE.//P44668

45 F-MAMMA1001305//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//9.9e-62:222:54//HOMO SAPIENS (HUMAN).//Q07960

50 F-MAMMA1001322//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//2.1e-09:46:60//HOMO SAPIENS (HUMAN).//P20931

55 F-MAMMA1001324//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)].//2.5e-43:128:50//FRIEND MURINE LEUKEMIA VIRUS (ISOLATE PVC-211) (F-MULV).//P26808

F-MAMMA1001330//HEMOGLOBIN ZETA CHAIN (FRAGMENTS).//0.30:51:37//MACROPUS EUGENII (TAMMAR WALLABY).//P81044

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5 F-MAMMA1001341//TRISTETRAPROLINE (TTP) (TIS11A) (TIS11) (ZFP-36) (GROWTH
FACTOR- INDUCIBLE NUCLEAR PROTEIN NUP475).//0.024:89:39//HOMO SAPIENS
(HUMAN).//P26651

10 F-MAMMA1001343//PROBABLE E5 PROTEIN.//0.60:64:29//HUMAN PAPILLOMAVIRUS TYPE
16.//P06927

F-MAMMA1001346//PROTEINASE INHIBITOR IIB (FRAGMENTS).//0.97:33:45//SOLANUM
TUBEROSUM (POTATO).//P01082

15 F-MAMMA1001383//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.2e-30:86:77//HOMO
SAPIENS (HUMAN).//P39194

20 F-MAMMA1001388//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//9.2e-91:195:
92//HOMO SAPIENS (HUMAN).//P02750

25 F-MAMMA1001397//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.5e-19:55:69//HOMO
SAPIENS (HUMAN).//P39188

F-MAMMA1001408//SALIVARY GLUE PROTEIN SGS-7 PRECURSOR.//0.60:45:
35//DROSOPHILA MELANOGASTER (FRUIT FLY).//P02841

30 F-MAMMA1001411//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-
ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//5.8e-06:153:
26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640

35 F-MAMMA1001419//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.3e-16:99:51//HOMO
SAPIENS (HUMAN).//P39194

40 F-MAMMA1001420//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!!/0.0018:23:65//HOMO
SAPIENS (HUMAN).//P39190

F-MAMMA1001435//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.7e-22:60:58//HOMO
SAPIENS (HUMAN).//P39195

45 F-MAMMA1001442

50 F-MAMMA1001446//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.2e-23:48:75//HOMO
SAPIENS (HUMAN).//P39194

55 F-MAMMA1001452//GENE 35 PROTEIN (GP35).//0.61:31:45//MYCOBACTERIOPHAGE
L5.//Q05245

F-MAMMA1001465//HYPOTHETICAL PROTEIN E-115.//0.0026:68:38//HUMAN ADENOVIRUS
TYPE 2.//P03290

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F-MAMMA1001476//URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE)
 (FRAGMENT).//3.7e-94:201:92//MUS MUSCULUS (MOUSE).//P52623
 5
 F-MAMMA1001487//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.6e-16:89:
 41//NYCTICEBUS COUCANG (SLOW LORIS).//P08548
 10
 F-MAMMA1001501//CALPAIN 1, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-
 ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU-TYPE).//6.2e-59:86:97//HOMO SAPIENS
 (HUMAN).//P07384
 15
 F-MAMMA1001502//HYPOTHETICAL 11.4 KD PROTEIN (ORF1).//0.21:79:
 30//STREPTOMYCES FRADIAE.//P26800
 20
 F-MAMMA1001510
 F-MAMMA1001522//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.67:98:
 31//STREPTOMYCES FRADIAE.//P20186
 25
 F-MAMMA1001547//PROBABLE MOLYBDENUM-PTERIN BINDING PROTEIN.//0.97:35:
 42//HAEMOPHILUS INFLUENZAE.//P45183
 30
 F-MAMMA1001551//HYPOTHETICAL PROTEIN MJ0458.1.//0.038:31:41//METHANOCOCCUS
 JANNASCHII.//P81308
 F-MAMMA1001575
 35
 F-MAMMA1001576//TUBULIN GAMMA CHAIN.//1.6e-86:162:99//XENOPUS LAEVIS (AFRICAN
 CLAWED FROG).//P23330
 40
 F-MAMMA1001590//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.0035:38:55//HOMO
 SAPIENS (HUMAN).//P39195
 F-MAMMA1001600//CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR.//0.85:53:
 33//HOMO SAPIENS (HUMAN).//P29279
 45
 F-MAMMA1001604//HYPOTHETICAL 11.1 KD PROTEIN C30D11.02C IN CHROMOSOME
 I.//0.14:82:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09902
 50
 F-MAMMA1001606//HIGH MOBILITY GROUP PROTEIN HMGI-C.//8.2e-05:77:37//HOMO
 SAPIENS (HUMAN).//P52926
 55
 F-MAMMA1001620//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//5.5e-05:24:66//HOMO
 SAPIENS (HUMAN).//P39195
 F-MAMMA1001627//CUTICLE COLLAGEN 40.//0.82:131:31//CAENORHABDITIS

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ELEGANS.//P34804

- 5 F-MAMMA1001630!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/8.6e-26:57:78//HOMO SAPIENS (HUMAN).//P39194
- 10 F-MAMMA1001633//ZINC FINGER PROTEIN 165.//6.9e-38:160:55//HOMO SAPIENS (HUMAN) .//P49910
- F-MAMMA1001635
- 15 F-MAMMA1001649//SPERM PROTAMINE P1.//0.39:31:41//TACHYGLOSSUS ACULEATUS ACULEATUS (AUSTRALIAN ECHIDNA).//P35311
- 20 F-MAMMA1001654//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PROTEIN KINASE 1).//5.6e-06:99:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P18160
- 25 F-MAMMA1001663//VERY HYPOTHETICAL XYLU PROTEIN.//0.99:27:37//ESCHERICHIA COLI.//P05056
- F-MAMMA1001670//CUTICLE COLLAGEN 1.//0.033:97:37//CAENORHABDITIS ELEGANS.//P08124
- 30 F-MAMMA1001671
- F-MAMMA1001679//PROCOLLAGEN ALPHA 2(IV) CHAIN PRECURSOR.//0.92:32:50//HOMO SAPIENS (HUMAN).//P08572
- 35 F-MAMMA1001683//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.00026: 147:34//STREPTOMYCES FRADIAE.//P20186
- 40 F-MAMMA1001686
- F-MAMMA1001692//SMALL HYDROPHOBIC PROTEIN (SMALL PROTEIN 1A).//1.0:34: 26//BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN A51908) (BRS).//P24616
- 45 F-MAMMA1001711!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.1e-28:56:69//HOMO SAPIENS (HUMAN).//P39194
- 50 F-MAMMA1001715!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.6e-08:39:71//HOMO SAPIENS (HUMAN).//P39188
- 55 F-MAMMA1001730//METALLOTHIONEIN-B (MTB).//1.0:17:64//STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN).//Q27287
- F-MAMMA1001735//TUBULIN BETA-5 CHAIN (CLASS-V).//5.1e-121:213:97//GALLUS GALLUS

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(CHICKEN).//P09653

F-MAMMA1001740

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F-MAMMA1001743//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.3e-09:100:42//HOMO SAPIENS (HUMAN).//P39195

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F-MAMMA1001744//POU DOMAIN PROTEIN 2.//0.97:59:38//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).//Q90270

15

F-MAMMA1001745//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.1e-43:199:42//HOMO SAPIENS (HUMAN).//P08547

F-MAMMA1001751//TWK-8 PROTEIN.//2.9e-15:77:36//CAENORHABDITIS ELEGANS.//P34410

20

F-MAMMA1001754//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.019:20:45//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645

25

F-MAMMA1001757//HYPOTHETICAL 9.2 KD PROTEIN IN RNPA 3'REGION.//0.94:30:43//PSEUDOMONAS PUTIDA.//P25753

F-MAMMA1001760//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//4.6e-34:103:59//HOMO SAPIENS (HUMAN).//P39191

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F-MAMMA1001764

35

F-MAMMA1001768//HYPOTHETICAL PROTEIN UL61.//0.042:167:33//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16818

40

F-MAMMA1001769//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.0e-29:97:69//HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1001771//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//3.3e-09:123:32//HOMO SAPIENS (HUMAN).//P51805

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F-MAMMA1001783//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.1e-09:55:61//HOMO SAPIENS (HUMAN).//P39188

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F-MAMMA1001785//RAS-RELATED PROTEIN RABC.//1.9e-06:120:25//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P34143

55

F-MAMMA1001788//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.3e-29:46:76//HOMO SAPIENS (HUMAN).//P08547

F-MAMMA1001790//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.7e-24:69:69//HOMO SAPIENS (HUMAN).//P39188

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F-MAMMA1001806//HYPOTHETICAL 21.2 KD PROTEIN IN TOR2-MNN4 INTERGENIC
 REGION.//0.95:58:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36042
 5 F-MAMMA1001812//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//8.8e-12:53:69//HOMO
 SAPIENS (HUMAN).//P39195
 10 F-MAMMA1001815//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.11:30:70//HOMO
 SAPIENS (HUMAN).//P08547
 15 F-MAMMA1001817//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.9e-16:86:55//HOMO
 SAPIENS (HUMAN).//P39188
 F-MAMMA1001818
 20 F-MAMMA1001820//VITTELLINE MEMBRANE PROTEIN VM26AB PRECURSOR (PROTEIN
 TU-4) (PROTEIN SV23).//0.0030:63:42//DROSOPHILA MELANOGASTER (FRUIT FLY)
 .//P13238
 25 F-MAMMA1001824//APTOTOXIN VII (PARALYTIC PEPTIDE VII) (PP VII).//0.99:26:
 34//APTOSTICHUS SCHLINGERI (TRAP-DOOR SPIDER).//P49271
 F-MAMMA1001836//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.6e-35:77:88//HOMO
 30 SAPIENS (HUMAN).//P39195
 F-MAMMA1001837//ZINC FINGER PROTEIN 191.//1.3e-27:106:58//HOMO SAPIENS (HUMAN)
 .//O14754
 35 F-MAMMA1001848//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.0e-19:92:58//HOMO
 SAPIENS (HUMAN).//P39188
 40 F-MAMMA1001851
 F-MAMMA1001854
 45 F-MAMMA1001858//ISOTOCIN-NEUROPHYSIN IT 1 PRECURSOR.//0.93:42:
 38//CATOSTOMUS COMMERSONI (WHITE SUCKER).//P15210
 F-MAMMA1001864//PROBABLE ABC TRANSPORTER PERMEASE PROTEIN MG189.//0.77:
 50 161:27//MYCOPLASMA GENITALIUM.//P47435
 F-MAMMA1001868//FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL-PROLYL CIS-TRANS
 ISOMERASE) (PPIASE) (EC 5.2.1.8) (PROLINE ROTAMASE) (NUCLEOLAR PROLINE
 55 ISOMERASE) (FKBP-70).//0.00013:219:26//SACCHAROMYCES CEREVISIAE (BAKER'S
 YEAST).//P38911

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F-MAMMA1001874//SPERM HISTONE P2 PRECURSOR (PROTAMINE MP2).//0.0075:76:31//MUS MUSCULUS (MOUSE).//P07978

5 F-MAMMA1001878//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).//0.020:10:80//LYCOPERSICON ESCULENTUM (TOMATO).//Q01157

F-MAMMA1001880

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F-MAMMA1001890//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/5.1e-34:56:83//HOMO SAPIENS (HUMAN).//P39192

15 F-MAMMA1001907//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.7e-12:44:68//HOMO SAPIENS (HUMAN).//P39194

20 F-MAMMA1001908//HYPOTHETICAL 16.2 KD PROTEIN IN PRP24-RRN9 INTERGENIC REGION.//0.00013:77:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q03525

F-MAMMA1001931//HYPOTHETICAL 118.2 KD PROTEIN F43C1.1 IN CHROMOSOME III.//0.41:106:29//CAENORHABDITIS ELEGANS.//Q09564

25

F-MAMMA1001956//OCTAPEPTIDE-REPEAT PROTEIN T2.//0.00053:149:30//MUS MUSCULUS (MOUSE).//Q06666

30 F-MAMMA1001963//HYPOTHETICAL PROTEIN IN NAC 5'REGION (ORF X) (FRAGMENT).//1.0:46:28//KLEBSIELLA AEROGENES.//Q08600

35 F-MAMMA1001969//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.7e-34:97:68//HOMO SAPIENS (HUMAN).//P08547

F-MAMMA1001970//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.2e-07:67:37//HOMO SAPIENS (HUMAN).//P08547

40

F-MAMMA1001992//PROTEIN Q300.//0.53:14:71//MUS MUSCULUS (MOUSE).//Q02722

45 F-MAMMA1002009//PROBABLE E5 PROTEIN.//0.17:56:32//HUMAN PAPILLOMAVIRUS TYPE 31.//P17385

50 F-MAMMA1002011//MYRISTOYLATED ALANINE-RICH C-KINASE SUBSTRATE (MARCKS) (PROTEIN KINASE C SUBSTRATE, 80 KD PROTEIN, LIGHT CHAIN) (PKCSL) (80K-L PROTEIN).//1.0:100:31//HOMO SAPIENS (HUMAN).//P29966

F-MAMMA1002032//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.1e-21:86:65//HOMO SAPIENS (HUMAN).//P39188

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F-MAMMA1002033//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/8.5e-20:67:58//HOMO SAPIENS (HUMAN).//P39188

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F-MAMMA1002041//MALE SPECIFIC SPERM PROTEIN MST84DC.//1.0:17:52//DROSOPHILA
 MELANOGASTER (FRUIT FLY).//Q01644
 5
 F-MAMMA1002042//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/0.19:45:46//HOMO
 SAPIENS (HUMAN).//P39192
 10
 F-MAMMA1002047//TYROSINE AMINOTRANSFERASE (EC 2.6.1.5) (L-TYROSINE:2-
 OXOGLUTARATE AMINOTRANSFERASE) (TAT).//0.0017:50:46//RATTUS NORVEGICUS (RAT)
 .//P04694
 15
 F-MAMMA1002056//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.2e-37:70:77//HOMO
 SAPIENS (HUMAN).//P39194
 20
 F-MAMMA1002058//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-08:26:76//HOMO
 SAPIENS (HUMAN).//P39188
 F-MAMMA1002068//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.0e-11:78:46//HOMO
 SAPIENS (HUMAN).//P08547
 25
 F-MAMMA1002078//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.96:26:46//COTURNIX
 COTURNIX JAPONICA (JAPANESE QUAIL).//P50682
 30
 F-MAMMA1002082//SUPPRESSOR PROTEIN SRP40.//0.23:95:32//SACCHAROMYCES
 CEREVISIAE (BAKER'S YEAST).//P32583
 35
 F-MAMMA1002084//HYPOTHETICAL 7.5 KD PROTEIN.//1.0:40:35//VACCINIA VIRUS (STRAIN
 COPENHAGEN).//P20520
 F-MAMMA1002093
 40
 F-MAMMA1002108//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.00079:
 143:33//STREPTOMYCES FRADIAE.//P20186
 45
 F-MAMMA1002118//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:43:34//METRIDIDIUM
 SENILE (BROWN SEA ANEMONE) (FRILLED SEA ANEMONE).//O47493
 F-MAMMA1002125//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.9e-14:60:68//HOMO
 SAPIENS (HUMAN).//P39192
 50
 F-MAMMA1002132
 F-MAMMA1002140//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.4e-24:69:65//HOMO
 SAPIENS (HUMAN).//P39188
 55
 F-MAMMA1002143//SERUM PROTEIN MSE55.//2.1e-16:166:43//HOMO SAPIENS (HUMAN)

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//Q00587

5 F-MAMMA1002145//36.4 KD PROLINE-RICH PROTEIN//0.00014:84:29//LYCOPERSICON
ESCULENTUM (TOMATO)//Q00451

F-MAMMA1002153

10 F-MAMMA1002155

F-MAMMA1002156//METALLOPROTEINASE INHIBITOR PRECURSOR//0.90:58:
15 34//STREPTOMYCES NIGRESCENS//P01077

F-MAMMA1002158

20 F-MAMMA1002170//40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN)//6.0e-66:157:
70//HOMO SAPIENS (HUMAN)//P15880

F-MAMMA1002174//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/6.5e-25:56:64//HOMO
25 SAPIENS (HUMAN)//P39188

F-MAMMA1002198//THIOREDOXIN PEROXIDASE 1 (THIOREDOXIN-DEPENDENT
PEROXIDE REDUCTASE 1) (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) (TSA) (PRP)
30 (NATURAL KILLER CELL ENHANCING FACTOR B) (NKEF-B)//9.0e-09:28:100//HOMO
SAPIENS (HUMAN)//P32119

F-MAMMA1002209//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-
35 135) (TAFII135) (TAFII-130) (TAFII130)//0.0023:132:33//HOMO SAPIENS (HUMAN)//O00268

F-MAMMA1002215//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR//0.00032:68:
35//HOMO SAPIENS (HUMAN)//P02452

40 F-MAMMA1002219//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1//0.0079:224:
24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P25386

45 F-MAMMA1002230

F-MAMMA1002236//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B
GDP-GTP EXCHANGE FACTOR)//1.4e-118:151:94//RATTUS NORVEGICUS (RAT)//P70541

50 F-MAMMA1002243//WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP)//0.028:
112:33//MUS MUSCULUS (MOUSE)//P70315

55 F-MAMMA1002250//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11)//0.0012:80:
32//ORYCTOLAGUS CUNICULUS (RABBIT)//P06333

F-MAMMA1002267//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6)//0.17:139:

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28//TRYPANOSOMA BRUCEI BRUCEI.//P24499

5 F-MAMMA1002268//60S RIBOSOMAL PROTEIN L22.//0.00026:163:30//DROSOPHILA
MELANOGASTER (FRUIT FLY).//P50887

10 F-MAMMA1002269//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE.//0.35:14:
57//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//Q48251

F-MAMMA1002282//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/6.1e-05:32:65//HOMO
SAPIENS (HUMAN).//P39192

15 F-MAMMA1002292//TROPOMYOSIN 2.//1.4e-05:100:30//SACCHAROMYCES CEREVISIAE
(BAKER'S YEAST).//P40414

20 F-MAMMA1002293//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/6.8e-25:127:44//HOMO
SAPIENS (HUMAN).//P39188

F-MAMMA1002294//ALPHA TRANS-INDUCING PROTEIN (ALPHA-TIF).//0.00011:138:
38//BOVINE HERPESVIRUS TYPE 1 (STRAIN P8-2).//P30020

25 F-MAMMA1002297//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.15:144:
30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323

30 F-MAMMA1002298//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.0e-05:40:50//MUS
MUSCULUS (MOUSE).//P05143

35 F-MAMMA1002299//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.84:
65:32//STRUTHIO CAMELUS (OSTRICH).//O21405

40 F-MAMMA1002308//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.3e-29:61:73//HOMO
SAPIENS (HUMAN).//P39188

F-MAMMA1002310//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)
.//0.00016:70:38//MUS MUSCULUS (MOUSE).//P15265

45 F-MAMMA1002311//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/9.4e-09:84:54//HOMO
SAPIENS (HUMAN).//P39189

50 F-MAMMA1002312//HYPOTHETICAL 10.8 KD PROTEIN IN GP30-RIII INTERGENIC REGION
(URF Y).//0.48:48:33//BACTERIOPHAGE T4.//P33084

F-MAMMA1002317

55 F-MAMMA1002319//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE
TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//0.011:128:27//MUS MUSCULUS
(MOUSE).//P11369

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F-MAMMA1002322//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/5.2e-20:92:57//HOMO
 SAPIENS (HUMAN).//P39195
 5
 F-MAMMA1002329//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.051:33:36//XENOPUS
 LAEVIS (AFRICAN CLAWED FROG).//P03931
 10
 F-MAMMA1002332//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.5e-20:116:51//HOMO
 SAPIENS (HUMAN).//P08547
 15
 F-MAMMA1002333//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.0017:214:31//BOS
 TAURUS (BOVINE).//P02453
 20
 F-MAMMA1002339//COPPER-METALLOTHIONEIN (CU-MT).//0.59:42:38//HELIX POMATIA
 (ROMAN SNAIL) (EDIBLE SNAIL).//P55947
 25
 F-MAMMA1002347//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.43:26:61//HOMO SAPIENS
 (HUMAN).//P39188
 30
 F-MAMMA1002351//HYPOTHETICAL PROTEIN MJ0304.//2.3e-07:139:25//METHANOCOCCUS
 JANNASCHII.//Q57752
 35
 F-MAMMA1002352
 F-MAMMA1002353//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00028:31:80//HOMO
 SAPIENS (HUMAN).//P39188
 40
 F-MAMMA1002355//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/4.2e-28:87:73//HOMO
 SAPIENS (HUMAN).//P39193
 45
 F-MAMMA1002356//RELAXIN.//0.95:31:35//SQUALUS ACANTHIAS (SPINY DOGFISH)
 .//P11953
 50
 F-MAMMA1002359//CHLOROPLAST 50S RIBOSOMAL PROTEIN L33.//0.93:44:
 36//GUILLARDIA THETA (CRYPTOMONAS PHI).//O78487
 55
 F-MAMMA1002360//LATE L2 MU CORE PROTEIN PRECURSOR (PROTEIN X).//0.94:30:
 43//BOVINE ADENOVIRUS TYPE 2 (MASTADENOVIRUS BOS2).//Q96626
 F-MAMMA1002361//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.0e-08:45:68//HOMO
 SAPIENS (HUMAN).//P39188
 F-MAMMA1002362//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.58:23:
 26//LUMBRICUS TERRESTRIS (COMMON EARTHWORM).//Q34942
 F-MAMMA1002380//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.23:100:

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27//DROSOPHILA SIMULANS (FRUIT FLY).//P13729

F-MAMMA1002384

5

F-MAMMA1002385//HYPOTHETICAL 40.9 KD PROTEIN IN ORC2-TIP1 INTERGENIC REGION.//3.8e-14:125:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38241

10

F-MAMMA1002392//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:17:58//BRANCHIOSTOMA LANCEOLATUM (COMMON LANCELET) (AMPHIOXUS).//O21003

15

F-MAMMA1002411//30S RIBOSOMAL PROTEIN S17.//0.85:49:32//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P73311

20

F-MAMMA1002413//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3) (FRAGMENT).//0.97:41:39//DROSOPHILA AFFINIS (FRUIT FLY).//P51926

F-MAMMA1002417//RFBJ PROTEIN.//0.99:31:35//SHIGELLA FLEXNERI.//P37786

25

F-MAMMA1002427//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.6e-33:135:59//HOMO SAPIENS (HUMAN).//P39194

30

F-MAMMA1002428//HYPOTHETICAL PROTEIN C18.//0.97:34:44//SWINEPOX VIRUS (STRAIN KASZA) (SPV).//P32217

F-MAMMA1002434//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/3.1e-36:56:78//HOMO SAPIENS (HUMAN).//P39189

35

F-MAMMA1002446

40

F-MAMMA1002454//EARLY NODULIN 20 PRECURSOR (N-20).//0.77:57:45//MEDICAGO TRUNCATULA (BARREL MEDIC).//P93329

F-MAMMA1002461//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//1.3e-05:193:32//CANIS FAMILIARIS (DOG).//P50551

45

F-MAMMA1002470//HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION.//1.0e-75:231:60//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38795

50

F-MAMMA1002475//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L4 (SNF2-BETA) (BRG-1 PROTEIN) (MITOTIC GROWTH AND TRANSCRIPTION ACTIVATOR) (BRAHMA PROTEIN HOMOLOG 1).//0.013:99:30//HOMO SAPIENS (HUMAN).//P51532

55

F-MAMMA1002480//NONSTRUCTURAL PROTEIN 5B.//1.0:23:43//HUMAN CORONAVIRUS (STRAIN 229E).//P19741

F-MAMMA1002485//STANNIOCALCIN PRECURSOR.//2.1e-23:88:46//HOMO SAPIENS

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(HUMAN).//P52823

5 F-MAMMA1002494//MOLT-INHIBITING HORMONE (MIH).//1.0:32:37//PROCAMBARUS CLARKII (RED SWAMP CRAYFISH).//P55848

10 F-MAMMA1002498//6.7 KD PROTEIN (ORF 5).//1.0:26:42//BARLEY YELLOW DWARF VIRUS (ISOLATE PAV) (BYDV).//P09517

F-MAMMA1002524//HYPOTHETICAL 117.8 KD PROTEIN IN STE2-FRS2 INTERGENIC REGION.//5.0e-26:222:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43571

15 F-MAMMA1002530//CYTOSOLIC PHOSPHOLIPASE A2 (EC 3.1.1.4) (CPLA2) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE) / LYSOPHOSPHOLIPASE (EC 3.1.1.5) .//4.5e-12:88:44//HOMO SAPIENS (HUMAN).//P47712

20 F-MAMMA1002545//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/4.3e-29:97:71//HOMO SAPIENS (HUMAN).//P39195

25 F-MAMMA1002554//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).//0.46:54:40//CRICETULUS GRISEUS (CHINESE HAMSTER).//P11414

30 F-MAMMA1002556//METALLOTHIONEIN 20-I ISOFORMS A AND B (MT-20-IA AND MT-20-IB) .//0.99:21:47//MYTILUS EDULIS (BLUE MUSSEL).//P80251

F-MAMMA1002566//TRANSCRIPTION FACTOR P65 (NUCLEAR FACTOR NF-KAPPA-B P65 SUBUNIT).//0.70:130:30//MUS MUSCULUS (MOUSE).//Q04207

35 F-MAMMA1002571//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (FRAGMENT).//0.54:45:51//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P35084

40 F-MAMMA1002573//PARATHYMOSIN.//1.5e-07:69:46//HOMO SAPIENS (HUMAN).//P20962

F-MAMMA1002585//MYOSIN LIGHT CHAIN 1, SLOW-TWITCH MUSCLE B/VENTRICULAR ISOFORM (FRAGMENT).//0.38:36:36//MUS MUSCULUS (MOUSE).//P09542

45 F-MAMMA1002590//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.99:22:77//HOMO SAPIENS (HUMAN).//P39195

50 F-MAMMA1002597//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.1e-18:44:70//HOMO SAPIENS (HUMAN).//P39194

55 F-MAMMA1002598//60S RIBOSOMAL PROTEIN L7.//1.8e-16:40:100//HOMO SAPIENS (HUMAN).//P18124

F-MAMMA1002603

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F-MAMMA1002612//30S RIBOSOMAL PROTEIN S16 (FRAGMENT)//1.0:29:37//THERMUS
AQUATICUS.//Q07348

5 F-MAMMA1002617//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25)
(FRAGMENT)//0.00041:81:34//RATTUS NORVEGICUS (RAT)//P10164

10 F-MAMMA1002618//ESCARGOT/SNAIL PROTEIN HOMOLOG (FRAGMENT)//0.11:18:
50//PSYCHODA CINEREA.//Q02027

F-MAMMA1002619//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3
(EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING
15 PROTEASE) (DEUBIQUITINATING ENZYME)//1.8e-13:110:40//CAENORHABDITIS
ELEGANS.//Q09931

20 F-MAMMA1002622//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//8.4e-05:53:58//HOMO
SAPIENS (HUMAN).//P39188

F-MAMMA1002623//PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE
PRECURSOR (EC 1.14.17.3) (PAM)//2.6e-07:37:78//HOMO SAPIENS (HUMAN).//P19021
25

F-MAMMA1002625

30 F-MAMMA1002629//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.4e-19:49:73//HOMO
SAPIENS (HUMAN).//P39188

F-MAMMA1002636//COLLAGEN ALPHA 2(VI) CHAIN (FRAGMENT)//1.7e-07:189:32//HOMO
SAPIENS (HUMAN).//P12110
35

F-MAMMA1002637//KINESIN LIGHT CHAIN (KLC)//7.7e-54:227:52//RATTUS NORVEGICUS
(RAT)//P37285

40 F-MAMMA1002646//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT
PROTEIN) (NF-H)//0.034:199:25//MUS MUSCULUS (MOUSE).//P19246

45 F-MAMMA1002650//TRANSCRIPTION REGULATOR PROTEIN BACH2 (BTB AND CNC
HOMOLOG 2)//1.7e-07:104:32//MUS MUSCULUS (MOUSE).//P97303

F-MAMMA1002655//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N)//1.0:25:
44//HOMO SAPIENS (HUMAN).//P22532
50

F-MAMMA1002662

55 F-MAMMA1002665//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.3e-07:54:57//HOMO
SAPIENS (HUMAN).//P39194

F-MAMMA1002671//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA

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LIGASE) (ACYL- ACTIVATING ENZYME).//1.4e-10:144:31//ESCHERICHIA COLI//P27550

5 F-MAMMA1002673//BREVICAN CORE PROTEIN PRECURSOR.//0.76:64:39//BOS TAURUS
(BOVINE).//Q28062

10 F-MAMMA1002684//HYPOTHETICAL 11.8 KD PROTEIN IN GP55-NRDG INTERGENIC
REGION.//0.094:77:27//BACTERIOPHAGE T4.//P07079

F-MAMMA1002685//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.0017:177:34//RATTUS
NORVEGICUS (RAT).//P02454

15 F-MAMMA1002698

F-MAMMA1002699//HYPOTHETICAL 45.1 KD PROTEIN IN RPS5-ZMS1 INTERGENIC
REGION.//1.2e-28:127:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47160

20 F-MAMMA1002701//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.0:14:92//HOMO SAPIENS
(HUMAN).//P39188

25 F-MAMMA1002708//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//7.9e-27:52:65//HOMO
SAPIENS (HUMAN).//P39193

30 F-MAMMA1002711//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.7e-24:54:75//HOMO
SAPIENS (HUMAN).//P39188

F-MAMMA1002721

35 F-MAMMA1002727//SOX-13 PROTEIN (FRAGMENT).//0.70:36:38//MUS MUSCULUS (MOUSE)
.//Q04891

40 F-MAMMA1002728//HYPOTHETICAL 6.0 KD PROTEIN.//1.0:25:44//THERMOPROTEUS
TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19305

45 F-MAMMA1002744//HYPOTHETICAL 13.4 KD PROTEIN IN ACT5-YCK1 INTERGENIC
REGION.//1.0:52:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38834

F-MAMMA1002746//HYPOTHETICAL 5.6 KD PROTEIN (ORF A-45).//1.0:22:40//SULFOLOBUS
VIRUS-LIKE PARTICLE SSV1.//P20198

50 F-MAMMA1002748

55 F-MAMMA1002754//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.1e-21:56:64//HOMO
SAPIENS (HUMAN).//P39188

F-MAMMA1002758//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.37:14:64//DROSOPHILA
MELANOGASTER (FRUIT FLY).//Q01645

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F-MAMMA1002764//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/4.7e-32:79:60//HOMO
 SAPIENS (HUMAN).//P39194
 5
 F-MAMMA1002765//PARATHYMOSIN.//0.79:63:28//BOS TAURUS (BOVINE).//P08814
 F-MAMMA1002769//GAR2 PROTEIN.//0.00037:192:27//SCHIZOSACCHAROMYCES POMBE
 10 (FISSION YEAST).//P41891
 F-MAMMA1002775//HYPOTHETICAL 36.7 KD PROTEIN C2F7.14C IN CHROMOSOME I.//5.4e-
 54:240:49//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09704
 15
 F-MAMMA1002780
 F-MAMMA1002782//MARGATOXIN (MGTX).//1.0:31:38//CENTRUROIDES MARGARITATUS
 20 (SCORPION).//P40755
 F-MAMMA1002796//ICE NUCLEATION PROTEIN.//0.0018:100:41//PSEUDOMONAS
 FLUORESCENS.//P09815
 25
 F-MAMMA1002807//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/9.3e-23:100:59//HOMO
 SAPIENS (HUMAN).//P39188
 30
 F-MAMMA1002820//NEUROTOXIN IV (LQQ IV).//1.0:18:50//LEIURUS QUINQUESTRIATUS
 QUINQUESTRIATUS (EGYPTIAN SCORPION).//P01489
 F-MAMMA1002830//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/4.7e-24:55:74//HOMO
 35 SAPIENS (HUMAN).//P39195
 F-MAMMA1002833//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.6e-31:95:73//HOMO
 SAPIENS (HUMAN).//P39189
 40
 F-MAMMA1002835//HYPOTHETICAL 42.1 KD PROTEIN F13G3.3 IN CHROMOSOME I.//1.0:54:
 37//CAENORHABDITIS ELEGANS.//Q19417
 45
 F-MAMMA1002838//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/2.5e-27:99:70//HOMO
 SAPIENS (HUMAN).//P39193
 F-MAMMA1002842//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.3e-13:65:63//HOMO
 50 SAPIENS (HUMAN).//P39195
 F-MAMMA1002843//METALLOTHIONEIN-II (MT-II).//0.97:19:47//MUS MUSCULUS (MOUSE)
 .//P02798
 55
 F-MAMMA1002844//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC
 REGION.//4.9e-08:119:36//AUTOGRAPHIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS

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(ACMNPV).//P41479

5 F-MAMMA1002858//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.98:37:37//PAN
TROGLODYTES (CHIMPANZEE).//Q35647

10 F-MAMMA1002868//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.8e-10:51:62//HOMO
SAPIENS (HUMAN).//P39188

15 F-MAMMA1002869//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS
PROTEIN).//1.8e-95:194:78//HOMO SAPIENS (HUMAN).//P48059

20 F-MAMMA1002871//G-PROTEIN COUPLED RECEPTOR HOMOLOG R33.//1.0:51:35//RAT
CYTOMEGALOVIRUS (STRAIN MAASTRICHT).//O12000

25 F-MAMMA1002880

30 F-MAMMA1002881//GLIOMA PATHOGENESIS-RELATED PROTEIN (RTVP-1 PROTEIN).//3.3e-
22:180:35//HOMO SAPIENS (HUMAN).//P48060

35 F-MAMMA1002886//MYOSIN HEAVY CHAIN IB (MYOSIN HEAVY CHAIN IL).//0.00011:148:
39//ACANTHAMOEBA CASTELLANII (AMOEBA).//P19706

40 F-MAMMA1002887

45 F-MAMMA1002890//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.030:142:
25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323

50 F-MAMMA1002892

55 F-MAMMA1002895//HYPOTHETICAL PROTEIN UL61.//0.00099:143:35//HUMAN
CYTOMEGALOVIRUS (STRAIN AD169).//P16818

60 F-MAMMA1002908//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).//0.12:44:
43//ORYCTOLAGUS CUNICULUS (RABBIT).//P06333

65 F-MAMMA1002909//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.00011:28:75//HOMO
SAPIENS (HUMAN).//P39188

70 F-MAMMA1002930//BOMBYXIN A-7 PRECURSOR (BBX-A7) (4K-PROTHORACICOTROPIC
HORMONE) (4K-PTTH).//0.99:45:46//BOMBYX MORI (SILK MOTH).//P26730

75 F-MAMMA1002937//ZINC FINGER PROTEIN 42 (MYELOID ZINC FINGER 1) (MZF-1).//6.5e-24:
147:34//HOMO SAPIENS (HUMAN).//P28698

80 F-MAMMA1002938//CERULOPLASMIN PRECURSOR (EC 1.16.3.1) (FERROXIDASE).//4.7e-
11:44:68//MUS MUSCULUS (MOUSE).//Q61147

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- F-MAMMA1002941//PROTEIN Q300.//0.0076:21:61//MUS MUSCULUS (MOUSE).//Q02722
- 5 F-MAMMA1002947//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//1.9e-08:
152:38//STREPTOMYCES FRADIAE.//P20186
- F-MAMMA1002964
- 10 F-MAMMA1002970///// ALU SUBFAMILY SB WARNING ENTRY !!!!!//0.0057:55:43//HOMO
SAPIENS (HUMAN).//P39189
- 15 F-MAMMA1002972//BRAIN-SPECIFIC HOMEBOX/POU DOMAIN PROTEIN 3A (BRN-3A)
(OCT-T1) (HOMEBOX/POU DOMAIN PROTEIN RDC-1).//0.84:53:41//HOMO SAPIENS
(HUMAN).//Q01851
- 20 F-MAMMA1002973///// ALU SUBFAMILY SC WARNING ENTRY !!!!!//4.6e-11:54:68//HOMO
SAPIENS (HUMAN).//P39192
- F-MAMMA1002982
- 25 F-MAMMA1002987//HYPOTHETICAL 11.9 KD PROTEIN IN RPC8-MFA2 INTERGENIC
REGION.//0.17:47:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53906
- 30 F-MAMMA1003003///// ALU SUBFAMILY SX WARNING ENTRY !!!!!//8.6e-09:30:73//HOMO
SAPIENS (HUMAN).//P39195
- F-MAMMA1003004///// ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.0071:41:58//HOMO
35 SAPIENS (HUMAN).//P39195
- F-MAMMA1003007//SPERM PROTAMINE P1.//0.0076:51:37//TACHYGLOSSUS ACULEATUS
ACULEATUS (AUSTRALIAN ECHIDNA).//P35311
- 40 F-MAMMA1003011//HISTONE MACRO-H2A.1.//1.8e-60:175:70//RATTUS NORVEGICUS (RAT)
//Q02874
- 45 F-MAMMA1003013//ACTIN BINDING PROTEIN.//0.097:83:31//SACCHAROMYCES EXIGUUS
(YEAST).//P38479
- F-MAMMA1003015
- 50 F-MAMMA1003019//MYOTUBULARIN.//0.022:56:37//HOMO SAPIENS (HUMAN).//Q13496
- F-MAMMA1003026//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.0014:208:27//ORGYIA
55 PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10341
- F-MAMMA1003031//PROBABLE E4 PROTEIN (E1^E4).//0.14:49:32//HUMAN

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PAPILLOMAVIRUS TYPE 6B.//P06459

- 5 F-MAMMA1003035//HYPOTHETICAL 24.4 KD PROTEIN IN LPD 3'REGION (ORF4).//5.1e-12:
112:34//ZYMOMONAS MOBILIS.//O66114
- 10 F-MAMMA1003039//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.4e-07:68:54//HOMO
SAPIENS (HUMAN).//P39188
- F-MAMMA1003040//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!!//2.8e-39:90:57//HOMO
SAPIENS (HUMAN).//P39190
- 15 F-MAMMA1003044
- F-MAMMA1003047//SPERM HISTONE P2 PRECURSOR (PROTAMINE 2).//0.18:25:44//BOS
TAURUS (BOVINE).//P19782
- 20 F-MAMMA1003049//PROBABLE E4 PROTEIN.//0.50:67:29//HUMAN PAPILLOMAVIRUS TYPE
6C.//P20969
- 25 F-MAMMA1003055//WEAK TOXIN CM-2.//0.99:23:30//NAJA HAJE HAJE (EGYPTIAN COBRA)
.//P01415
- 30 F-MAMMA1003056//EXPORTED PROTEIN 7 (FRAGMENT).//1.0:52:32//STREPTOCOCCUS
PNEUMONIAE.//P35597
- F-MAMMA1003057//MD6 PROTEIN.//1.5e-85:168:95//MUS MUSCULUS (MOUSE).//Q60584
- 35 F-MAMMA1003066//REGB PROTEIN.//1.0:62:27//PSEUDOMONAS AERUGINOSA.//Q03381
- F-MAMMA1003089//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!!//5.1e-15:44:77//HOMO
SAPIENS (HUMAN).//P39190
- 40 F-MAMMA1003099//ENDOTHELIAL ACTIN-BINDING PROTEIN (ABP-280) (NONMUSCLE
FILAMIN) (FILAMIN 1).//4.8e-20:80:62//HOMO SAPIENS (HUMAN).//P21333
- 45 F-MAMMA1003104//PHOTOSYSTEM I REACTION CENTRE SUBUNIT VIII.//0.98:22:
40//SYNECHOCOCCUS ELONGATUS NAEGELI.//P25900
- 50 F-MAMMA1003113//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (FRAGMENTS).//0.67:
35:45//GALLUS GALLUS (CHICKEN).//P02467
- 55 F-MAMMA1003127//MYOSIN I ALPHA (MMI-ALPHA).//5.2e-34:141:56//MUS MUSCULUS
(MOUSE).//P46735
- F-MAMMA1003135//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC
REGION.//3.6e-05:91:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47170

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F-MAMMA1003140

5 F-MAMMA1003146//MALE SPECIFIC SPERM PROTEIN MST87F.//1.0:33:36//DROSOPHILA
MELANOGASTER (FRUIT FLY).//P08175

10 F-MAMMA1003150//HYPOTHETICAL 84.3 KD PROTEIN ZK945.10 IN CHROMOSOME II.//4.4e-
10:254:30//CAENORHABDITIS ELEGANS.//Q09625

F-MAMMA1003166//BRAIN PROTEIN H5.//4.0e-42:182:48//HOMO SAPIENS (HUMAN)
15 .//O43236

F-NT2RM1000001//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGENIC
REGION (ORF70).//0.15:38:34//ASTASIA LONGA (EUGLENOPHYCEAN ALGA).//P34779

20 F-NT2RM1000018

F-NT2RM1000032//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.51:17:41//CYPRINUS
25 CARPIO (COMMON CARP).//P24948

F-NT2RM1000035//3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE (EC
1.1.1.34) (HMG-COA REDUCTASE).//0.00011:114:27//BLATTELLA GERMANICA (GERMAN
30 COCKROACH).//P54960

F-NT2RM1000037//METALLOTHIONEIN-II (MT-II).//0.025:19:47//SCYLLA SERRATA (MUD
CRAB).//P02806

35 F-NT2RM1000039//VITELLINE MEMBRANE VM34CA PROTEIN PRECURSOR.//0.00083:84:
33//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q06521

40 F-NT2RM1000055//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.//1.1e-07:34:
55//PLASMODIUM LOPHURAE.//P04929

F-NT2RM1000059//MYOCYTE-SPECIFIC ENHANCER FACTOR 2B (SERUM RESPONSE
45 FACTOR-LIKE PROTEIN 2) (XMEF2) (RSRFR2).//0.18:83:36//HOMO SAPIENS (HUMAN)
//Q02080

F-NT2RM1000062//PROLINE-RICH PEPTIDE P-B.//0.54:34:44//HOMO SAPIENS (HUMAN)
50 .//P02814

F-NT2RM1000080//HYPOTHETICAL 35.7 KD PROTEIN SLR1128.//2.1e-20:119:
40//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P72655

55 F-NT2RM1000086//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS:
PEPTIDE P-D] (FRAGMENT).//0.20:56:35//HOMO SAPIENS (HUMAN).//P10162

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F-NT2RM1000092//COLLAGEN-LIKE PROTEIN.//0.0017:44:45//HERPESVIRUS SAIMIRI
(SUBGROUP C / STRAIN 488).//P22576

5 F-NT2RM1000118//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B
REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).//5.7e-07:109:
28//NEUROSPORA CRASSA.//P87072

10 F-NT2RM1000119//TRANSCRIPTIONAL REGULATOR IE63 (VMW63) (ICP27).//0.0050:135:
32//HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).//P28276

15 F-NT2RM1000127//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//0.032:68:
32//SORGHUM VULGARE (SORGHUM).//P24152

20 F-NT2RM1000131//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF)
.//0.82:33:39//BOS TAURUS (BOVINE).//P37359

25 F-NT2RM1000132//NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-A SUBUNIT
PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-13KD-A) (CI-13KD-A).//2.7e-59:124:
91//HOMO SAPIENS (HUMAN).//O75380

F-NT2RM1000153//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//2.5e-08:148:
29//HOMO SAPIENS (HUMAN).//P49902

30 F-NT2RM1000186//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B
REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).//1.9e-07:109:
27//NEUROSPORA CRASSA.//P87072

35 F-NT2RM1000187//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
HELICASE SPAC10F6.02C.//1.0e-12:94:46//SCHIZOSACCHAROMYCES POMBE (FISSION
YEAST).//O42643

40 F-NT2RM1000199//CUTICLE COLLAGEN 12 PRECURSOR.//0.46:130:
33//CAENORHABDITIS ELEGANS.//P20630

45 F-NT2RM1000242//PUTATIVE ATP SYNTHASE J CHAIN, MITOCHONDRIAL (EC 3.6.1.34)
.//0.85:38:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O13931

50 F-NT2RM1000244//HYPOTHETICAL 131.5 KD PROTEIN C02F12.7 IN CHROMOSOME
X.//0.0055:98:36//CAENORHABDITIS ELEGANS.//Q11102

F-NT2RM1000252//TRICHOHYALIN.//2.9e-06:88:36//OVIS ARIES (SHEEP).//P22793

55 F-NT2RM1000256//GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE
[ISOMERIZING] (EC 2.6.1.16) (HEXOSEPHOSPHATE AMINOTRANSFERASE) (D-FRUCTOSE-
6- PHOSPHATE AMIDOTRANSFERASE) (GFAT).//2.9e-54:153:67//MUS MUSCULUS (MOUSE)
.//P47856

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5 F-NT2RM1000257//MAGO NASHI PROTEIN.//5.9e-64:136:89//DROSOPHILA
MELANOGASTER (FRUIT FLY).//P49028

F-NT2RM1000260

10 F-NT2RM1000271//GALACTOKINASE (EC 2.7.1.6).//0.99:41:39//BACILLUS
SUBTILIS.//P39574

15 F-NT2RM1000272//HYPOTHETICAL 55.5 KD PROTEIN ZK1128.2 IN CHROMOSOME
III.//8.8e-25:131:45//CAENORHABDITIS ELEGANS.//Q09357

20 F-NT2RM1000280//VACUOLAR ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-ATPASE D
SUBUNIT) (V- ATPASE 28 KD ACCESSORY PROTEIN).//2.5e-63:121:94//BOS TAURUS
(BOVINE).//P39942

25 F-NT2RM1000300//TREACLE PROTEIN (TREACHER COLLINS SYNDROME PROTEIN)
.//0.51:145:26//HOMO SAPIENS (HUMAN).//Q13428

F-NT2RM1000314

30 F-NT2RM1000318//50S RIBOSOMAL PROTEIN L23.//0.83:28:35//AQUIFEX
AEOLICUS.//O66433

F-NT2RM1000341

35 F-NT2RM1000354//HYPOTHETICAL 5.8 KD PROTEIN IN PUHA 5'REGION (ORF55).//0.95:43:
37//RHODOBACTER CAPSULATUS (RHODOPSEUDOMONAS CAPSULATA).//P26159

40 F-NT2RM1000355//SPERM-SPECIFIC PROTEIN PHI-1.//0.0016:73:43//MYTILUS EDULIS
(BLUE MUSSEL).//Q04621

F-NT2RM1000365//HYPOTHETICAL PROTEIN KIAA0140.//3.5e-10:83:49//HOMO SAPIENS
(HUMAN).//Q14153

45 F-NT2RM1000377//DUAL SPECIFICITY PROTEIN PHOSPHATASE 9 (EC 3.1.3.48) (EC
3.1.3.16) (MITOGEN-ACTIVATED PROTEIN KINASE PHOSPHATASE 4) (MAP KINASE
PHOSPHATASE 4) (MKP-4).//4.9e-18:113:38//HOMO SAPIENS (HUMAN).//Q99956

50 F-NT2RM1000388//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC
REGION.//0.00023:67:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53915

55 F-NT2RM1000394//HISTONE H3.3 (H3.B) (H3.3Q).//4.7e-52:71:91//HOMO SAPIENS
(HUMAN), MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), ORYCTOLAGUS
CUNICULUS (RABBIT), GALLUS GALLUS (CHICKEN), SPISULA SOLIDISSIMA (ATLANTIC
SURF-CLAM), DROSOPHILA MELANOGASTER (FRUIT FLY), AND DROSOPHILA HYDEI

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(FRUIT FLY).//P06351

5 F-NT2RM1000399//ENDOTHELIN-2 PRECURSOR (ET-2) (FRAGMENT).//0.92:24:45//CANIS FAMILIARIS (DOG).//P12064

10 F-NT2RM1000421//CUTICLE COLLAGEN 2C (FRAGMENT).//0.12:93:33//HAEMONCHUS CONTORTUS.//P16252

F-NT2RM1000430//PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (PELP) .//0.13:86:31//NICOTIANA TABACUM (COMMON TOBACCO).//Q03211

15 F-NT2RM1000499//HYPOTHETICAL PROTEIN KIAA0041 (FRAGMENT).//2.9e-17:75:49//HOMO SAPIENS (HUMAN).//Q15057

20 F-NT2RM1000539//HYPOTHETICAL 10.4 KD PROTEIN IN FTR1-SPT15 INTERGENIC REGION.//2.9e-16:82:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40089

F-NT2RM1000553//GLYCOLIPID TRANSFER PROTEIN (GLTP).//6.4e-06:103:33//SUS SCROFA (PIG).//P17403

25 F-NT2RM1000555//UNR PROTEIN.//8.7e-77:105:95//RATTUS NORVEGICUS (RAT).//P18395

30 F-NT2RM1000563//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS) .//0.15:20:50//HOMO SAPIENS (HUMAN).//P30808

35 F-NT2RM1000623//CLARA CELL PHOSPHOLIPID-BINDING PROTEIN PRECURSOR (CCPBP) (CLARA CELLS 10 KD SECRETORY PROTEIN) (CC10).//0.17:70:34//HOMO SAPIENS (HUMAN).//P11684

40 F-NT2RM1000648//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//2.0e-22:133:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43636

F-NT2RM1000661//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF) (GIFB).//0.0060:24:33//HOMO SAPIENS (HUMAN).//P25713

45 F-NT2RM1000666//COLD SHOCK PROTEIN SCOF.//9.1e-07:67:41//STREPTOMYCES COELICOLOR.//P48859

50 F-NT2RM1000669//CHLOROPLAST 50S RIBOSOMAL PROTEIN L31.//0.071:69:31//PORPHYRA PURPUREA.//P51290

55 F-NT2RM1000672//SIGNAL RECOGNITION PARTICLE SEC65 SUBUNIT (FRAGMENT).//0.27:42:42//KLUYVEROMYCES LACTIS (YEAST).//O13475

F-NT2RM1000691//RETINOBLASTOMA BINDING PROTEIN 2 (RBBP-2).//4.3e-42:241:42//HOMO SAPIENS (HUMAN).//P29375

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- 5 F-NT2RM1000699//N2,N2-DIMETHYLGUANOSINE TRNA METHYLTRANSFERASE
PRECURSOR (EC 2.1.1.32)//0.94:48:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)
./P15565
- 10 F-NT2RM1000702//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 1./0.0013:
139:25//DROSOPHILA MELANOGASTER (FRUIT FLY)//P26308
- 15 F-NT2RM1000725//BASIC PROLINE-RICH PEPTIDE P-E (IB-9)//1.0:15:60//HOMO SAPIENS
(HUMAN)//P02811
- 20 F-NT2RM1000741//STATHMIN (CLONE XO20) (FRAGMENT)//1.0:53:32//XENOPUS LAEVIS
(AFRICAN CLAWED FROG)//Q09005
- 25 F-NT2RM1000742//HYPOTHETICAL 24.1 KD PROTEIN IN DHFR 3'REGION (ORF2)//1.0:54:
42//HERPESVIRUS SAIMIRI (STRAIN 484-77)//P25049
- 30 F-NT2RM1000746//HYPOTHETICAL 16.8 KD PROTEIN C29E6.04 IN CHROMOSOME I./0.11:
87:21//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09858
- 35 F-NT2RM1000770//DXS6673E PROTEIN./2.0e-38:190:48//HOMO SAPIENS (HUMAN)
./Q14202
- 40 F-NT2RM1000772//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1./4.3e-12:141:
30//PODOSPORA ANSERINA//Q00808
- 45 F-NT2RM1000780//MALE SPECIFIC SPERM PROTEIN MST87F./0.98:34:38//DROSOPHILA
MELANOGASTER (FRUIT FLY)//P08175
- 50 F-NT2RM1000781
- 55 F-NT2RM1000800//24.1 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION./7.9e-11:135:
34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P28707
- F-NT2RM1000802//ALPHA-AMYLASE INHIBITOR PAIM I (PIG PANCREATIC ALPHA-AMYLASE
INHIBITOR OF MICROBES I)/0.43:62:35//STREPTOMYCES OLIVACEOVIRIDIS
(STREPTOMYCES CORCHORUSII)//P09921
- F-NT2RM1000811
- F-NT2RM1000826//UNR PROTEIN./1.1e-110:144:83//RATTUS NORVEGICUS (RAT)
./P18395
- F-NT2RM1000829//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)/1.0:38:
34//DROSOPHILA SIMULANS (FRUIT FLY)//P50270

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F-NT2RM1000833//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.4e-62:145:841/CANIS FAMILIARIS (DOG).//P38377

5 F-NT2RM1000850//TESTIS-SPECIFIC PROTEIN KINASE 1 (EC 2.7.1.-).//6.1e-08:136:33//RATTUS NORVEGICUS (RAT).//Q63572

10 F-NT2RM1000852//ATP-DEPENDENT RNA HELICASE ROK1.//1.6e-34:212:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P45818

F-NT2RM1000857//HISTONE H1.M6.1.//0.76:31:48//TRYPANOSOMA CRUZI.//P40273

15 F-NT2RM1000867//MICROSOMAL SIGNAL PEPTIDASE 10.8 KD SUBUNIT (EC 3.4.-).//0.0082:76:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P46965

20 F-NT2RM1000874//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.38:12:58//HOMO SAPIENS (HUMAN).//P30808

25 F-NT2RM1000882//CYTOCHROME B5.//9.0e-13:92:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40312

F-NT2RM1000883//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.79:22:59//HOMO SAPIENS (HUMAN).//P30808

30 F-NT2RM1000885//HYPOTHETICAL 5.8 KD PROTEIN.//0.76:18:38//CLOVER YELLOW MOSAIC VIRUS (CYMV).//P16485

35 F-NT2RM1000894//DNA-DIRECTED RNA POLYMERASE I135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT).//6.2e-70:153:88//RATTUS NORVEGICUS (RAT).//O54888

40 F-NT2RM1000898//ACTIN, CYTOPLASMIC (ACTIN, MICRONUCLEAR).//4.3e-12:159:28//OXYTRICHA FALLAX.//P02583

45 F-NT2RM1000905//GLUTATHIONE S-TRANSFERASE 1-1 (EC 2.5.1.18) (CLASS-THETA).//0.98:39:35//LUCILIA CUPRINA (GREENBOTTLE FLY) (AUSTRALIAN SHEEP BLOWFLY).//P42860

50 F-NT2RM1000924//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//1.3e-11:169:28//CAENORHABDITIS ELEGANS.//P46577

F-NT2RM1000927//CUTICLE COLLAGEN 1.//0.00048:141:31//CAENORHABDITIS ELEGANS.//P08124

55 F-NT2RM1000962//HYPOTHETICAL 35.8 KD PROTEIN C4F8.04 IN CHROMOSOME I.//7.1e-13:169:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14180

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F-NT2RM1000978//HYPOTHETICAL 20.2 KD PROTEIN IN MNN4-PTK1 INTERGENIC REGION.//0.61:82:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36045

5 F-NT2RM1001003//ALPHA-2 CATENIN (ALPHA N-CATENIN) (NEURAL ALPHA-CATENIN) .//1.6e-21:211:31//GALLUS GALLUS (CHICKEN).//P30997

10 F-NT2RM1001008//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//3.2e-15:119:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09701

F-NT2RM1001043//ENDOTHELIN-1 (ET-1) (FRAGMENT).//0.78:32:34//MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MONKEY).//Q28469

15 F-NT2RM1001044

F-NT2RM1001059//LORICRIN.//8.6e-08:108:39//HOMO SAPIENS (HUMAN).//P23490

20 F-NT2RM1001066//METALLOTHIONEIN-LIKE PROTEIN TYPE 2.//0.99:24:50//LYCOPERSICON ESCULENTUM (TOMATO).//Q43513

25 F-NT2RM1001072//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 1 (EC 3.1.4.11) (PLC-GAMMA-1) (PHOSPHOLIPASE C-GAMMA-1) (PLC-II) (PLC-148).//4.7e-15:148:33//HOMO SAPIENS (HUMAN).//P19174

30 F-NT2RM1001074//HYPOTHETICAL PROTEIN F-215.//8.6e-05:126:30//HUMAN ADENOVIRUS TYPE 2.//P03291

35 F-NT2RM1001082//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//6.5e-19:75:54//HOMO SAPIENS (HUMAN).//P39195

F-NT2RM1001085//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.49:29:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643

40 F-NT2RM1001092//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//2.8e-42:200:38//HOMO SAPIENS (HUMAN).//P51522

45 F-NT2RM1001102//HYPOTHETICAL 62.8 KD PROTEIN IN TAF145-YOR1 INTERGENIC REGION.//1.7e-18:161:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53331

50 F-NT2RM1001105//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//4.0e-05:157:35//STREPTOMYCES FRADIAE.//P20186

F-NT2RM1001112//NONHISTONE CHROMOSOMAL PROTEIN HMG-17.//0.18:20:55//BOS TAURUS (BOVINE).//P02313

55 F-NT2RM1001115

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- F-NT2RM1001139//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR (GRP 1.8)//2.0e-25:156:46//PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN) //P10496
- 5 F-NT2RM2000006//MITOCHONDRIAL RIBOSOMAL PROTEIN S12//0.76:45:35//LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE)//Q34940
- 10 F-NT2RM2000013//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2)//3.9e-87:238:65//DROSOPHILA MELANOGASTER (FRUIT FLY)//P25167
- 15 F-NT2RM2000030//TOXINS 1 AND 2//0.98:21:42//TRIMERESURUS WAGLERI (WAGLER'S PIT VIPER) (TROPIDOLAEMUS WAGLERI)//P24335
- 20 F-NT2RM2000032//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00059:53:49//HOMO SAPIENS (HUMAN)//P39188
- F-NT2RM2000042//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N)//1.0:68:26//HOMO SAPIENS (HUMAN)//P22532
- 25 F-NT2RM2000092//HYPOTHETICAL 67.5 KD PROTEIN IN PRPS4-STE20 INTERGENIC REGION//7.0e-11:80:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38748
- 30 F-NT2RM2000093//OVARY MATURATING PARSIN (OMP)//1.0:26:38//LOCUSTA MIGRATORIA (MIGRATORY LOCUST)//P80045
- 35 F-NT2RM2000101//HYPOTHETICAL 39.3 KD PROTEIN C02B8.6 IN CHROMOSOME X//3.3e-09:56:35//CAENORHABDITIS ELEGANS//Q11096
- 40 F-NT2RM2000124//CAMP-DEPENDENT PROTEIN KINASE, ALPHA-CATALYTIC SUBUNIT (EC 2.7.1.37) (PKA C-ALPHA)//3.1e-35:77:96//MUS MUSCULUS (MOUSE)//P05132
- F-NT2RM2000191//3',5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA)//3.3e-05:181:27//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)//Q23917
- 45 F-NT2RM2000192//REPLICATION PROTEIN E1 (FRAGMENTS)//0.019:148:25//COTTONTAIL RABBIT (SHOPE) PAPILLOMAVIRUS (STRAIN WASHINGTON B) (CRPV)//P51894
- 50 F-NT2RM2000239//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//0.00032:111:32//MUS MUSCULUS (MOUSE)//P05143
- F-nnnnnnnnnnn//METALLOTHIONEIN-LIKE PROTEIN TYPE 2//0.046:59:33//LYCOPERSICON ESCULENTUM (TOMATO)//Q43512
- 55 F-NT2RM2000250//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35)

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(LAMININ-BINDING PROTEIN) (LECTIN L-29).//0.054:46:34//RATTUS NORVEGICUS (RAT)
//P08699

5 F-NT2RM2000259//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN)
(IER 2.9/ER2.6).//0.27:112:33//BOVINE HERPES VIRUS TYPE 1 (STRAIN JURA).//P29128

10 F-NT2RM2000260//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//4.7e-22:191:35//MUS
MUSCULUS (MOUSE).//P05143

15 F-NT2RM2000287//HYPOTHETICAL 11.8 KD PROTEIN C1B3.02C IN CHROMOSOME
I.//5.0e-19:83:53//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O13868

20 F-NT2RM2000322//DIAMINOPIMELATE DECARBOXYLASE (EC 4.1.1.20) (DAP
DECARBOXYLASE).//0.47:117:29//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI)
//P56129

25 F-NT2RM2000359//SPORE GERMINATION PROTEIN 270-11.//0.12:83:36//DICTYOSTELIUM
DISCOIDEUM (SLIME MOLD).//P22698

30 F-NT2RM2000363//BREAKPOINT CLUSTER REGION PROTEIN.//1.3e-16:203:30//HOMO
SAPIENS (HUMAN).//P11274

35 F-NT2RM2000368//DEK PROTEIN.//0.00027:100:32//HOMO SAPIENS (HUMAN).//P35659

40 F-NT2RM2000371//POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8)
(POLYNUCLEOTIDE PHOSPHORYLASE) (PNPASE).//6.8e-36:170:47//ESCHERICHIA
COLI.//P05055

45 F-NT2RM2000374//NODAL PRECURSOR.//1.1e-32:64:95//MUS MUSCULUS (MOUSE)
//P43021

50 F-NT2RM2000395//IMMEDIATE-EARLY PROTEIN IE180.//0.31:41:43//PSEUDORABIES
VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675

55 F-NT2RM2000402//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE
PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE
ENDOCYTIC INTERMEDIATE COMPONENT).//1.2e-30:228:32//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST).//P32802

60 F-NT2RM2000407//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//0.032:105:30//HOMO
SAPIENS (HUMAN).//P51805

65 F-NT2RM2000420//METALLOTHIONEIN (MT).//0.88:42:38//PLEURONECTES PLATESSA
(PLAICE).//P07216

F-NT2RM2000422//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//2.0e-

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117:237:87//RATTUS NORVEGICUS (RAT).//Q08469

5 F-NT2RM2000452//HYPOTHETICAL 63.6 KD PROTEIN IN YPT52-GCN3 INTERGENIC
REGION.//1.1e-08:157:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36113

F-NT2RM2000469//70 KD ANTIGEN.//0.050:207:23//SHIGELLA FLEXNERI.//P18010

10 F-NT2RM2000490//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.022:25:44//HOMO
SAPIENS (HUMAN).//P02811

15 F-NT2RM2000502//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.0037:17:
58//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645

F-NT2RM2000504//HYPOTHETICAL 99.0 KD PROTEIN SPBC119.17.//1.7e-22:195:
27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O42908

20 F-NT2RM2000522//RAS-RELATED PROTEIN RABA (FRAGMENT).//3.6e-05:67:
29//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P34141

25 F-NT2RM2000540//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III.//8.4e-
33:214:38//CAENORHABDITIS ELEGANS.//Q18262

30 F-NT2RM2000556//HYPOTHETICAL PROTEIN KIAA0288 (HA6116).//1.7e-09:133:36//HOMO
SAPIENS (HUMAN).//P56524

35 F-NT2RM2000566//INTEGRIN ALPHA-6 PRECURSOR (VLA-6) (CD49F).//2.2e-60:244:
51//HOMO SAPIENS (HUMAN).//P23229

F-NT2RM2000567//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//2.3e-09:192:34//MUS
MUSCULUS (MOUSE).//P05143

40 F-NT2RM2000569//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//9.0e-08:43:72//HOMO
SAPIENS (HUMAN).//P39188

45 F-NT2RM2000577//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE-TRNA
LIGASE) (ILERS).//9.1e-54:225:45//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P73505

50 F-NT2RM2000581//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//0.079:
111:34//HOMO SAPIENS (HUMAN).//Q15427

F-NT2RM2000588//HYPOTHETICAL PROTEIN KIAA0288 (HA6116).//2.3e-09:193:32//HOMO
SAPIENS (HUMAN).//P56524

55 F-NT2RM2000594//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.18:33:42//HOMO SAPIENS
(HUMAN).//P02811

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F-NT2RM2000599//DNA (CYTOSINE-5)-METHYLTRANSFERASE (EC 2.1.1.37) (DNA METHYLTRANSFERASE) (DNA METASE) (MCMT) (M.MMUI).//1.5e-09:68:45//MUS MUSCULUS (MOUSE).//P13864

5 F-NT2RM2000609//GRANULIN 2.//0.83:42:35//CYPRINUS CARPIO (COMMON CARP) .//P81014

10 F-NT2RM2000612//ZINC FINGER PROTEIN GCS1.//7.2e-05:155:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P35197

15 F-NT2RM2000623//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//1.8e-09:196:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323

20 F-NT2RM2000624//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.070:113:27//DROSOPHILA ERECTA (FRUIT FLY).//P13730

F-NT2RM2000635//SPERM PROTAMINE P1.//0.54:47:38//ANTECHINUS STUARTII.//P42129

25 F-NT2RM2000636//OUTER MEMBRANE PROTEIN H.8 PRECURSOR.//0.096:62:35//NEISSERIA GONORRHOEAE.//P11910

F-NT2RM2000639//HYPOTHETICAL PROTEIN MJ0243.//0.99:32:34//METHANOCOCCUS JANNASCHII.//Q57694

30 F-NT2RM2000649//NEURONAL CALCIUM SENSOR 1 (NCS-1).//0.00049:70:35//RATTUS NORVEGICUS (RAT), AND GALLUS GALLUS (CHICKEN).//P36610

35 F-NT2RM2000669//50S RIBOSOMAL PROTEIN L34.//1.0:34:44//BACILLUS SUBTILIS.//P05647

40 F-NT2RM2000691//ACTIN-LIKE PROTEIN 3 (ACTIN-2).//7.0e-116:243:87//HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE).//P32391

45 F-NT2RM2000714//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-I) .//3.8e-21:174:35//HOMO SAPIENS (HUMAN).//Q15404

50 F-NT2RM2000718//HYPOTHETICAL 52.9 KD SERINE-RICH PROTEIN C11G7.01 IN CHROMOSOME I.//0.0022:174:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST) .//O13695

F-NT2RM2000735//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//1.6e-102:246:74//HOMO SAPIENS (HUMAN).//P28160

55 F-NT2RM2000740//HYPOTHETICAL 131.1 KD HELICASE IN ALG7-ENP1 INTERGENIC REGION.//8.5e-51:212:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38144

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F-NT2RM2000795//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//9.0e-41:125:53//HOMO SAPIENS (HUMAN).//P39189

5 F-NT2RM2000821//COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP).//1.1e-128:291:89//RATTUS NORVEGICUS (RAT).//P23514

10 F-NT2RM2000837//CYCLIN-DEPENDENT KINASE INHIBITOR 1C (CYCLIN-DEPENDENT KINASE INHIBITOR P57) (P57KIP2).//3.9e-05:113:36//HOMO SAPIENS (HUMAN).//P49918

F-NT2RM2000951//HYPOTHETICAL 60.3 KD PROTEIN R08D7.7 IN CHROMOSOME III.//2.5e-49:273:39//CAENORHABDITIS ELEGANS.//P30646

15 F-NT2RM2000952//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H) (FRAGMENT).//0.037:234:23//RATTUS NORVEGICUS (RAT).//P16884

20 F-NT2RM2000984//HYPOTHETICAL 54.7 KD PROTEIN F37A4.1 IN CHROMOSOME III.//6.3e-44:216:43//CAENORHABDITIS ELEGANS.//P41879

25 F-NT2RM2001004//SYNAPSINS IA AND IB.//0.15:178:32//RATTUS NORVEGICUS (RAT).//P09951

F-NT2RM2001035//CCR4-ASSOCIATED FACTOR 1 (CAF1).//1.4e-87:188:90//MUS MUSCULUS (MOUSE).//Q60809

30 F-NT2RM2001065//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.53:122:31//TRYPANOSOMA BRUCEI BRUCEI.//P24499

35 F-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//3.4e-13:171:30//CAENORHABDITIS ELEGANS.//P46577

40 F-NT2RM2001105//SPORE COAT PROTEIN SP96.//7.8e-06:141:34//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P14328

F-NT2RM2001131//PROBABLE EUKARYOTIC INITIATION FACTOR C17C9.03.//2.3e-18:249:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10475

45 F-NT2RM2001141//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III.//0.050:134:26//CAENORHABDITIS ELEGANS.//P34681

50 F-NT2RM2001152

F-NT2RM2001177//COLLAGEN ALPHA 1(XIV) CHAIN PRECURSOR (UNDULIN).//0.86:42:40//GALLUS GALLUS (CHICKEN).//P32018

55 F-NT2RM2001194//SMOOTHELIN.//4.7e-05:77:32//HOMO SAPIENS (HUMAN).//P53814

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F-NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//1.7e-18:218:35//MUS MUSCULUS (MOUSE)//P05143

5 F-NT2RM2001201//CYSTEINE STRING PROTEIN (CCCS1)//0.041:22:59//TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY)//P56101

10 F-NT2RM2001221//KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP10) //1.3e-13:183:32//RATTUS NORVEGICUS (RAT)//P97924

15 F-NT2RM2001238//GLUTAMINASE, KIDNEY ISOFORM PRECURSOR (EC 3.5.1.2) (GLS) (L-GLUTAMINE AMIDOHYDROLASE)//6.5e-121:218:98//RATTUS NORVEGICUS (RAT)//P13264

F-NT2RM2001243//HYPOTHETICAL 200.0 KD PROTEIN IN GZF3-IME2 INTERGENIC REGION//0.00019:177:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P42945

20 F-NT2RM2001247//LEGUMIN B (FRAGMENT)//0.22:54:35//PISUM SATIVUM (GARDEN PEA) //P14594

25 F-NT2RM2001256//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR)//1.8e-109:207:98//MUS MUSCULUS (MOUSE)//P53995

30 F-NT2RM2001291//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)//0.016:22:40//HOMO SAPIENS (HUMAN)//P22531

F-NT2RM2001306//REF(2)P PROTEIN//0.61:51:33//DROSOPHILA MELANOGASTER (FRUIT FLY)//P14199

35 F-NT2RM2001312//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//7.2e-11:33:72//HOMO SAPIENS (HUMAN)//P39195

F-NT2RM2001319

40

F-NT2RM2001324//ZYXIN//5.1e-22:91:38//GALLUS GALLUS (CHICKEN)//Q04584

45 F-NT2RM2001345//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1//7.4e-10:159:27//PODOSPORA ANSERINA//Q00808

50 F-NT2RM2001360//ACCESSORY GLAND PEPTIDE PRECURSOR (PARAGONIAL PEPTIDE B)//1.0:27:48//DROSOPHILA MELANOGASTER (FRUIT FLY)//P05623

F-NT2RM2001370//NAPE PROTEIN//0.98:44:31//PARACOCCLUS DENITRIFICANS (SUBSP. THIOSPHAERA PANTOTROPHA)//Q56348

55 F-NT2RM2001393//VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN LV-1C; LIPOVITELLIN LV-2]//0.0024:163:31//CHTHYOMYZON UNICUSPUS (SILVER LAMPREY)//Q91062

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F-NT2RM2001420

- 5 F-NT2RM2001424//HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U)
./2.4e-41:140:59//HOMO SAPIENS (HUMAN).//Q00839
- 10 F-NT2RM2001499//HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1)
(CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL
LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RETROVIRUS RECEPTOR
HOMOLOG).//3.7e-71:201:68//HOMO SAPIENS (HUMAN).//P30825
- 15 F-NT2RM2001504//CUTICLE COLLAGEN 2./0.028:41:39//CAENORHABDITIS
ELEGANS.//P17656
- 20 F-NT2RM2001524//HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III./6.7e-
47:190:42//CAENORHABDITIS ELEGANS.//Q09316
- 25 F-NT2RM2001544//TELOMERE-BINDING PROTEIN 51 KD SUBUNIT./0.0027:136:
33//EUPLOTES CRASSUS.//Q06184
- F-NT2RM2001547//HYPOTHETICAL 48.6 KD PROTEIN IN BET1-PAN1 INTERGENIC
REGION./8.5e-18:91:50//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40564
- 30 F-NT2RM2001575//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A))
(RO(SS-A)).//3.9e-35:212:41//HOMO SAPIENS (HUMAN).//P19474
- 35 F-NT2RM2001582//RESA PROTEIN./0.0033:72:27//BACILLUS SUBTILIS.//P35160
- F-NT2RM2001588//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//1.0e-06:
115:32//ZEA MAYS (MAIZE).//P14918
- 40 F-NT2RM2001592//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN)
./0.033:156:23//HOMO SAPIENS (HUMAN).//P26371
- 45 F-NT2RM2001605//RETINOBLASTOMA BINDING PROTEIN 2 (RBBP-2).//1.1e-116:249:
82//HOMO SAPIENS (HUMAN).//P29375
- 50 F-NT2RM2001613//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT./1.2e-97:
192:100//RATTUS NORVEGICUS (RAT).//P38378
- F-NT2RM2001632//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR./0.00068:145:
28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323
- 55 F-NT2RM2001635//NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE
MEMBRANE PROTEIN OF 121 KD) (P145).//1.1e-39:235:47//RATTUS NORVEGICUS (RAT)
./P52591

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- 5 F-NT2RM2001637//HYPOTHETICAL BHLF1 PROTEIN.//0.075:197:29//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
- 10 F-NT2RM2001641//NADH-CYTOCHROME B5 REDUCTASE (EC 1.6.2.2) (B5R).//0.013:29:68//HOMO SAPIENS (HUMAN).//P00387
- 15 F-NT2RM2001648//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//3.2e-65:132:100//CANIS FAMILIARIS (DOG).//P38377
- 20 F-NT2RM2001652//PROTEIN TRANSPORT PROTEIN SEC7.//1.6e-32:261:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P11075
- 25 F-NT2RM2001659//CARBOXYPEPTIDASE A INHIBITOR.//0.83:30:46//ASCARIS SUUM (PIG ROUNDWORM) (ASCARIS LUMBRICOIDES).//P19399
- 30 F-NT2RM2001664//IKI3 PROTEIN.//1.3e-31:265:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06706
- 35 F-NT2RM2001668//TONB PROTEIN.//0.32:39:41//XANTHOMONAS CAMPESTRIS (PV. CAMPESTRIS).//O34261
- 40 F-NT2RM2001670//ZINC FINGER PROTEIN 174.//3.6e-21:172:39//HOMO SAPIENS (HUMAN).//Q15697
- 45 F-NT2RM2001671//HYPOTHETICAL 118.6 KD PROTEIN C29E6.03C IN CHROMOSOME I.//1.6e-10:229:24//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09857
- 50 F-NT2RM2001675//DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52) (DHDPS).//1.0:184:21//METHANOCOCCUS JANNASCHII.//Q57695
- 55 F-NT2RM2001681//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1).//0.0039:199:22//DROSOPHILA MELANOGASTER (FRUIT FLY).//P54399
- F-NT2RM2001688//HYPOTHETICAL 28.1 KD PROTEIN IN SIPU-PBPC INTERGENIC REGION.//2.6e-21:162:33//BACILLUS SUBTILIS.//P42966
- F-NT2RM2001695//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//4.9e-41:60:81//HOMO SAPIENS (HUMAN).//P39194
- F-NT2RM2001696//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//9.8e-16:126:38//AUTOGRAPHIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479
- F-NT2RM2001698//PENAEIDIN-3B PRECURSOR (P3-B).//0.36:52:34//PENAEUS VANNAMEI (PENOEID SHRIMP) (EUROPEAN WHITE SHRIMP).//P81059

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- 5 F-NT2RM2001699//TRANSCRIPTION INITIATION FACTOR TFIIID 30 KD SUBUNIT (TAFII-30) (TAFII30).//0.0012:79:40//HOMO SAPIENS (HUMAN).//Q12962
- F-NT2RM2001700//ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC (EC 1.3.99.-) (VLCAD) (FRAGMENT).//1.0e-30:140:53//MUS MUSCULUS (MOUSE).//P50544
- 10 F-NT2RM2001706//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!1.5e-33:95:75//HOMO SAPIENS (HUMAN).//P39195
- F-NT2RM2001716//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR.//0.010:116:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) .//P47179
- 15 F-NT2RM2001718//METHYL-ACCEPTING CHEMOTAXIS PROTEIN TLPB.//0.00029:77: 37//BACILLUS SUBTILIS.//P39217
- F-NT2RM2001723//POSTERIOR PITUITARY PEPTIDE.//0.94:26:53//BOS TAURUS (BOVINE) .//P01154
- 25 F-NT2RM2001727//E7 PROTEIN.//0.91:46:34//HUMAN PAPILLOMAVIRUS TYPE 23.//P50781
- F-NT2RM2001730//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//4.9e-07:139:29//CAENORHABDITIS ELEGANS.//Q09931
- 30 F-NT2RM2001743//PROENKEPHALIN A PRECURSOR.//0.75:65:35//CAVIA PORCELLUS (GUINEA PIG).//P47969
- F-NT2RM2001753//HYPOTHETICAL PROTEIN KIAA0210.//1.5e-14:119:36//HOMO SAPIENS (HUMAN).//Q92609
- 40 F-NT2RM2001760//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//8.3e-58: 119:99//CANIS FAMILIARIS (DOG).//P38377
- 45 F-NT2RM2001768//HYPOTHETICAL PROTEIN UL25.//0.45:77:32//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16761
- 50 F-NT2RM2001771//ZINC FINGER PROTEIN 135.//4.6e-80:224:60//HOMO SAPIENS (HUMAN) .//P52742
- 55 F-NT2RM2001782//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1- PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//7.0e-06:61:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41940

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F-NT2RM2001784//HYPOTHETICAL PROTEIN UL61.//0.00070:145:33//HUMAN
 CYTOMEGALOVIRUS (STRAIN AD169).//P16818
 5
 F-NT2RM2001785//LINOLEOYL-COA DESATURASE (EC 1.14.99.25) (DELTA(6)-
 DESATURASE).//1.5e-08:127:32//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//Q08871
 10
 F-NT2RM2001797//ZINC FINGER PROTEIN 135.//1.6e-73:267:49//HOMO SAPIENS (HUMAN)
 .//P52742
 F-NT2RM2001800//HYPOTHETICAL HELICASE MG018/MG017/MG016 HOMOLOG.//3.9e-12:
 15 171:33//MYCOPLASMA PNEUMONIAE.//P75093
 F-NT2RM2001803//IKI3 PROTEIN.//1.6e-38:283:36//SACCHAROMYCES CEREVISIAE
 (BAKER'S YEAST).//Q06706
 20
 F-NT2RM2001805//COLD SHOCK-LIKE PROTEIN CSPH.//0.51:46:32//SALMONELLA
 TYPHIMURIUM.//O33793
 25
 F-NT2RM2001813//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN
 C14B1.4 IN CHROMOSOME III.//5.0e-05:82:32//CAENORHABDITIS ELEGANS.//Q17963
 F-NT2RM2001823//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2).//3.6e-
 30 49:233:45//HOMO SAPIENS (HUMAN).//O14647
 F-NT2RM2001839//RETICULOCALBIN 1 PRECURSOR.//5.2e-65:222:56//HOMO SAPIENS
 (HUMAN).//Q15293
 35
 F-NT2RM2001840//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//9.6e-33:102:68//HOMO
 SAPIENS (HUMAN).//P39194
 40
 F-NT2RM2001855//BASP1 PROTEIN.//0.054:120:30//HOMO SAPIENS (HUMAN).//P80723
 F-NT2RM2001867//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC
 REGION.//4.1e-19:88:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53867
 45
 F-NT2RM2001879//HYPOTHETICAL 47.3 KD PROTEIN C22G7.07C IN CHROMOSOME
 I.//5.9e-15:76:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09800
 50
 F-NT2RM2001886//HYPOTHETICAL 126.9 KD PROTEIN C22G7.04 IN CHROMOSOME
 I.//1.4e-41:249:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09798
 55
 F-NT2RM2001896//HYPOTHETICAL 83.2 KD PROTEIN IN KAR4-PBN1 INTERGENIC
 REGION.//2.1e-59:197:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25582
 F-NT2RM2001903//HYPOTHETICAL PROTEIN MJ0263.//0.070:132:31//METHANOCOCCUS

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JANNASCHII./O06917

- 5 F-NT2RM2001930//THROMBOSPONDIN 2 PRECURSOR./7.1e-05:53:47//MUS MUSCULUS (MOUSE)./Q03350
- 10 F-NT2RM2001935//PUTATIVE CUTICLE COLLAGEN F55C10.3./0.00046:116:35//CAENORHABDITIS ELEGANS./Q21184
- 15 F-NT2RM2001936//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION./4.5e-27:216:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)./P28320
- 20 F-NT2RM2001950//HIRUDIN HV1 (BUFRUDIN)./0.59:43:34//HIRUDINARIA MANILLENSIS (BUFFALO LEECH)./P81492
- 25 F-NT2RM2001982//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-8 SUBUNIT (G GAMMA-C)./0.72:35:42//BOS TAURUS (BOVINE)./P50154
- 30 F-NT2RM2001983//PROLINE-RICH PEPTIDE P-B./0.00035:23:52//HOMO SAPIENS (HUMAN)./P02814
- 35 F-NT2RM2001989//NUCLEOLAR PROTEIN NOP4 (NUCLEOLAR PROTEIN NOP77)./8.6e-24:197:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)./P37838
- 40 F-NT2RM2001997
- 45 F-NT2RM2001998//IMMEDIATE-EARLY PROTEIN IE180./0.076:92:27//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV)./P11675
- 50 F-NT2RM2002004//SLF1 PROTEIN./3.5e-06:235:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)./Q12034
- 55 F-NT2RM2002014//HYPOTHETICAL PROTEIN HI0568./2.1e-17:235:29//HAEMOPHILUS INFLUENZAE./P71353
- 60 F-NT2RM2002030//GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE [ISOMERIZING] (EC 2.6.1.16) (HEXOSEPHOSPHATE AMINOTRANSFERASE) (D-FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE) (GFAT)./9.5e-105:271:76//MUS MUSCULUS (MOUSE)./P47856
- 65 F-NT2RM2002049//SMALL PROLINE-RICH PROTEIN 2-1./0.099:41:41//HOMO SAPIENS (HUMAN)./P35326
- 70 F-NT2RM2002055//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13./0.012:217:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)./Q07878
- 75 F-NT2RM2002088//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X

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(HNRNP X) (CBP).//1.1e-09:65:53//MUS MUSCULUS (MOUSE).//Q61990

5 F-NT2RM2002091//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC
REGION.//0.072:74:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214

10 F-NT2RM2002100//ATP-DEPENDENT RNA HELICASE ROK1.//4.5e-50:289:
41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P45818

15 F-NT2RM2002109//NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112)
(TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C).//1.4e-14:203:32//RATTUS NORVEGICUS
(RAT).//Q03351

20 F-NT2RM2002128//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
.//0.0025:139:31//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437

25 F-NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12.//9.2e-20:42:
73//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).//P47805

30 F-NT2RM2002145//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT 12
PRECURSOR.//0.0085:200:26//TRITICUM AESTIVUM (WHEAT).//P08488

35 F-NT2RM2002178//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//5.8e-05:56:39//BOS
TAURUS (BOVINE).//P25508

40 F-NT2RM2002580//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y
PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).//2.9e-14:96:
37//PETROMYZON MARINUS (SEA LAMPREY).//P25210

45 F-NT2RM4000024//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC
2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//8.6e-95:271:67//DROSOPHILA
MELANOGASTER (FRUIT FLY).//P25167

50 F-NT2RM4000027//INTERFERON-ACTIVATABLE PROTEIN 202 (IFI-202).//0.99:72:31//MUS
MUSCULUS (MOUSE).//P15091

55 F-NT2RM4000030//LAS1 PROTEIN.//1.4e-14:184:32//SACCHAROMYCES CEREVISIAE
(BAKER'S YEAST).//P36146

F-NT2RM4000046//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT).//0.99:120:28//RATTUS
NORVEGICUS (RAT).//P13941

F-NT2RM4000061

55 F-NT2RM4000085//ATP-DEPENDENT RNA HELICASE A (NUCLEAR DNA HELICASE II)
(NDH II) (DEAD BOX PROTEIN 9) (MHEL-5).//8.5e-40:263:38//MUS MUSCULUS (MOUSE)
.//O70133

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- 5 F-NT2RM4000086//HYPOTHETICAL PROTEIN HI1497.//1.0:27:37//HAEMOPHILUS INFLUENZAE.//P44221
- F-NT2RM4000104//ZINC FINGER PROTEIN 134.//1.0e-26:64:56//HOMO SAPIENS (HUMAN).//P52741
- 10 F-NT2RM4000139//PREPROTEIN TRANSLOCASE SECE SUBUNIT.//0.99:38:42//THERMOTOGA MARITIMA.//P35874
- 15 F-NT2RM4000155//THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.3) (THREONINE-TRNA LIGASE) (THRRS).//6.3e-34:181:40//HOMO SAPIENS (HUMAN).//P26639
- 20 F-NT2RM4000156//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//4.6e-12:142:33//NICOTIANA TABACUM (COMMON TOBACCO).//P13983
- F-NT2RM4000167//KINESIN-LIKE PROTEIN KIF4.//3.4e-123:269:91//MUS MUSCULUS (MOUSE).//P33174
- 25 F-NT2RM4000169//M PROTEIN, SEROTYPE 2.2 PRECURSOR.//9.7e-10:229:26//STREPTOCOCCUS PYOGENES.//P50469
- 30 F-NT2RM4000191//P68-LIKE PROTEIN.//2.1e-11:104:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P24783
- F-NT2RM4000197//CUTICLE PROTEIN CP463 (CPCP463).//0.84:29:37//CANCER PAGURUS (ROCK CRAB).//P81587
- 35 F-NT2RM4000199//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//1.8e-06:187:34//HOMO SAPIENS (HUMAN).//P10162
- 40 F-NT2RM4000200//HYPOTHETICAL 9.4 KD PROTEIN IN FLAL 3'REGION (ORF3).//0.52:42:40//BACILLUS LICHENIFORMIS.//P22754
- 45 F-NT2RM4000202//COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN).//0.00044:168:32//ORYCTOLAGUS CUNICULUS (RABBIT).//P14282
- F-NT2RM4000210//EXTENSIN PRECURSOR.//0.27:129:27//DAUCUS CAROTA (CARROT).//P06599
- 50 F-NT2RM4000215//MAK16 PROTEIN.//2.0e-65:234:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P10962
- 55 F-NT2RM4000229//GAR2 PROTEIN.//0.13:217:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891

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- F-NT2RM4000233//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//0.047:108:30//HOMO SAPIENS (HUMAN).//P51805
- 5 F-NT2RM4000244//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.67:59:27//BALAENOPTERA PHYSALUS (FINBACK WHALE) (COMMON RORQUAL).//P24947
- 10 F-NT2RM4000251//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.0059:108:35//MUS MUSCULUS (MOUSE).//P05143
- 15 F-NT2RM4000265//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//8.1e-38:70:70//HOMO SAPIENS (HUMAN).//P39188
- F-NT2RM4000290//TRANSDUCIN-LIKE ENHANCER PROTEIN 3 (ESG3).//1.6e-115:209:94//HOMO SAPIENS (HUMAN).//Q04726
- 20 F-NT2RM4000324//PRESPORE PROTEIN DP87 PRECURSOR.//0.14:136:30//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//Q04503
- 25 F-NT2RM4000327//HYPOTHETICAL 8.9 KD PROTEIN IN IE0-IE1 INTERGENIC REGION.//0.91:73:28//AUTOGRAPHIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41703
- 30 F-NT2RM4000344//YME1 PROTEIN HOMOLOG (EC 3.4.24.-).//9.4e-78:241:55//CAENORHABDITIS ELEGANS.//P54813
- 35 F-NT2RM4000349//CYSTEINE STRING PROTEIN (CCCS1).//0.055:22:59//TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).//P56101
- F-NT2RM4000354//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//4.6e-26:208:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24371
- 40 F-NT2RM4000356//COAT PROTEIN.//0.11:105:36//SATELLITE TOBACCO MOSAIC VIRUS (STMV).//P17574
- 45 F-NT2RM4000366//IMMEDIATE-EARLY PROTEIN.//1.2e-05:215:24//HERPES VIRUS SAIMIRI (STRAIN 11).//Q01042
- 50 F-NT2RM4000368//HYPOTHETICAL 7.3 KD PROTEIN IN RPBA-GP46 INTERGENIC REGION.//0.54:46:36//BACTERIOPHAGE RB69.//O64300
- F-NT2RM4000386//RHSC PROTEIN PRECURSOR.//0.0096:162:29//ESCHERICHIA COLI.//P16918
- 55 F-NT2RM4000395//HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION.//4.5e-66:256:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43616

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F-NT2RM4000414//HYPOTHETICAL 6.0 KD PROTEIN IN THI12 5'REGION.//0.13:33:
48//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53820

5 F-NT2RM4000421//MRNA TRANSPORT REGULATOR MTR10.//5.0e-13:171:
29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q99189

10 F-NT2RM4000425/////ALU SUBFAMILY SP WARNING ENTRY !!!!!//2.1e-25:46:80//HOMO
SAPIENS (HUMAN).//P39193

15 F-NT2RM4000433//CUTICLE COLLAGEN 3A3.//2.5e-06:77:38//HAEMONCHUS
CONTORTUS.//P16253

F-NT2RM4000457//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME
I.//4.3e-09:215:22//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10297

20 F-NT2RM4000471//TRNA SPLICING PROTEIN SPL1.//6.7e-73:163:65//CANDIDA ALBICANS
(YEAST).//P87185

25 F-NT2RM4000486//COLLAGEN ALPHA 2(VI) CHAIN PRECURSOR.//0.0012:121:34//GALLUS
GALLUS (CHICKEN).//P15988

30 F-NT2RM4000496//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6)
(RNA POLYMERASE II SUBUNIT 1).//5.9e-09:175:35//SCHIZOSACCHAROMYCES POMBE
(FISSION YEAST).//P36594

35 F-NT2RM4000511//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.020:122:
31//DROSOPHILA SIMULANS (FRUIT FLY).//P13729

F-NT2RM4000514//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.46:68:
32//ARTEMIA SANFRANCISCANA (BRINE SHRIMP) (ARTEMIA FRANCISCANA).//Q37708

40 F-NT2RM4000515//GAR2 PROTEIN.//3.2e-05:198:27//SCHIZOSACCHAROMYCES POMBE
(FISSION YEAST).//P41891

45 F-NT2RM4000520//HYPOTHETICAL 7.5 KD PROTEIN (ORF 63).//0.011:55:38//SPINACIA
OLERACEA (SPINACH).//P08974

50 F-NT2RM4000531//ZINC FINGER PROTEIN 169 (FRAGMENT).//3.6e-44:244:42//HOMO
SAPIENS (HUMAN).//Q14929

F-NT2RM4000532//PUTATIVE MEMBRANE PROTEIN 53.//1.0:47:34//HERPES VIRUS SAIMIRI
(STRAIN 11).//Q01049

55 F-NT2RM4000534//HYPOTHETICAL 5.9 KD PROTEIN IN WRBA-PUTA INTERGENIC
REGION.//0.75:26:46//ESCHERICHIA COLI.//P56614

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- F-NT2RM4000585//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P16; CORE PROTEIN P26]//0.019:86:34//HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE SBLIS Y) (HIV-2) //P12450
- 5 F-NT2RM4000590//RING CANAL PROTEIN (KELCH PROTEIN)//5.0e-23:224:29//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q04652
- 10 F-NT2RM4000595//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III//3.8e-62:226:50//CAENORHABDITIS ELEGANS//P34284
- 15 F-NT2RM4000603//SRC SUBSTRATE CORTACTIN (AMPLAXIN) (EMS1 ONCOGENE)//0.077:132:22//HOMO SAPIENS (HUMAN)//Q14247
- 20 F-NT2RM4000611//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN C14B1.4 IN CHROMOSOME III//1.9e-06:82:32//CAENORHABDITIS ELEGANS//Q17963
- F-NT2RM4000616//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME)//5.3e-79:213:62//ESCHERICHIA COLI//P27550
- 25 F-NT2RM4000674//HYPOTHETICAL SYMPORTER SLL1374//1.3e-11:147:32//SYNECHOCYSTIS SP. (STRAIN PCC 6803)//P74168
- 30 F-NT2RM4000689
- F-NT2RM4000698//CHORION CLASS HIGH-CYSTEINE HCA PROTEIN 12 PRECURSOR (HC-A.12)//0.26:45:33//BOMBYX MORI (SILK MOTH)//P05687
- 35 F-NT2RM4000700//THIOPHENE AND FURAN OXIDATION PROTEIN THDF//0.95:165:25//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE)//P53364
- 40 F-NT2RM4000712//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME)//2.2e-82:152:63//CAENORHABDITIS ELEGANS//P34547
- 45 F-NT2RM4000717//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR//0.80:54:40//DROSOPHILA SIMULANS (FRUIT FLY)//P13729
- 50 F-NT2RM4000733//OCTAPEPTIDE-REPEAT PROTEIN T2//1.5e-08:139:28//MUS MUSCULUS (MOUSE)//Q06666
- F-NT2RM4000734//GASTRULA ZINC FINGER PROTEIN XLCGF26.1 (FRAGMENT)//7.2e-20:205:28//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P18715
- 55 F-NT2RM4000741//SPERM PROTAMINE P1//0.89:52:38//ISOODON MACROURUS (SHORT-NOSED BANDICOOT)//P42136

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F-NT2RM4000751//ZINC FINGER PROTEIN 26 (ZFP-26) (MKR3 PROTEIN) (FRAGMENT)
 .//5.2e-77:246:52//MUS MUSCULUS (MOUSE).//P10076
 5
 F-NT2RM4000764//KERATIN, GLYCINE/TYROSINE-RICH OF HAIR.//0.062:33:42//OVIS ARIES
 (SHEEP).//Q02958
 10 F-NT2RM4000778
 F-NT2RM4000779//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//0.014:53:
 45//VOLVOX CARTERI.//P21997
 15 F-NT2RM4000787//BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-
 1).//0.00011:73:39//MUS MUSCULUS (MOUSE).//P98063
 20 F-NT2RM4000790//SPORE COAT PROTEIN SP96.//0.00083:157:29//DICTYOSTELIUM
 DISCOIDEUM (SLIME MOLD).//P14328
 F-NT2RM4000795//CHOLINESTERASE PRECURSOR (EC 3.1.1.8) (ACYLCHOLINE
 25 ACYLHYDROLASE) (CHOLINE ESTERASE II) (BUTYRYLCHOLINE ESTERASE)
 (PSEUDOCHELINESTERASE).//7.4e-41:271:36//HOMO SAPIENS (HUMAN).//P06276
 F-NT2RM4000796//5-METHYLCYTOSINE-SPECIFIC RESTRICTION ENZYME B (EC 3.1.21.-)
 30 .//0.28:82:30//ESCHERICHIA COLI.//P15005
 F-NT2RM4000798//PROTEIN TRANSPORT PROTEIN SEC7.//4.7e-38:165:
 48//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P11075
 35 F-NT2RM4000813//METALLOTHIONEIN-IB.//0.0025:25:44//OVIS ARIES (SHEEP).//P09577
 F-NT2RM4000820
 40 F-NT2RM4000833//HYPOTHETICAL PROTEIN MJ1136.//6.5e-42:206:41//METHANOCOCCUS
 JANNASCHII.//Q58536
 F-NT2RM4000848//BRAIN-SPECIFIC HOMEODOMAIN/POU DOMAIN PROTEIN 3A (BRN-3A)
 45 (BRN-3.0).//0.00060:159:33//MUS MUSCULUS (MOUSE).//P17208
 F-NT2RM4000852//SMALL PROLINE-RICH PROTEIN 2B (SPR-2B).//0.0076:13:69//HOMO
 50 SAPIENS (HUMAN).//P35325
 F-NT2RM4000855//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//0.0060:68:44//HOMO
 SAPIENS (HUMAN).//P39194
 55 F-NT2RM4000887//RTS1 PROTEIN (SCS1 PROTEIN).//0.23:153:24//SACCHAROMYCES
 CEREVISIAE (BAKER'S YEAST).//P38903

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- 5 F-NT2RM4000895//HYPOTHETICAL 53.5 KD PROTEIN IN PHO2-POL3 INTERGENIC
REGION.//3.3e-09:80:46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43123
- 10 F-NT2RM4000950//HYPOTHETICAL PROTEIN MJ0572.//0.090:68:29//METHANOCOCCUS
JANNASCHII.//Q57992
- 15 F-NT2RM4000971//KINESIN LIGHT CHAIN (KLC).//0.79:201:24//LOLIGO PEALEII (LONGFIN
SQUID).//P46825
- 20 F-NT2RM4000979//MYOSIN REGULATORY LIGHT CHAIN 2, NONSARCOMERIC (MYOSIN
RLC).//1.2e-07:25:96//HOMO SAPIENS (HUMAN).//P19105
- 25 F-NT2RM4000996//ZINC FINGER PROTEIN 37 (ZFP-37) (MALE GERM CELL SPECIFIC ZINC
FINGER PROTEIN).//1.4e-56:253:46//MUS MUSCULUS (MOUSE).//P17141
- 30 F-NT2RM4001002
- 35 F-NT2RM4001016//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT
PROTEIN P12; CORE SHELL PROTEIN P30].//0.25:101:31//FBR MURINE OSTEOSARCOMA
VIRUS.//P29175
- 40 F-NT2RM4001032//CUTICLE COLLAGEN 2.//2.6e-07:130:39//CAENORHABDITIS
ELEGANS.//P17656
- 45 F-NT2RM4001047//MO25 PROTEIN.//5.6e-107:252:80//MUS MUSCULUS (MOUSE).//Q06138
- 50 F-NT2RM4001054//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//9.0e-109:
209:94//CANIS FAMILIARIS (DOG).//P38377
- 55 F-NT2RM4001084//HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN UXUR-IADA
INTERGENIC REGION.//0.57:95:30//ESCHERICHIA COLI.//P39376
- 60 F-NT2RM4001092//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME
III.//2.5e-47:231:47//CAENORHABDITIS ELEGANS.//Q09531
- 65 F-NT2RM4001116//HYPOTHETICAL 216.3 KD PROTEIN R06F6.8 IN CHROMOSOME
II.//1.3e-08:243:23//CAENORHABDITIS ELEGANS.//Q09417
- 70 F-NT2RM4001140//HOMEBOX PROTEIN MSH-D.//7.1e-13:103:38//BRACHYDANIO RERIO
(ZEBRAFISH) (ZEBRA DANIO).//Q01704
- 75 F-NT2RM4001151//SYNAPSINS IA AND IB (BRAIN PROTEIN 4.1).//0.26:96:34//HOMO
SAPIENS (HUMAN).//P17600
- 80 F-NT2RM4001155//ADRENAL MEDULLA 50 KD PROTEIN.//3.6e-103:201:91//BOS TAURUS

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(BOVINE).//Q27969

- 5 F-NT2RM4001160//GLUTATHIONE S-TRANSFERASE (EC 2.5.1.18) (CLASS-PHI)
(FRAGMENTS).//1.0:33:36//BRASSICA OLERACEA (CAULIFLOWER).//P48438 F-
NT2RM4001187//PREPROTEIN TRANSLOCASE SECA SUBUNIT.//0.44:158:
27//MYCOPLASMA GENITALIUM.//P47318
- 10 F-NT2RM4001191//LONG NEUROTOXIN 2 (TOXIN C).//0.99:44:43//ASTROTIA STOKESI
(STOKES'S SEA SNAKE) (DSTEIRA STOKESI).//P01381
- 15 F-NT2RM4001200//ZINC FINGER PROTEIN 135.//2.2e-82:245:59//HOMO SAPIENS (HUMAN)
./P52742
- 20 F-NT2RM4001203//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC
REGION.//0.028:94:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214
- F-NT2RM4001204//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//0.0096:
182:34//HOMO SAPIENS (HUMAN).//Q15428
- 25 F-NT2RM4001217//RING CANAL PROTEIN (KELCH PROTEIN).//2.1e-21:221:
29//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
- 30 F-NT2RM4001256//CBP3 PROTEIN PRECURSOR.//0.30:55:32//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST).//P21560
- 35 F-NT2RM4001258//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.00031:
132:39//STREPTOMYCES FRADIAE.//P20186
- 40 F-NT2RM4001309//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7)
[CONTAINS: BASIC PEPTIDE P-F] (FRAGMENT).//0.048:132:28//HOMO SAPIENS (HUMAN)
./P02812
- 45 F-NT2RM4001313//PHOSPHATIDYLINOSITOL 3-KINASE VPS34-LIKE (EC 2.7.1.137) (PI3-
KINASE) (PTDINS-3-KINASE) (PI3K).//2.6e-37:124:65//DICTYOSTELIUM DISCOIDEUM (SLIME
MOLD).//P54676
- 50 F-NT2RM4001316//ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC
PRECURSOR (EC 1.3.99.3) (MCAD).//1.7e-10:185:30//RATTUS NORVEGICUS (RAT).//P08503
- 55 F-NT2RM4001320//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR
(RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//1.5e-08:197:26//MUS
MUSCULUS (MOUSE).//P52734
- F-NT2RM4001340//UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4 PROTEIN).//7.7e-14:82:
36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32626

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- F-NT2RM4001344//HYPOTHETICAL GTP-BINDING PROTEIN IN POP2-HOL1 INTERGENIC REGION.//3.3e-16:128:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53742
- 5 F-NT2RM4001347//HYPOTHETICAL 76.9 KD PROTEIN IN RPM2-TUB1 INTERGENIC REGION.//0.067:111:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04511
- F-NT2RM4001371
- 10 F-NT2RM4001382//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.//1.0e-08:82:39//PLASMODIUM LOPHURAE.//P04929
- 15 F-NT2RM4001384
- F-NT2RM4001410//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//2.1e-08:185:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323
- 20 F-NT2RM4001411//EARLY NODULIN 20 PRECURSOR (N-20).//5.3e-05:105:38//MEDICAGO TRUNCATULA (BARREL MEDIC).//P93329
- 25 F-NT2RM4001412//GTPASE-ACTIVATING PROTEIN (GAP) (RAS P21 PROTEIN ACTIVATOR) (P120GAP) (RASGAP).//6.2e-17:109:41//RATTUS NORVEGICUS (RAT).//P50904
- F-NT2RM4001414//ZINC FINGER PROTEIN 177.//8.3e-06:54:50//HOMO SAPIENS (HUMAN)
- 30 .//Q13360
- F-NT2RM4001437//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//2.1e-24:87:65//HOMO SAPIENS (HUMAN).//P39192
- 35 F-NT2RM4001444//PROBABLE ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS) (FRAGMENT).//2.6e-45:197:47//CIONA INTESTINALIS.//Q94425
- 40 F-NT2RM4001454//HYPOTHETICAL PROTEIN KIAA0041 (FRAGMENT).//0.0060:95:29//HOMO SAPIENS (HUMAN).//Q15057
- 45 F-NT2RM4001455//PROBABLE E5B PROTEIN.//0.41:44:36//HUMAN PAPILLOMAVIRUS TYPE 6B.//P06461
- F-NT2RM4001483//ZINC FINGER PROTEIN 136.//1.7e-28:85:64//HOMO SAPIENS (HUMAN)
- 50 .//P52737
- F-NT2RM4001489//PTB-ASSOCIATED SPLICING FACTOR (PSF).//0.086:111:34//HOMO SAPIENS (HUMAN).//P23246
- 55 F-NT2RM4001519//ACID UREASE ALPHA SUBUNIT (EC 3.5.1.5) (UREA AMIDOHYDROLASE).//0.82:51:47//LACTOBACILLUS FERMENTUM.//P26929

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F-NT2RM4001522//TROPOMYOSIN.//0.030:117:23//SCHIZOSACCHAROMYCES POMBE
 (FISSION YEAST).//Q02088
 5 F-NT2RM4001557
 F-NT2RM4001565//HYPOTHETICAL 44.3 KD PROTEIN C1F7.07C IN CHROMOSOME I.//0.99:
 10 42:40//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09919
 F-NT2RM4001566//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-
 ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//0.054:190:
 15 23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640
 F-NT2RM4001569//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
 PROTEIN (ACTIVATED PROTEIN KINASE C RECEPTOR HOMOLOG).//0.72:64:
 20 31//TRYPANOSOMA BRUCEI BRUCEI.//Q94775
 F-NT2RM4001582
 F-NT2RM4001592//DNA REPAIR PROTEIN RAD9.//0.00037:198:31//SACCHAROMYCES
 25 CEREVISIAE (BAKER'S YEAST).//P14737
 F-NT2RM4001594//IMMEDIATE-EARLY PROTEIN IE180.//1.9e-05:147:34//PSEUDORABIES
 30 VIRUS (STRAIN KAPLAN) (PRV).//P33479
 F-NT2RM4001597//THIOL:DISULFIDE INTERCHANGE PROTEIN TLPA (CYTOCHROME C
 BIOGENESIS PROTEIN TLPA).//5.7e-06:122:29//BRADYRHIZOBIUM JAPONICUM.//P43221
 35 F-NT2RM4001605//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN
 NUP155) (155 KD NUCLEOPORIN) (P140).//1.7e-128:249:96//RATTUS NORVEGICUS (RAT)
 40 .//P37199
 F-NT2RM4001611//SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3).//1.5e-35:128:
 47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36024
 F-NT2RM4001629//MAGUK P55 SUBFAMILY MEMBER 3 (MPP3 PROTEIN) (DISCS, LARGE
 45 HOMOLOG 3).//5.8e-42:254:37//HOMO SAPIENS (HUMAN).//Q13368
 F-NT2RM4001650//HOMEBOX PROTEIN HOX-A4 (CHOX-1.4).//0.62:19:57//GALLUS
 50 GALLUS (CHICKEN).//P17277
 F-NT2RM4001662//PROTEIN KINASE C, ALPHA TYPE (EC 2.7.1.-) (PKC-ALPHA).//0.29:90:
 32//HOMO SAPIENS (HUMAN).//P17252
 55 F-NT2RM4001666//HYPOTHETICAL 48.6 KD PROTEIN IN ALPA-GABP INTERGENIC
 REGION.//1.1e-31:137:44//ESCHERICHIA COLI.//P37339

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- 5 F-NT2RM4001682//PROBABLE 60S RIBOSOMAL PROTEIN L22.//0.98:55:29//CAENORHABDITIS ELEGANS.//P52819
- 5 F-NT2RM4001710//HYPOTHETICAL PROTEIN KIAA0039 (FRAGMENT).//0.56:113:28//HOMO SAPIENS (HUMAN).//Q15054
- 10 F-NT2RM4001714//SEPTIN 2 HOMOLOG (FRAGMENT).//1.4e-108:255:77//HOMO SAPIENS (HUMAN).//Q14141
- 15 F-NT2RM4001715//HYPOTHETICAL PROTEIN C19G10.16 IN CHROMOSOME I (FRAGMENT).//2.1e-36:148:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10342
- 20 F-NT2RM4001731//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III.//1.1e-05:90:33//CAENORHABDITIS ELEGANS.//P34284
- 20 F-NT2RM4001741//TALIN.//1.1e-106:208:99//MUS MUSCULUS (MOUSE).//P26039
- 25 F-NT2RM4001746//EBNA-1 NUCLEAR PROTEIN.//1.6e-09:155:38//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03211
- 30 F-NT2RM4001754//COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR.//0.93:158:33//HOMO SAPIENS (HUMAN).//P29400
- 30 F-NT2RM4001758//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).//5.1e-113:277:79//HOMO SAPIENS (HUMAN).//P27448
- 35 F-NT2RM4001776//MYOSIN I ALPHA (MMI-ALPHA).//2.2e-73:262:54//MUS MUSCULUS (MOUSE).//P46735
- 40 F-NT2RM4001783//ZINC FINGER PROTEIN HRX (ALL-1) (FRAGMENT).//5.3e-26:169:39//MUS MUSCULUS (MOUSE).//P55200
- 45 F-NT2RM4001810//MALE SPECIFIC SPERM PROTEIN MST84DB.//2.3e-05:68:42//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643
- 45 F-NT2RM4001813//RHODOCETIN ALPHA SUBUNIT.//2.3e-05:115:34//AGKISTRODON RHODOSTOMA (MALAYAN PIT VIPER) (CALLOSELASMA RHODOSTOMA).//P81397
- 50 F-NT2RM4001819//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR) (CELL SURFACE GLYCOPROTEIN F4/80).//1.7e-06:159:25//MUS MUSCULUS (MOUSE).//Q61549
- 55 F-NT2RM4001823//ZINC FINGER PROTEIN ZIC1 (ZINC FINGER PROTEIN OF THE CEREBELLUM 1).//2.6e-18:114:40//MUS MUSCULUS (MOUSE).//P46684

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- F-NT2RM4001828//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//4.0e-81:
253:59//HOMO SAPIENS (HUMAN).//P51523
- 5 F-NT2RM4001836//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//0.21:176:
30//NEPHILA CLAVIPES (ORB SPIDER).//P46804
- 10 F-NT2RM4001841//PROLINE-RICH PEPTIDE P-B.//0.046:27:40//HOMO SAPIENS (HUMAN)
//P02814
- 15 F-NT2RM4001842//HYPOTHETICAL 7.0 KD PROTEIN B03B8.1 IN CHROMOSOME III.//0.98:
35:42//CAENORHABDITIS ELEGANS.//Q11104
- F-NT2RM4001856//HYPOTHETICAL 75.2 KD PROTEIN IN ACS1-GCV3 INTERGENIC
REGION.//2.3e-37:242:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39722
- 20 F-NT2RM4001858//T-BOX PROTEIN VEGT (T-BOX PROTEIN BRAT) (T-BOX PROTEIN
ANTIPODEAN).//1.8e-23:78:64//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P87377
- 25 F-NT2RM4001865//NEURONAL CALCIUM SENSOR 2 (NCS-2).//0.012:83:
28//CAENORHABDITIS ELEGANS.//P36609
- 30 F-NT2RM4001876//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC
REGION PRECURSOR.//3.8e-10:242:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)
//P47179
- 35 F-NT2RM4001880//EC PROTEIN HOMOLOG.//0.22:59:32//ARABIDOPSIS THALIANA
(MOUSE-EAR CRESS).//P93746
- F-NT2RM4001905//60S RIBOSOMAL PROTEIN L40 (CEP52).//0.57:20:60//HOMO SAPIENS
(HUMAN), RATTUS NORVEGICUS (RAT), AND GALLUS GALLUS (CHICKEN).//P14793
- 40 F-NT2RM4001922
- 45 F-NT2RM4001930//PUTATIVE GLUCOSYLTRANSFERASE C08B11.8 (EC 2.4.1.-).//5.5e-45:
167:53//CAENORHABDITIS ELEGANS.//Q09226
- F-NT2RM4001938//RTOA PROTEIN (RATIO-A).//0.0036:120:32//DICTYOSTELIUM
DISCOIDEUM (SLIME MOLD).//P54681
- 50 F-NT2RM4001940//IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-1 (FRAGMENT).//0.32:
31:48//HOMO SAPIENS (HUMAN).//P78415
- 55 F-NT2RM4001953//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//2.2e-43:56:85//HOMO
SAPIENS (HUMAN).//P39192
- F-NT2RM4001965//IG ALPHA-1 CHAIN C REGION.//0.56:73:34//GORILLA GORILLA GORILLA

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(LOWLAND GORILLA).//P20758

- 5 F-NT2RM4001969//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//0.0016:140:27//HOMO SAPIENS (HUMAN).//P04280
- 10 F-NT2RM4001979//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.9e-21:103:51//HOMO SAPIENS (HUMAN).//P51523
- 15 F-NT2RM4001984//HYPOTHETICAL PROTEIN LAMBDA-SP5.//0.0034:50:40//MUS MUSCULUS (MOUSE).//P15974
- 20 F-NT2RM4001987//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PROTEIN).//6.9e-17:115:31//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q08180
- 25 F-NT2RM4002013//HYPOTHETICAL 54.5 KD TRP-ASP REPEATS CONTAINING PROTEIN ZC302.2 IN CHROMOSOME V.//0.0062:117:28//CAENORHABDITIS ELEGANS.//Q23256
- 30 F-NT2RM4002018//SPORE COAT PROTEIN SP96.//4.3e-06:203:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P14328
- 35 F-NT2RM4002034//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//0.78:132:25//HOMO SAPIENS (HUMAN).//P98171
- 40 F-NT2RM4002044//VITELLOGENIN I PRECURSOR (MINOR VITELLOGENIN) [CONTAINS: LIPOVITELLIN I (LVI); PHOSVITIN (PV); LIPOVITELLIN II (LVII); YGP42].//0.062:201:24//GALLUS GALLUS (CHICKEN).//P87498
- 45 F-NT2RM4002054//DUPLICATE PROCYCLIN.//0.0079:44:52//TRYPANOSOMA BRUCEI BRUCEI.//P14044
- 50 F-NT2RM4002055//PUTATIVE Z PROTEIN.//0.82:39:30//OVIS ARIES (SHEEP).//P08105
- 55 F-NT2RM4002062//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE-TRNA LIGASE) (ASPRS).//7.0e-37:80:52//THERMUS AQUATICUS (SUBSP. THERMOPHILUS).//P36419
- 60 F-NT2RM4002063//SARCOSINE OXIDASE (EC 1.5.3.1).//2.2e-25:216:31//BACILLUS SP. (STRAIN NS-129).//P23342
- 65 F-NT2RM4002066//HYPOTHETICAL PROTEIN KIAA0192 (FRAGMENT).//1.1e-94:260:71//HOMO SAPIENS (HUMAN).//Q93074
- 70 F-NT2RM4002067//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.5e-15:51:70//HOMO SAPIENS (HUMAN).//P39188

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- F-NT2RM4002073//ELASTIN PRECURSOR (TROPOLASTIN).//4.9e-05:88:36//HOMO SAPIENS (HUMAN).//P15502
- 5 F-NT2RM4002075//RING CANAL PROTEIN (KELCH PROTEIN).//7.2e-43:220:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
- 10 F-NT2RM4002093//POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTB) (HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN I) (HNRNP I) (57 KD RNA-BINDING PROTEIN PPTB-1).//1.8e-93:255:72//HOMO SAPIENS (HUMAN).//P26599
- 15 F-NT2RM4002109//KINESIN-LIKE PROTEIN KIF4.//3.7e-101:260:78//MUS MUSCULUS (MOUSE).//P33174
- 20 F-NT2RM4002128//HYPOTHETICAL PROTEIN IN CYCB 3'REGION PRECURSOR (ORF2) (FRAGMENT).//0.91:49:32//PARACOCUS DENITRIFICANS.//P29969
- F-NT2RM4002140//GROUCHO PROTEIN (ENHANCER OF SPLIT M9/10).//0.36:104:22//DROSOPHILA MELANOGASTER (FRUIT FLY).//P16371
- 25 F-NT2RM4002145//SLIT PROTEIN PRECURSOR.//8.6e-13:127:33//DROSOPHILA MELANOGASTER (FRUIT FLY).//P24014
- 30 F-NT2RM4002146//MAGO NASHI PROTEIN.//7.9e-69:143:91//DROSOPHILA MELANOGASTER (FRUIT FLY).//P49028
- 35 F-NT2RM4002161//DUAL SPECIFICITY PROTEIN PHOSPHATASE (EC 3.1.3.48) (EC 3.1.3.16).//0.0062:99:26//CHLAMYDOMONAS EUGAMETOS.//Q39491
- F-NT2RM4002174//MRP PROTEIN.//4.5e-50:183:55//ESCHERICHIA COLI.//P21590
- 40 F-NT2RM4002189//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//2.6e-14:233:29//HOMO SAPIENS (HUMAN).//Q02817
- 45 F-NT2RM4002194//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//0.92:108:28//HOMO SAPIENS (HUMAN).//P51805
- F-NT2RM4002205//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).//5.8e-39:122:72//RATTUS NORVEGICUS (RAT).//Q07803
- 50 F-NT2RM4002213//HYPOTHETICAL 88.4 KD PROTEIN B0464.7 IN CHROMOSOME III.//9.9e-27:110:43//CAENORHABDITIS ELEGANS.//Q03565
- 55 F-NT2RM4002226//GTPASE ACTIVATING PROTEIN ROTUND.//1.3e-21:147:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//P40809
- F-NT2RM4002251//PROTEIN EF-7 (FRAGMENT).//0.00082:45:42//MUS MUSCULUS

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(MOUSE).//P97805

- 5 F-NT2RM4002256//COLD-REGULATED PROTEIN 1 (FRAGMENT).//0.00015:114:42//HORDEUM VULGARE (BARLEY).//P23251
- 10 F-NT2RM4002266//CUTICLE COLLAGEN 2.//0.00013:142:33//CAENORHABDITIS ELEGANS.//P17656
- 15 F-NT2RM4002278//HYPOTHETICAL 22.2 KD PROTEIN IN NSR1-TIF4631 INTERGENIC REGION.//1.0:40:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53288
- 20 F-NT2RM4002281
- 25 F-NT2RM4002287//GAR2 PROTEIN.//0.00055:225:23//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891
- 30 F-NT2RM4002294//HYPOTHETICAL PROTEIN KIAA0281 (HA6725).//1.1e-60:152:75//HOMO SAPIENS (HUMAN).//Q92556
- 35 F-NT2RM4002301//GENERAL STRESS PROTEIN CTC (FRAGMENT).//0.56:43:39//BACILLUS CALDOLYTICUS.//P42832
- 40 F-NT2RM4002323//NONHISTONE CHROMOSOMAL PROTEIN HMG-17.//0.0080:73:35//BOS TAURUS (BOVINE).//P02313
- 45 F-NT2RM4002339//METALLOTHIONEIN 10-III (MT-10-III).//0.67:34:38//MYTILUS EDULIS (BLUE MUSSEL).//P80248
- 50 F-NT2RM4002344//METALLOTHIONEIN-I (MT-I).//0.84:41:31//MUS MUSCULUS (MOUSE).//P02802
- 55 F-NT2RM4002373//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT DY10 PRECURSOR.//0.0019:190:28//TRITICUM AESTIVUM (WHEAT).//P10387
- F-NT2RM4002374//5E5 ANTIGEN.//0.0059:170:32//RATTUS NORVEGICUS (RAT).//Q63003
- F-NT2RM4002383//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//0.13:17:88//HOMO SAPIENS (HUMAN).//P39193
- F-NT2RM4002390
- F-NT2RM4002398//HNRNP ARGININE N-METHYLTRANSFERASE (EC 2.1.1.-) (ODP1 PROTEIN).//0.034:110:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38074
- F-NT2RM4002409//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME).//4.0e-20:179:31//METHANOTHRIX

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SOEHNGENII./P27095

5 F-NT2RM4002438///// ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.7e-15:41:95//HOMO
SAPIENS (HUMAN)./P39194

10 F-NT2RM4002446//CRYPTDIN-RELATED PROTEIN 4C-1 PRECURSOR (CRS4C)./0.0058:
24:50//MUS MUSCULUS (MOUSE)./P17534

10 F-NT2RM4002452//METALLOTHIONEIN 10-II (MT-10-II)./0.83:48:37//MYTILUS EDULIS
(BLUE MUSSEL)./P80247

15 F-NT2RM4002457///// ALU SUBFAMILY SC WARNING ENTRY !!!!!/4.9e-07:52:63//HOMO
SAPIENS (HUMAN)./P39192

20 F-NT2RM4002460//C-HORDEIN (CLONE PC-919) (FRAGMENT)./0.92:43:30//HORDEUM
VULGARE (BARLEY)./P17992

25 F-NT2RM4002479//RNA HELICASE-LIKE PROTEIN DB10./1.7e-28:200:41//NICOTIANA
SYLVESTRIS (WOOD TOBACCO)./P46942

30 F-NT2RM4002482//HYPOTHETICAL 65.9 KD PROTEIN YPR065W./8.8e-26:123:
49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)./Q12514 F-NT2RM4002493//LARVAL
CUTICLE PROTEIN I PRECURSOR./0.17:126:27//DROSOPHILA MIRANDA (FRUIT FLY)
./P91627

35 F-NT2RM4002499///// ALU SUBFAMILY SQ WARNING ENTRY !!!!!/9.4e-34:92:80//HOMO
SAPIENS (HUMAN)./P39194

35 F-NT2RM4002504///// ALU SUBFAMILY SB WARNING ENTRY !!!!!/3.4e-19:55:83//HOMO
SAPIENS (HUMAN)./P39189

40 F-NT2RM4002527//WD-40 REPEAT PROTEIN MSI2./3.0e-07:193:27//ARABIDOPSIS
THALIANA (MOUSE-EAR CRESS)./O22468

45 F-NT2RM4002532//AEROLYSIN REGULATORY PROTEIN./0.97:19:47//AEROMONAS
SOBRIA./P09165

50 F-NT2RM4002534//MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L32 PRECURSOR
(YML32)./0.76:86:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)./P25348

50 F-NT2RM4002558//LONG-CHAIN FATTY ACID TRANSPORT PROTEIN (FATP)./4.2e-55:204:
50//MUS MUSCULUS (MOUSE)./Q60714

55 F-NT2RM4002565//CHYMOTRYPSIN/ELASTASE ISOINHIBITORS 2 TO 5./1.0:16:
62//ASCARIS SUUM (PIG ROUNDWORM) (ASCARIS LUMBRICOIDES)./P07852

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F-NT2RM4002567//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION.//2.7e-10:184:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40032

5 F-NT2RM4002571//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN- UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC: POLYPEPTIDE, N- ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1).//2.4e-25:124: 47//HOMO SAPIENS (HUMAN).//Q10472

10 F-NT2RM4002593//HYPOTHETICAL 9.1 KD PROTEIN IN TETB-EXOA INTERGENIC REGION.//0.95:36:38//BACILLUS SUBTILIS.//P37509

15 F-NT2RM4002594//MSP1 PROTEIN HOMOLOG.//9.0e-68:227:60//CAENORHABDITIS ELEGANS.//P54815

20 F-NT2RM4002623//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS).//3.3e-54:243:47//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P73851

F-NT2RP1000018//SUPPRESSOR PROTEIN SRP40.//0.0023:131:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583

25 F-NT2RP1000035//RING CANAL PROTEIN (KELCH PROTEIN).//1.0e-06:63: 34//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

30 F-NT2RP1000040//LETHAL NEUROTOXIN TX1.//0.69:21:47//PHONEUTRIA NIGRIVENTER (BRAZILIAN ARMED SPIDER).//P17727

35 F-NT2RP1000063//HYPOTHETICAL 25.1 KD PROTEIN IN SMC3-MRPL8 INTERGENIC REGION.//3.8e-14:130:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40359

F-NT2RP1000086//HYPOTHETICAL 9.4 KD PROTEIN IN RNPA-THDF INTERGENIC REGION.//0.16:44:40//ESCHERICHIA COLI.//P22847

40 F-NT2RP1000101//45.8 KD PROTEIN IN SHM1-MRPL37 INTERGENIC REGION.//1.9e-06:74: 32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38344

45 F-NT2RP1000111//COP1 REGULATORY PROTEIN (FUSCA PROTEIN FUS1).//2.7e-19:135: 36//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P43254

50 F-NT2RP1000112//DUAL SPECIFICITY PROTEIN KINASE TTK (EC 2.7.1.-) (PYT).//1.2e-39: 91:62//HOMO SAPIENS (HUMAN).//P33981

F-NT2RP1000124//ATP-DEPENDENT . PROTEASE LA 2 (EC 3.4.21.53).//0.074:131: 24//MYXOCOCCUS XANTHUS.//P36774

55 F-NT2RP1000130//HEPATOMA-DERIVED GROWTH FACTOR (HDGF).//1.5e-49:186:56//MUS MUSCULUS (MOUSE).//P51859

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- 5 F-NT2RP1000163//METALLOTHIONEIN (MT).//0.98:41:34//PLEURONECTES PLATESSA (PLAICE).//P07216
- F-NT2RP1000170//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.85:64:35//HOMO SAPIENS (HUMAN).//P10162
- 10 F-NT2RP1000174//IMMEDIATE-EARLY PROTEIN IE180.//0.00056:89:37//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479
- F-NT2RP1000191//NIFU PROTEIN.//0.53:78:35//FRANKIA ALNI.//P46045
- 15 F-NT2RP1000202//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//9.1e-21:148:39//HOMO SAPIENS (HUMAN).//Q01485
- 20 F-NT2RP1000243//HYPOTHETICAL PROTEIN MJ1136.//1.4e-37:219:36//METHANOCOCCUS JANNASCHII.//Q58536
- F-NT2RP1000259//HYPOTHETICAL PROTEIN TP0318.//0.18:25:44//TREPONEMA PALLIDUM.//O83338
- 25 F-NT2RP1000272//SPLICING FACTOR, ARGININE/SERINE-RICH 3 (PRE-MRNA SPLICING FACTOR SRP20) (X16 PROTEIN).//1.6e-18:133:36//HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE).//P23152
- 30 F-NT2RP1000324
- 35 F-NT2RP1000326//HYPOTHETICAL 29.8 KD PROTEIN ZC97.1 IN CHROMOSOME III.//1.0e-23:129:36//CAENORHABDITIS ELEGANS.//P34599
- F-NT2RP1000333//ANTI-SILENCING PROTEIN 1.//2.5e-45:147:57//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32447
- 40 F-NT2RP1000348//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//4.8e-14:119:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25343
- 45 F-NT2RP1000357//TRYPOMASTIGOTE DECAY-ACCELERATING FACTOR (T-DAF) (FRAGMENT).//1.0:43:32//TRYPANOSOMA CRUZI.//Q26327
- 50 F-NT2RP1000358//HYPOTHETICAL 84.4 KD PROTEIN IN RPC2/RET1 3'REGION.//7.9e-28:244:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39744
- F-NT2RP1000363//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//2.2e-07:178:30//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437
- 55 F-NT2RP1000376//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//1.5e-

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20:254:31//HOMO SAPIENS (HUMAN).//P16157

- 5 F-NT2RP1000409//CYTOCHROME C3 (CYTOCHROME C7) (C551.5).//1.0:34:26//DESULFUROMONAS ACETOXIDANS (CHLOROPSEUDOMONAS ETHYLICA).//P00137
- 10 F-NT2RP1000413//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAP1 PROTEIN).//3.7e-131:230:97//RATTUS NORVEGICUS (RAT).//P55161
- F-NT2RP1000416//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.83:54:40//DROSOPHILA SIMULANS (FRUIT FLY).//P13729
- 15 F-NT2RP1000418//HYPOTHETICAL 9.9 KD PROTEIN IN GCVT-SPOIIIAA INTERGENIC REGION.//0.24:91:35//BACILLUS SUBTILIS.//P49779
- 20 F-NT2RP1000439//HYPOTHETICAL 100.5 KD PROTEIN C1B9.04 IN CHROMOSOME I.//0.13:172:22//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10429
- 25 F-NT2RP1000443//QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA- CRYSTALLIN).//1.9e-08:167:24//HOMO SAPIENS (HUMAN).//Q08257
- F-NT2RP1000460//NUCLEAR MOVEMENT PROTEIN NUDC.//1.0e-18:149:34//EMERICELLA NIDULANS (ASPERGILLUS NIDULANS).//P17624
- 30 F-NT2RP1000470//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//1.3e-43:180:47//CAENORHABDITIS ELEGANS.//P34580
- 35 F-NT2RP1000478//TUBULIN BETA-6 CHAIN (CLASS-VI).//1.5e-45:85:63//GALLUS GALLUS (CHICKEN).//P09207
- 40 F-NT2RP1000481//HYPOTHETICAL 5.8 KD PROTEIN IN PUHA 5'REGION (ORF55).//0.083:21:47//RHODOBACTER CAPSULATUS (RHODOPSEUDOMONAS CAPSULATA).//P26159
- 45 F-NT2RP1000493//POSSIBLE DNA-REPAIR PROTEIN XP-E (POSSIBLE XERODERMA PIGMENTOSUM GROUP E PROTEIN) (UV-DAMAGED DNA-BINDING PROTEIN) (UV-DDB).//6.6e-11:139:31//CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET).//P33194
- F-NT2RP1000513//60S RIBOSOMAL PROTEIN L22.//0.017:92:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//P50887
- 50 F-NT2RP1000522//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//0.0055:86:36//MUS MUSCULUS (MOUSE).//Q61068
- 55 F-NT2RP1000547//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.2e-09:69:36//CRICETULUS GRISEUS (CHINESE HAMSTER).//P49020

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- 5 F-NT2RP1000574//HOMEBOX PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1)//6.0e-39:
141:65//MUS MUSCULUS (MOUSE)//P97367
- 5 F-NT2RP1000577//PUTATIVE ATP-DEPENDENT RNA HELICASE YDL031W//0.00016:48:
45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q12389
- 10 F-NT2RP1000581//VON WILLEBRAND FACTOR PRECURSOR//0.00017:61:50//HOMO
SAPIENS (HUMAN)//P04275
- 15 F-NT2RP1000609//LINOLEOYL-COA DESATURASE (EC 1.14.99.25) (DELTA(6)-
DESATURASE)//4.4e-07:128:31//SYNECHOCYSTIS SP. (STRAIN PCC 6803)//Q08871
- 20 F-NT2RP1000629//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT
ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD
SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM
CHAIN)//4.2e-70:167:86//MUS MUSCULUS (MOUSE)//P35585
- 25 F-NT2RP1000630//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC
REGION PRECURSOR//0.0011:238:21//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)
//P47179
- 30 F-NT2RP1000677//COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR//0.99:71:33//HOMO
SAPIENS (HUMAN)//Q07092
- 35 F-NT2RP1000688//!!! ALU SUBFAMILY SP WARNING ENTRY !!!//0.0024:19:94//HOMO
SAPIENS (HUMAN)//P39193
- F-NT2RP1000695//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III//2.2e-
30:185:37//CAENORHABDITIS ELEGANS//Q18262
- 40 F-NT2RP1000701//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP)//3.2e-65:128:
93//RATTUS NORVEGICUS (RAT)//P54319
- 45 F-NT2RP1000721//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-
135) (TAFII135) (TAFII-130) (TAFII130)//2.3e-06:139:34//HOMO SAPIENS (HUMAN)//O00268
- 50 F-NT2RP1000730//MYOSIN LIGHT CHAIN 1, SLOW-TWITCH MUSCLE B/VENTRICULAR
ISOFORM (FRAGMENT)//0.89:40:40//MUS MUSCULUS (MOUSE)//P09542
- F-NT2RP1000733//METALLOTHIONEIN-LIKE PROTEIN CRS5//0.024:24:
45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P41902
- 55 F-NT2RP1000738//SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2
PRECURSOR (PRP-1 / PRP-3) (PRP-2 / PRP-4) (PIF-F / PIF-S) (PROTEIN A / PROTEIN C)
[CONTAINS: PEPTIDE P-C]//0.040:82:36//HOMO SAPIENS (HUMAN)//P02810

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- 5 F-NT2RP1000746//HYPOTHETICAL 27.1 KD PROTEIN UFD4-CAP1 INTERGENIC REGION.//2.0e-30:170:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33201
- 10 F-NT2RP1000767//PSEUDOMONAPEPSIN PRECURSOR (EC 3.4.23.37) (PEPSTATIN-INSENSITIVE CARBOXYL PROTEINASE).//0.99:75:34//PSEUDOMONAS SP. (STRAIN 101).//P42790
- 15 F-NT2RP1000782//CELL SURFACE GLYCOPROTEIN A15 (T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1).//2.3e-23:159:35//HOMO SAPIENS (HUMAN).//P41732
- 20 F-NT2RP1000796//CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) (SPRP).//0.00018:79:32//SUS SCROFA (PIG).//P35323
- 25 F-NT2RP1000825//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//3.1e-37:89:64//HOMO SAPIENS (HUMAN).//Q07960
- 30 F-NT2RP1000833//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.32:29:48//HOMO SAPIENS (HUMAN).//P22531
- 35 F-NT2RP1000834//2-ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-.-).//6.4e-67:202:68//RATTUS NORVEGICUS (RAT).//P70473
- 40 F-NT2RP1000836//HYPOTHETICAL 7.3 KD PROTEIN IN 100 KD PROTEIN REGION.//1.0:35:54//HUMAN ADENOVIRUS TYPE 41.//P23691
- 45 F-NT2RP1000846//SMALL PROLINE-RICH PROTEIN 2-1.//0.013:35:48//HOMO SAPIENS (HUMAN).//P35326
- 50 F-NT2RP1000851//PERIOD CLOCK PROTEIN (FRAGMENT).//0.082:28:57//DROSOPHILA SALTANS (FRUIT FLY).//Q04536
- 55 F-NT2RP1000856//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//2.5e-26:190:30//MUS MUSCULUS (MOUSE).//O35566
- F-NT2RP1000860//POTENTIAL TRANSCRIPTIONAL ADAPTOR.//0.13:86:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q02336
- F-NT2RP1000902//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//7.6e-11:200:35//CAENORHABDITIS ELEGANS.//Q09531

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F-NT2RP1000915//HYPOTHETICAL GTP-BINDING PROTEIN IN PMI40-PAC2 INTERGENIC REGION.//1.4e-06:88:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40010

5 F-NT2RP1000916//SUPPRESSOR PROTEIN SRP40.//0.40:90:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583

10 F-NT2RP1000943//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//0.099:75:34//HOMO SAPIENS (HUMAN).//Q02817

15 F-NT2RP1000944//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//7.6e-06:65:41//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10341

20 F-NT2RP1000947//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//3.6e-12:27:77//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), AND XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P51669

25 F-NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).//2.8e-15:169:28//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-NT2RP1000958//HYPOTHETICAL GTP-BINDING PROTEIN IN PMI40-PAC2 INTERGENIC REGION.//4.2e-16:162:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40010

30 F-NT2RP1000959//CORNIFIN A (SMALL PROLINE-RICH PROTEIN IA) (SPR-IA) (SPRK).//0.0031:34:44//HOMO SAPIENS (HUMAN).//P35321

35 F-NT2RP1000966//NUCLEOLIN (PROTEIN C23).//1.5e-52:110:95//HOMO SAPIENS (HUMAN).//P19338

40 F-NT2RP1000980//LIGHT-HARVESTING PROTEIN B-1015, ALPHA CHAIN PRECURSOR (ANTENNA PIGMENT PROTEIN, ALPHA CHAIN).//0.87:37:45//RHODOPSEUDOMONAS VIRIDIS.//P04123

F-NT2RP1000988

45 F-NT2RP1001011//PROTEIN P19.//0.96:30:50//BACTERIOPHAGE PRD1.//P17638

50 F-NT2RP1001013//DNA-BINDING PROTEIN 65 (PROTEIN GP65).//1.0:20:45//BACTERIOPHAGE T4.//P16012

F-NT2RP1001014

55 F-NT2RP1001033//TUBULIN GAMMA CHAIN.//2.5e-16:112:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P25295

F-NT2RP1001073//HYPOTHETICAL 10.4 KD PROTEIN IN FTR1-SPT15 INTERGENIC

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REGION.//7.6e-16:82:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40089

5 F-NT2RP1001079//SARCOSINE OXIDASE (EC 1.5.3.1).//4.8e-15:95:40//ARTHROBACTER
SP. (STRAIN TE1826).//P40873

10 F-NT2RP1001080//PROBABLE ATP-DEPENDENT RNA HELICASE DBP9.//2.4e-29:126:
46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06218

F-NT2RP1001113//SMALL PROLINE-RICH PROTEIN 2-1.//0.49:38:39//HOMO SAPIENS
(HUMAN).//P35326

15 F-NT2RP1001173//RHOMBOTIN-1 (CYSTEINE RICH PROTEIN TTG-1) (T-CELL
TRANSLOCATION PROTEIN 1) (LIM-ONLY PROTEIN 1).//0.99:54:37//HOMO SAPIENS
(HUMAN).//P25800

20 F-NT2RP1001177//HISTONE MACRO-H2A.1.//1.6e-29:85:76//RATTUS NORVEGICUS (RAT)
.//Q02874

25 F-NT2RP1001185

F-NT2RP1001199//NEUROTOXIN I.//1.0:23:47//CENTRUROIDES SCULPTURATUS (BARK
SCORPION).//P01491

30 F-NT2RP1001247//TRANSFORMING GROWTH FACTOR BETA 4 PRECURSOR (TGF-BETA
4) (ENDOMETRIAL BLEEDING-ASSOCIATED FACTOR).//3.3e-08:28:89//HOMO SAPIENS
(HUMAN).//O00292

35 F-NT2RP1001248//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.33:49:
28//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1).//P18804

40 F-NT2RP1001253//GLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.3.1.10)
(GLUCOSAMINE-6- PHOSPHATE DEAMINASE) (GNPDA) (OSCILLIN) (KIAA0060).//3.8e-46:
115:81//HOMO SAPIENS (HUMAN).//P46926

45 F-NT2RP1001286//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-
BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35)
(LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-34 GALACTOSIDE-BINDING LECTIN).//0.16:
48:37//MUS MUSCULUS (MOUSE).//P16110

50 F-NT2RP1001294//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//6.1e-05:92:
34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12024

55 F-NT2RP1001302//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.2e-05:92:
33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12024

F-NT2RP1001310//PROBABLE E4 PROTEIN.//0.99:109:26//HUMAN PAPILLOMAVIRUS TYPE

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5.//P06924

5 F-NT2RP1001311//SODIUM/HYDROGEN EXCHANGER 5 (NA(+)/H(+)) EXCHANGER 5) (NHE-5) (FRAGMENT).//0.99:94:31//HOMO SAPIENS (HUMAN).//Q14940

10 F-NT2RP1001313//CYTOCHROME B5.//9.0e-13:92:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40312

15 F-NT2RP1001361//NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-B14.5B) (CI-B14.5B).//1.2e-47:117:74//BOS TAURUS (BOVINE).//Q02827

20 F-NT2RP1001385//CELL DIVISION PROTEIN FTSN.//0.64:107:28//ESCHERICHIA COLI.//P29131

25 F-NT2RP1001395//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (FRAGMENTS).//0.25:35:45//GALLUS GALLUS (CHICKEN).//P02467

30 F-NT2RP1001410//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//2.2e-41:129:67//CAENORHABDITIS ELEGANS.//P91917

35 F-NT2RP1001424//UREASE ACCESSORY PROTEIN UREF (FRAGMENT).//0.87:24:45//ESCHERICHIA COLI.//Q03286

40 F-NT2RP1001432//CYSTEINE PROTEINASE INHIBITOR B (CYSTATIN B) (SCB).//1.0:35:42//HELIANTHUS ANNUUS (COMMON SUNFLOWER).//Q10993

45 F-NT2RP1001449//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//0.053:37:37//OVIS ARIES (SHEEP).//P26372

50 F-NT2RP1001457//HYPOTHETICAL 57.0 KD TRP-ASP REPEATS CONTAINING PROTEIN IN CPR4-SSK22 INTERGENIC REGION.//2.9e-16:159:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25382

55 F-NT2RP1001466//HYPOTHETICAL PROTEIN MJ0284.//5.3e-15:162:35//METHANOCOCCUS JANNASCHII.//Q57732

F-NT2RP1001475//HYPOTHETICAL 195.1 KD PROTEIN IN DNA43-UBI1 INTERGENIC REGION.//0.69:119:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40457

F-NT2RP1001482//PROTEASOME COMPONENT C9 (EC 3.4.99.46) (MACROPAIN SUBUNIT C9) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C9).//1.0:58:32//HOMO SAPIENS (HUMAN).//P25789

F-NT2RP1001494//MALE STERILITY PROTEIN 2.//2.4e-12:84:42//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q08891

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- 5 F-NT2RP1001543//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//6.3e-37:94:52//SPIRODELA POLYRRHIZA.//P42803
- 10 F-NT2RP1001546//LEUKOCYTE SURFACE ANTIGEN CD53 (CELL SURFACE GLYCOPROTEIN CD53).//9.3e-11:98:29//HOMO SAPIENS (HUMAN).//P19397
- 15 F-NT2RP1001569//SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA).//2.2e-64:159:84//MUS MUSCULUS (MOUSE).//P47758
- F-NT2RP1001616//HYPOTHETICAL 13.5 KD PROTEIN C45G9.7 IN CHROMOSOME III.//9.2e-05:49:42//CAENORHABDITIS ELEGANS.//Q09506
- F-NT2RP1001665//REGB PROTEIN.//0.99:29:37//PSEUDOMONAS AERUGINOSA.//Q03381
- 20 F-NT2RP2000001//SMALL PROLINE-RICH PROTEIN 2-1.//0.64:36:41//HOMO SAPIENS (HUMAN).//P35326
- 25 F-NT2RP2000006//DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40).//1.7e-19:74:52//HOMO SAPIENS (HUMAN).//P25685
- F-NT2RP2000007//TROPOMYOSIN, FIBROBLAST AND EPITHELIAL MUSCLE-TYPE (TM36) (TME1) (TM1).//0.93:126:23//HOMO SAPIENS (HUMAN).//P06468
- 30 F-NT2RP2000008//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946) (FRAGMENT).//4.2e-35:156:54//HOMO SAPIENS (HUMAN).//Q06730
- 35 F-NT2RP2000027//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.95:41:39//MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MONKEY).//P50665
- 40 F-NT2RP2000032//BAX PROTEIN, CYTOPLASMIC ISOFORM GAMMA.//1.0:35:34//HOMO SAPIENS (HUMAN).//Q07815
- 45 F-NT2RP2000040//BASIC PROLINE-RICH PEPTIDE IB-1.//0.0024:58:36//HOMO SAPIENS (HUMAN).//P04281
- 50 F-NT2RP2000045//DNAJ PROTEIN.//1.1e-12:42:66//THERMUS AQUATICUS (SUBSP. THERMOPHILUS).//Q56237
- F-NT2RP2000054//GONADOLIBERIN III PRECURSOR (GONADOTROPIN-RELEASING HORMONE III) (GNRH-III) (LH-RH III) (LULIBERIN III).//0.20:46:36//ONCORHYNCHUS MASOU (CHERRY SALMON) (MASU SALMON).//P30973
- 55 F-NT2RP2000056//PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3.48) (R-PTP- EPSILON).//1.3e-18:45:100//MUS MUSCULUS (MOUSE).//P49446

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F-NT2RP2000067//HOMEBOX PROTEIN HOX-A5 (S12-B) (FRAGMENT).//0.71:44:
 40//SALMO SALAR (ATLANTIC SALMON).//P09637
 5
 F-NT2RP2000070//INSULIN.//0.94:30:43//HYSTRIX CRISTATA (CRESTED PORCUPINE)
 .//P01328
 10 F-NT2RP2000076//ETS-LIKE PROTEIN POINTED P1 (D-ETS-2).//0.0013:76:
 40//DROSOPHILA MELANOGASTER (FRUIT FLY).//P51022
 F-NT2RP2000077//U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (U1-C).//0.24:49:
 15 40//HOMO SAPIENS (HUMAN).//P09234
 F-NT2RP2000079//PLATELET FACTOR 4 (PF-4).//0.15:52:30//SUS SCROFA (PIG).//P30034
 20 F-NT2RP2000088//HYPOTHETICAL 13.6 KD PROTEIN IN SPT4-ROM1 INTERGENIC
 REGION.//1.0:36:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53245
 F-NT2RP2000091//HYPOTHETICAL PROTEIN HI0149 PRECURSOR.//0.22:38:
 25 47//HAEMOPHILUS INFLUENZAE.//P43953
 F-NT2RP2000097//VIRUS ATTACHMENT PROTEIN (O61R).//0.75:33:36//AFRICAN SWINE
 FEVER VIRUS (STRAIN BA71V) (ASFV).//P32510
 30 F-NT2RP2000098
 F-NT2RP2000108//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.4e-09:50:70//HOMO
 35 SAPIENS (HUMAN).//P39195
 F-NT2RP2000114//WISKOTT-ALDRICH SYNDROME PROTEIN (WASP).//0.024:52:44//HOMO
 SAPIENS (HUMAN).//P42768
 40 F-NT2RP2000120//5.8 KD PROTEIN IN HMC OPERON (ORF 4).//0.67:37:
 32//DESULFOVIBRIO VULGARIS (STRAIN HILDENBOROUGH).//P33391
 45 F-NT2RP2000126//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1).//1.5e-
 23:94:47//HOMO SAPIENS (HUMAN).//O14646
 F-NT2RP2000133//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//5.6e-10:
 50 82:39//HOMO SAPIENS (HUMAN).//Q15427
 F-NT2RP2000147//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT
 ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD
 55 SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM
 CHAIN).//6.7e-89:96:98//MUS MUSCULUS (MOUSE).//P35585

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F-NT2RP2000153//PEPTIDYLPROLYL ISOMERASE CYP-1 (EC 5.2.1.8) (PEPTIDYLPROLYL
CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE).//1.7e-05:136:33//BRUGIA
MALAYI.//Q27450

5 F-NT2RP2000157//MLO2 PROTEIN.//2.7e-06:62:40//SCHIZOSACCHAROMYCES POMBE
(FISSION YEAST).//Q09329

10 F-NT2RP2000161//DIS3 PROTEIN HOMOLOG.//2.7e-33:173:45//CAENORHABDITIS
ELEGANS.//Q17632

15 F-NT2RP2000173//HYPOTHETICAL 10.5 KD PROTEIN IN SODA-COMGA INTERGENIC
REGION.//0.99:62:25//BACILLUS SUBTILIS.//P54499

F-NT2RP2000175//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.19:41:43//DROSOPHILA
MELANOGASTER (FRUIT FLY).//Q01643

20 F-NT2RP2000183//DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (NEURAL
SPECIFIC PROTEIN NSP60).//4.1e-19:114:44//BOS TAURUS (BOVINE).//O02675

25 F-NT2RP2000195//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.99:30:33//MICROTUS
PENNSYLVANICUS (MEADOW VOLE).//P24949

30 F-NT2RP2000205//MERCURIC TRANSPORT PROTEIN PERIPLASMIC COMPONENT
PRECURSOR (PERIPLASMIC MERCURY ION BINDING PROTEIN) (MERCURY SCAVENGER
PROTEIN).//0.098:88:25//SHEWANELLA PUTREFACIENS (PSEUDOMONAS PUTREFACIENS)
.//Q54463

35 F-NT2RP2000208//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.020:19:
57//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645

40 F-NT2RP2000224//PUTATIVE CUTICLE COLLAGEN C09G5.4.//0.0058:159:
32//CAENORHABDITIS ELEGANS.//Q09455

F-NT2RP2000232//P55-C-FOS PROTO-ONCOGENE PROTEIN (FRAGMENT).//1.0:44:
38//OVIS ARIES (SHEEP).//O02761

45 F-NT2RP2000233//GASTRIN/CHOLECYSTOKININ TYPE B RECEPTOR (CCK-B RECEPTOR)
(CCK-BR).//0.34:53:43//CANIS FAMILIARIS (DOG).//P30552

50 F-NT2RP2000239//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25)
(FRAGMENT).//0.019:69:33//RATTUS NORVEGICUS (RAT).//P10164

55 F-NT2RP2000248//OVOMUCOID (FRAGMENT).//0.88:18:55//POLYPLECTRON EMPHANUM
(PALAWAN PEACOCK-PHEASANT).//P52250

F-NT2RP2000257//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//6.4e-09:83:

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37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40556

5 F-NT2RP2000258//MYOSIN II HEAVY CHAIN, NON MUSCLE.//0.081:217:
28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P08799

10 F-NT2RP2000270//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.4e-17:80:57//HOMO
SAPIENS (HUMAN).//P39188

F-NT2RP2000274//HYPOTHETICAL 5.8 KD PROTEIN.//0.082:22:45//CLOVER YELLOW
MOSAIC VIRUS (CYMV).//P16485

15 F-NT2RP2000283//HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III.//0.39:
38:34//CAENORHABDITIS ELEGANS.//P34535

20 F-NT2RP2000288

F-NT2RP2000289//HYPOTHETICAL 9.4 KD PROTEIN IN RNPA-THDF INTERGENIC
REGION.//0.40:38:42//ESCHERICHIA COLI.//P22847

25 F-NT2RP2000297//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1)
.//2.3e-62:206:47//HOMO SAPIENS (HUMAN).//Q03923

30 F-NT2RP2000298//CUTICLE COLLAGEN 12 PRECURSOR.//0.55:81:40//CAENORHABDITIS
ELEGANS.//P20630

F-NT2RP2000310//RUBREDOXIN (RD).//0.13:43:41//TREPONEMA PALLIDUM.//O83956

35 F-NT2RP2000327//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:46:30//GADUS
MORHUA (ATLANTIC COD).//P15996

40 F-NT2RP2000328//HYPOTHETICAL 86.6 KD PROTEIN IN PFK1-TDS4 INTERGENIC
REGION.//2.0e-21:198:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53313

45 F-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10)
(AK3).//1.8e-91:155:92//BOS TAURUS (BOVINE).//P08760

F-NT2RP2000337//PROTEIN A54.//0.75:48:35//VACCINIA VIRUS (STRAIN WR), AND
VACCINIA VIRUS (STRAIN COPENHAGEN).//P21072

50 F-NT2RP2000346//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN
MYD116.//9.7e-13:114:42//MUS MUSCULUS (MOUSE).//P17564

55 F-NT2RP2000369//CALTRIN (CALCIUM TRANSPORT INHIBITOR).//0.98:47:34//MUS
MUSCULUS (MOUSE).//Q09098

F-NT2RP2000412//SHORT NEUROTOXIN D PRECURSOR.//0.66:57:36//AIPYSURUS LAEVIS

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(OLIVE SEA SNAKE)//P19960

- 5 F-NT2RP2000414//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F)
./1.0e-27:96:67//HOMO SAPIENS (HUMAN)//P52597
- 10 F-NT2RP2000420//ZINC FINGER PROTEIN 191./0.16:47:38//HOMO SAPIENS (HUMAN)
./O14754
- 15 F-NT2RP2000422//PUTATIVE PHOSPHOACETYLGLUCOSAMINE MUTASE (EC 5.4.2.3)
(ACETYLGLUCOSAMINE PHOSPHOMUTASE) (N-ACETYLGLUCOSAMINE-PHOSPHATE
MUTASE)./3.6e-19:148:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09687
- 20 F-NT2RP2000438//TUBULIN GAMMA CHAIN./0.86:190:27//RETICULOMYXA
FILOSA//P54405
- 25 F-NT2RP2000448//OXYSTEROL-BINDING PROTEIN./3.7e-13:140:42//HOMO SAPIENS
(HUMAN)//P22059
- 30 F-NT2RP2000459//NEURONAL PROTEIN 3.1 (P311 PROTEIN)./1.0:45:35//HOMO SAPIENS
(HUMAN)//Q16612
- 35 F-NT2RP2000498//!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/0.062:25:68//HOMO
SAPIENS (HUMAN)//P39194
- 40 F-NT2RP2000503
- 45 F-NT2RP2000510//TOXIN IV-5./1.0:51:33//TITYUS BAHIIENSIS (BRAZILIAN SCORPION)
./P56608
- 50 F-NT2RP2000516//SLYX PROTEIN./1.0:52:32//ESCHERICHIA COLI//P30857
- 55 F-NT2RP2000523//PHORBOLIN I (FRAGMENTS)./1.4e-06:36:47//HOMO-SAPIENS (HUMAN)
./P31941
- 60 F-NT2RP2000603//ALPHA/BETA-GLIADIN PRECURSOR (PROLAMIN) (CLASS A-III)./0.93:
119:26//TRITICUM AESTIVUM (WHEAT)//P04723
- 65 F-NT2RP2000617//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE)./0.056:16:
62//OVIS ARIES (SHEEP), AND CAPRA HIRCUS (GOAT)//P04102
- 70 F-NT2RP2000634//NEDD-4 PROTEIN (EC 6.3.2.-) (KIAA0093) (FRAGMENT)./1.8e-05:128:
28//HOMO SAPIENS (HUMAN)//P46934
- 75 F-NT2RP2000644//HYPOTHETICAL PROTEIN HI1566 PRECURSOR./0.85:48:
39//HAEMOPHILUS INFLUENZAE//P44257

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- F-NT2RP2000656//EARLY GROWTH RESPONSE PROTEIN 1 (EGR-1) (NERVE GROWTH FACTOR-INDUCED PROTEIN A) (NGFI-A)//1.0:111:24//RATTUS NORVEGICUS (RAT) //P08154
- 5 F-NT2RP2000658//URONATE ISOMERASE (EC 5.3.1.12) (GLUCURONATE ISOMERASE) (URONIC ISOMERASE)//0.49:79:31//ESCHERICHIA COLI//P42607
- 10 F-NT2RP2000668//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2) (45 KD MEROZOITE SURFACE ANTIGEN)//0.020:115:30//PLASMODIUM FALCIPARUM (ISOLATE 3D7)//P50498
- 15 F-NT2RP2000678//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.00085:38:68//HOMO SAPIENS (HUMAN)//P39188
- 20 F-NT2RP2000704//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.2e-17:55:74//HOMO SAPIENS (HUMAN)//P39188
- F-NT2RP2000710//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS)//8.9e-47:106:59//TREPONEMA PALLIDUM//O83950
- 25 F-NT2RP2000715
- F-NT2RP2000731//CONIDIATION-SPECIFIC PROTEIN 10//0.094:31:41//NEUROSPORA CRASSA//P10713
- 30 F-NT2RP2000758//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.00027:31:74//HOMO SAPIENS (HUMAN)//P39188
- 35 F-NT2RP2000764//NIFS PROTEIN//2.7e-27:175:47//ANABAENA SP. (STRAIN PCC 7120) //P12623
- 40 F-NT2RP2000809//HYPOTHETICAL PROTEIN MG381 HOMOLOG//0.91:85:25//MYCOPLASMA PNEUMONIAE//P75219
- F-NT2RP2000812//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A)//2.8e-07:133:31//MUS MUSCULUS (MOUSE)//Q99104
- 45 F-NT2RP2000814//40S RIBOSOMAL PROTEIN S27A//0.93:44:38//LYCOPERSICON ESCULENTUM (TOMATO), AND SOLANUM TUBEROSUM (POTATO)//P27083
- 50 F-NT2RP2000816//HYPOTHETICAL 88.4 KD PROTEIN B0464.7 IN CHROMOSOME III//3.3e-21:123:39//CAENORHABDITIS ELEGANS//Q03565
- 55 F-NT2RP2000819//TROPOMYOSIN 5, CYTOSKELETAL TYPE//1.0:71:30//MUS MUSCULUS (MOUSE)//P21107

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- F-NT2RP2000841//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//0.0011:133:26//MUS MUSCULUS (MOUSE).//P27671
- 5 F-NT2RP2000842//LYSOPHOSPHATIDIC ACID RECEPTOR (EDG-2).//6.4e-13:22:95//HOMO SAPIENS (HUMAN).//Q92633
- 10 F-NT2RP2000845//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR (MSTI).//0.92:24:41//MEDICAGO SCUTELLATA (SNAIL MEDIC).//P80321
- 15 F-NT2RP2000863//N-MYC PROTO-ONCOGENE PROTEIN.//0.010:148:27//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P24793
- F-NT2RP2000880//PROBABLE TRANSLATION INITIATION FACTOR IF-2.//4.0e-100:199:94//HOMO SAPIENS (HUMAN).//O60841
- 20 F-NT2RP2000892//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN].//0.43:45:44//MUS MUSCULUS (MOUSE).//P28481
- 25 F-NT2RP2000931//MATRIN 3.//2.8e-46:104:92//RATTUS NORVEGICUS (RAT).//P43244
- F-NT2RP2000932//2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDENT RNAASE) (RNASE L) (RIBONUCLEASE 4) (FRAGMENT).//3.9e-07:113:31//MUS MUSCULUS (MOUSE).//Q05921
- 30 F-NT2RP2000938//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID).//0.026:59:45//RATTUS NORVEGICUS (RAT).//Q01956
- 35 F-NT2RP2000943//HYPOTHETICAL PROTEIN KIAA0079 (HA3543).//5.9e-18:161:42//HOMO SAPIENS (HUMAN).//P53992
- 40 F-NT2RP2000965//INNER CENTROMERE PROTEIN (INCENP).//0.062:156:25//GALLUS GALLUS (CHICKEN).//P53352
- 45 F-NT2RP2000970//EC PROTEIN HOMOLOG.//1.0:50:30//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P93746
- F-NT2RP2000985//HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC REGION.//2.5e-06:53:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36159
- 50 F-NT2RP2000987//INSECT TOXIN 4 (INSECT TOXIN AAH IT4).//1.0:32:34//ANDROCTONUS AUSTRALIS HECTOR (SAHARA SCORPION).//P21150
- 55 F-NT2RP2001036//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.2e-33:65:81//HOMO SAPIENS (HUMAN).//P39193
- F-NT2RP2001044//HIRUSTASIN.//0.97:15:66//HIRUDO MEDICINALIS (MEDICINAL LEECH)

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//P80302

5 F-NT2RP2001056//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.0e-24:85:65//HOMO SAPIENS (HUMAN)//P39194

10 F-NT2RP2001065//BOWMAN-BIRK TYPE SEED TRYPSIN AND CHYMOTRYPSIN INHIBITOR (BTCI)//0.41:50:32//VIGNA UNGUICULATA (COWPEA)//P17734

F-NT2RP2001070//PROBABLE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMP OXIDASE) (FPRA PROTEIN)//6.2e-18:64:48//MYXOCOCCUS XANTHUS//P21159

15 F-NT2RP2001081//SYNAPTOTAGMIN IV//7.8e-16:94:46//RATTUS NORVEGICUS (RAT) //P50232

20 F-NT2RP2001094//METALLOTHIONEIN-I (MT-I)//1.0:24:33//RATTUS NORVEGICUS (RAT) //P02803

25 F-NT2RP2001119//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/7.5e-11:61:63//HOMO SAPIENS (HUMAN)//P39195

F-NT2RP2001127//XE169 PROTEIN (SMCX PROTEIN) (FRAGMENTS)//1.0e-47:155:58//MUS MUSCULUS (MOUSE)//P41230

30 F-NT2RP2001137//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS)//0.10:68:39//BOS TAURUS (BOVINE)//P25508

35 F-NT2RP2001149//!!!! ALU SUBFAMILY J WARNING ENTRY!!!!/1.1e-13:81:59//HOMO SAPIENS (HUMAN)//P39188

40 F-NT2RP2001168//PROTEIN KINASE C SUBSTRATE 80 KD PROTEIN (FRAGMENTS) //0.0071:77:33//RATTUS NORVEGICUS (RAT)//P20468

F-NT2RP2001173//CYTOSKELETON-ASSOCIATED PROTEIN CKAPI (TUBULIN FOLDING COFACTOR B)//1.0:36:41//HOMO SAPIENS (HUMAN)//Q99426

45 F-NT2RP2001174//ZINC FINGER PROTEIN 137//7.2e-11:65:43//HOMO SAPIENS (HUMAN) //P52743

50 F-NT2RP2001196//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3)//1.0:95: 26//CAPRA HIRCUS (GOAT)//Q36346

55 F-NT2RP2001218//HYPOTHETICAL 59.2 KD PROTEIN IN MOB1-SGA1 INTERGENIC REGION//0.00024:80:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40486

F-NT2RP2001226//RABPHILIN-3A (FRAGMENT)//4.6e-05:121:39//MUS MUSCULUS (MOUSE)//P47708

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- 5 F-NT2RP2001233//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//3.2e-61:153:56//HOMO SAPIENS (HUMAN).//P16415
- 10 F-NT2RP2001245//SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN).//4.9e-05:230:21//HOMO SAPIENS (HUMAN).//Q15431
- 15 F-NT2RP2001268//HOMEBOX PROTEIN CEH-32.//0.23:159:25//CAENORHABDITIS ELEGANS.//Q23175
- 20 F-NT2RP2001277
- F-NT2RP2001290//BETA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-BETA) (SNAP-ALPHA HOMOLOG) (BRAIN PROTEIN I47) (FRAGMENT).//1.0e-86:131:97//MUS MUSCULUS (MOUSE).//P28663
- 25 F-NT2RP2001295
- F-NT2RP2001312//N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLUCOSAMINE-6-SULFATASE).//0.64:80:33//CAPRA HIRCUS (GOAT).//P50426
- 30 F-NT2RP2001327//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//1.0e-36:118:65//HOMO SAPIENS (HUMAN).//Q13829
- 35 F-NT2RP2001328//PROBABLE E5 PROTEIN.//1.0:46:41//HUMAN PAPILLOMAVIRUS TYPE 33.//P06426
- 40 F-NT2RP2001347//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//4.5e-19:66:62//HOMO SAPIENS (HUMAN).//P39193
- F-NT2RP2001366//SPERM-SPECIFIC PROTEIN PHI-1.//0.66:55:32//MYTILUS EDULIS (BLUE MUSSEL).//Q04621
- 45 F-NT2RP2001378//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHI1D) (FRAGMENT).//0.060:78:33//HOMO SAPIENS (HUMAN).//Q14003
- 50 F-NT2RP2001381//26S PROTEASE REGULATORY SUBUNIT 8 (SUG1 HOMOLOG) (XSUG1).//1.0:167:26//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P46470
- 55 F-NT2RP2001392//KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIA3.//0.0080:82:32//OVIS ARIES (SHEEP).//P02441
- F-NT2RP2001394//POLYHOMEOTIC-PROXIMAL CHROMATIN PROTEIN.//0.024:39:53//DROSOPHILA MELANOGASTER (FRUIT FLY).//P39769
- F-NT2RP2001397//G2/MITOTIC-SPECIFIC CYCLIN B2.//1.4e-46:125:78//MESOCRICETUS

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AURATUS (GOLDEN HAMSTER).//P37883

5 F-NT2RP2001420//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4
AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//0.00018:113:38//HOMO
SAPIENS (HUMAN).//P04280

10 F-NT2RP2001423//HYPOTHETICAL 9.4 KD PROTEIN IN GP31-CD INTERGENIC REGION
(ORF A).//0.90:23:43//BACTERIOPHAGE T4.//P17307

15 F-NT2RP2001427//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.2e-11:38:68//HOMO
SAPIENS (HUMAN).//P39188

F-NT2RP2001436//DYNEIN LIGHT INTERMEDIATE CHAIN 2, CYTOSOLIC (LIC53/55) (LIC-2)
//0.25:124:28//RATTUS NORVEGICUS (RAT).//Q62698

20 F-NT2RP2001440//14-3-3 PROTEIN GAMMA (PROTEIN KINASE C INHIBITOR PROTEIN-1)
(KCIP-1).//4.8e-62:145:90//RATTUS NORVEGICUS (RAT).//P35214

25 F-NT2RP2001445

F-NT2RP2001449//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD
SUBUNIT (CPSF 100 KD SUBUNIT).//9.5e-118:226:95//BOS TAURUS (BOVINE).//Q10568

30 F-NT2RP2001450

F-NT2RP2001467//SHORT NEUROTOXIN 1 (TOXIN V-II-1).//1.0:25:40//BUNGARUS
FASCIATUS (BANDED KRAIT).//P10808

35 F-NT2RP2001506

40 F-NT2RP2001511//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME
III.//0.49:124:29//CAENORHABDITIS ELEGANS.//P34681

F-NT2RP2001520//VITAMIN D-DEPENDENT CALCIUM-BINDING PROTEIN, INTESTINAL
(CABP) (CALBINDIN D9K).//0.035:71:33//HOMO SAPIENS (HUMAN).//P29377

45 F-NT2RP2001526

50 F-NT2RP2001536//METALLOTHIONEIN-I (MT-1).//1.0:19:42//COLUMBA LIVIA (DOMESTIC
PIGEON).//P15786

F-NT2RP2001560//CUTICLE COLLAGEN 12 PRECURSOR.//0.0018:144:
35//CAENORHABDITIS ELEGANS.//P20630

55 F-NT2RP2001569//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.7e-31:102:67//HOMO
SAPIENS (HUMAN).//P39194

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5 F-NT2RP2001576//SMP3 PROTEIN.//0.00016:75:36//SACCHAROMYCES CEREVISIAE
 (BAKER'S YEAST).//Q04174
 F-NT2RP2001581//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//0.040:46:36//HOMO
 SAPIENS (HUMAN).//P51805
 10 F-NT2RP2001597//PROBABLE E4 PROTEIN.//0.00042:113:34//HUMAN PAPILLOMAVIRUS
 TYPE 5.//P06924
 F-NT2RP2001601
 15 F-NT2RP2001613//HOMEBOX PROTEIN SAX-1 (CHOX-3) (FRAGMENT).//0.14:59:
 32//GALLUS GALLUS (CHICKEN).//P19601
 20 F-NT2RP2001628//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.056:140:
 33//SACCHAROMYCES CEREVISIAE (BAKER'S
 YEAST).//P32323
 25 F-NT2RP2001634//ALPHA-CATENIN.//7.1e-12:152:35//DROSOPHILA MELANOGASTER
 (FRUIT FLY).//P35220
 30 F-NT2RP2001660//HYPOTHETICAL 80.4 KD PROTEIN IN SMC3-MRPL8 INTERGENIC
 REGION.//0.43:119:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40358
 35 F-NT2RP2001663//ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-
 LYASE) (NON- NEURAL ENOLASE) (NNE) (PHOSPHOPYRUVATE HYDRATASE).//1.2e-26:
 126:56//HOMO SAPIENS (HUMAN).//P06733
 40 F-NT2RP2001675//HYPOTHETICAL 107.7 KD PROTEIN IN RPSO 5'REGION (ORF1).//0.25:
 148:25//CAMPYLOBACTER JEJUNI.//Q46089
 F-NT2RP2001677//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25)
 (FRAGMENT).//0.010:101:31//RATTUS NORVEGICUS (RAT).//P10164
 45 F-NT2RP2001678//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.6e-18:83:61//HOMO
 SAPIENS (HUMAN).//P39188
 50 F-NT2RP2001699//PROTEIN C14.//0:98:51:31//VACCINIA VIRUS (STRAIN COPENHAGEN)
 .//P21045
 55 F-NT2RP2001720//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2) (ALLELIC
 FORM 1).//0.16:145:30//PLASMODIUM FALCIPARUM (ISOLATE CAMP / MALAYSIA).//Q99317
 F-NT2RP2001721//MALE-SPECIFIC LETHAL-2 PROTEIN.//0.00090:48:39//DROSOPHILA

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MELANOGASTER (FRUIT FLY).//P50534

5 F-NT2RP2001740//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.50:43:25//BOS TAURUS
(BOVINE).//P20072

10 F-NT2RP2001748//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS:
PEPTIDE P-D] (FRAGMENT).//0.77:111:28//HOMO SAPIENS (HUMAN).//P10162

F-NT2RP2001762

15 F-NT2RP2001813//PHOTOSYSTEM I REACTION CENTRE SUBUNIT VIII (PSI-I).//1.0:22:
40//PICEA ABIES (NORWAY SPRUCE) (PICEA EXCELSA).//O47040

20 F-NT2RP2001839//SCY1 PROTEIN.//6.8e-17:204:27//SACCHAROMYCES CEREVISIAE
(BAKER'S YEAST).//P53009

F-NT2RP2001861//D15KZ1 PROTEIN (FRAGMENT).//0.31:56:39//MUS MUSCULUS (MOUSE)
./Q61466

25 F-NT2RP2001869//CORNEODESMOSIN (S PROTEIN) (FRAGMENT).//0.97:78:30//SUS
SCROFA (PIG).//O19084

30 F-NT2RP2001876//ALLOGRAFT INFLAMMATORY FACTOR-1 (AIF-1) (IONIZED CALCIUM
BINDING ADAPTER MOLECULE 1).//3.5e-36:106:66//HOMO SAPIENS (HUMAN).//P55008

35 F-NT2RP2001883//CATHEPSIN L (EC 3.4.22.15).//0.95:29:41//OVIS ARIES (SHEEP)
./Q10991

40 F-NT2RP2001898//TYPE II INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE
PRECURSOR (EC 3.1.3.56) (5PTASE) (FRAGMENT).//1.6e-84:185:88//HOMO SAPIENS
(HUMAN).//P32019

F-NT2RP2001900//ACTIN-LIKE PROTEIN ARP5.//1.1e-17:180:34//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST).//P53946

45 F-NT2RP2001907//HYPHAL WALL PROTEIN 1 (CELL ELONGATION PROTEIN 2).//0.13:108:
27//CANDIDA ALBICANS (YEAST).//P46593

50 F-NT2RP2001926//HYPOTHETICAL 7.6 KD PROTEIN YCF33.//0.55:57:26//CYANOPHORA
PARADOXA.//P48273

F-NT2RP2001936

55 F-NT2RP2001943//HYPOTHETICAL 57.7 KD PROTEIN IN AIP1-CTF13 INTERGENIC
REGION.//1.8e-13:208:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04305

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F-NT2RP2001946//HYPOTHETICAL 13.0 KD PROTEIN IN ALGR3 3'REGION.//0.59:76:28//PSEUDOMONAS AERUGINOSA.//P21485

5 F-NT2RP2001947//ZINC FINGER PROTEIN DAN (N03).//0.53:68:29//RATTUS NORVEGICUS (RAT).//Q06880

10 F-NT2RP2001969//CHLOROPLAST 30S RIBOSOMAL PROTEIN S18.//0.0015:52:34//CHLORELLA VULGARIS.//P56353

15 F-NT2RP2001976//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A).//9.5e-07:201:22//MUS MUSCULUS (MOUSE).//Q99104

F-NT2RP2001985//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.016:90:32//MUS MUSCULUS (MOUSE).//P05142

20 F-NT2RP2001991//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//8.0e-14:47:76//RATTUS NORVEGICUS (RAT).//Q08469

25 F-NT2RP2002025//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//2.9e-30:211:42//GALLUS GALLUS (CHICKEN).//P35331

30 F-NT2RP2002032//FLOCCULANT-ACTIVE PROTEINS MO2.1 AND MO2.2.//0.23:20:40//MORINGA OLEIFERA (HORSERADISH TREE) (MORINGA PTERYGOSPERMA).//P24303

F-NT2RP2002033//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//0.88:27:62//HOMO SAPIENS (HUMAN).//P39193

35 F-NT2RP2002041

40 F-NT2RP2002046//MATING PROCESS PROTEIN MID2 (SERINE-RICH PROTEIN SMS1) (PROTEIN KINASE A INTERFERENCE PROTEIN).//1.0:85:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36027

F-NT2RP2002047

45 F-NT2RP2002058//DOM34 INTERACTING PROTEIN 2.//9.4e-25:165:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12220

50 F-NT2RP2002066//TIGHT JUNCTION PROTEIN ZO-1 (TIGHT JUNCTION PROTEIN 1).//5.7e-12:108:41//HOMO SAPIENS (HUMAN).//Q07157

55 F-NT2RP2002070//CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) (FRAGMENT).//0.88:28:50//ASTERINA PECTINIFERA (STARFISH).//P11958

F-NT2RP2002076//TRP-ASP REPEATS CONTAINING PROTEIN RBA-2.//0.0031:124:27//CAENORHABDITIS ELEGANS.//P90916

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- 5 F-NT2RP2002078//KERATIN, GLYCINE/TYROSINE-RICH OF HAIR.//0.82:30:40//OVIS ARIES (SHEEP).//Q02958
- 10 F-NT2RP2002079//OUTER DENSE FIBER PROTEIN.//0.34:41:39//HOMO SAPIENS (HUMAN).//Q14990
- 15 F-NT2RP2002099//HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U).//5.2e-08:81:48//HOMO SAPIENS (HUMAN).//Q00839
- 20 F-NT2RP2002105//COLLAGEN 1(X) CHAIN PRECURSOR.//0.0012:100:34//BOS TAURUS (BOVINE).//P23206
- 25 F-NT2RP2002124//EARLY GROWTH RESPONSE PROTEIN 1 (EGR-1) (KROX24) (TRANSCRIPTION FACTOR ETR103) (ZINC FINGER PROTEIN 225) (AT225).//0.74:72:31//HOMO SAPIENS (HUMAN).//P18146
- 30 F-NT2RP2002137//NEUROTOXIN B-II.//1.0:27:44//CEREBRATULUS LACTEUS (MILKY RIBBON WORM).//P01526
- 35 F-NT2RP2002154//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-34 GALACTOSIDE-BINDING LECTIN).//0.0029:112:34//MUS MUSCULUS (MOUSE).//P16110
- 40 F-NT2RP2002172
- 45 F-NT2RP2002185//UBIQUITIN-LIKE PROTEIN DSK2.//1.8e-07:87:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48510
- 50 F-NT2RP2002192
- 55 F-NT2RP2002193//CUTICLE COLLAGEN 40.//0.0062:70:37//CAENORHABDITIS ELEGANS.//P34804
- 60 F-NT2RP2002208//PEROXISOME ASSEMBLY PROTEIN PEX10 (PEROXIN-10).//0.00011:45:40//HOMO SAPIENS (HUMAN).//060683
- 65 F-NT2RP2002219
- 70 F-NT2RP2002231//V-TYPE SODIUM ATP SYNTHASE SUBUNIT E (EC 3.6.1.34) (NA(+)-TRANSLOCATING ATPASE SUBUNIT E).//1.0:68:32//ENTEROCOCCUS HIRAE.//P43436
- 75 F-NT2RP2002235//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACTOR ICP34.5).//0.0022:66:45//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN CVG-2).//P37318

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F-NT2RP2002252//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).//0.071:110:31//CRICETULUS GRISEUS (CHINESE HAMSTER) //P11414

5

F-NT2RP2002256//CYTOCHROME P450 26 (EC 1.14.-.-) (RETINOIC ACID-METABOLIZING CYTOCHROME) (P450RAI) (RETINOIC ACID 4-HYDROXYLASE).//3.1e-31:75:84//MUS MUSCULUS (MOUSE).//O55127

10

F-NT2RP2002259//L-MYC-1 PROTO-ONCOGENE PROTEIN.//1.9e-17:41:90//HOMO SAPIENS (HUMAN).//P12524

15

F-NT2RP2002270//HYPOTHETICAL 26.0 KD PROTEIN IN CYB5-LEU4 INTERGENIC REGION.//2.1e-27:164:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53930

20

F-NT2RP2002292//IMMEDIATE-EARLY PROTEIN RSP40.//0.018:107:23//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P24827

25

F-NT2RP2002312//PHOSPHATIDATE CYTIDYLYLTRANSFERASE (EC 2.7.7.41) (CDP-DIGLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE).//1.4e-52:174:55//HOMO SAPIENS (HUMAN).//Q92903

30

F-NT2RP2002316//HISTONE H1.C6/H1.C9.//1.0:40:40//TRYPANOSOMA CRUZI.//P40269

F-NT2RP2002325//PEROXISOMAL MEMBRANE PROTEIN PMP30A (PMP31) (PEROXIN 11A) .//2.2e-06:145:26//CANDIDA BOIDINII (YEAST).//Q00316

35

F-NT2RP2002333//HYPOTHETICAL 39.1 KD PROTEIN IN RNPB-SOHA INTERGENIC REGION (ORF 3).//0.30:86:32//ESCHERICHIA COLI.//P23524

40

F-NT2RP2002373//SYNAPSINS IA AND IB.//0.080:145:31//BOS TAURUS (BOVINE).//P17599

45

F-NT2RP2002385//ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: KNOB PROTEIN GP70; SPIKE PROTEIN P15E; R PROTEIN].//0.021:66:28//MINK CELL FOCUS-FORMING MURINE LEUKEMIA VIRUS (ISOLATE CI-3).//P03388

F-NT2RP2002394

50

F-NT2RP2002408//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.00030:107:37//BOS TAURUS (BOVINE).//P02453

F-NT2RP2002426

55

F-NT2RP2002439//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//0.00032:79:32//PLASMODIUM BERGHEI (STRAIN ANKA).//P23093

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F-NT2RP2002442//HESA PROTEIN //6.0e-16:163:30//PLECTONEMA BORYANUM.//P46037

F-NT2RP2002457

5

F-NT2RP2002464//HYPOTHETICAL 60.7 KD PROTEIN C56F8.17C IN CHROMOSOME
I.//9.3e-18:165:32//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10264

10

F-NT2RP2002475//CYSTEINE-RICH HEART PROTEIN (HCRHP).//0.91:45:35//HOMO
SAPIENS (HUMAN).//P50238

15

F-NT2RP2002479//ATP-BINDING CASSETTE TRANSPORTER 7 PRECURSOR (ABC
TRANSPORTER 7 PROTEIN).//6.8e-96:186:94//HOMO SAPIENS (HUMAN).//O75027

20

F-NT2RP2002498//HYPOTHETICAL MERCURIC RESISTANCE PROTEIN MERC.//0.65:37:
45//PSEUDOMONAS AERUGINOSA.//P04139

25

F-NT2RP2002504//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN
NUP155) (155 KD NUCLEOPORIN) (P140).//1.2e-123:240:92//RATTUS NORVEGICUS (RAT)
.//P37199

30

F-NT2RP2002520//ACIDIC PROLINE-RICH PROTEIN HP43A PRECURSOR.//0.94:83:
28//MESOCRICETUS AURATUS (GOLDEN HAMSTER).//P06680

35

F-NT2RP2002537//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//4.0e-
10:194:23//CAENORHABDITIS ELEGANS.//Q11073

F-NT2RP2002546

40

F-NT2RP2002549//G2/MITOTIC-SPECIFIC CYCLIN C13-1 (A-LIKE CYCLIN) (FRAGMENT)
.//0.98:65:30//DAUCUS CAROTA (CARROT).//P25010

45

F-NT2RP2002591//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.6e-19:60:
61//HOMO SAPIENS (HUMAN).//P51523

50

F-NT2RP2002595//ANNEXIN VII (SYNEXIN).//1.2e-15:121:49//XENOPUS LAEVIS (AFRICAN
CLAWED FROG).//Q92125

55

F-NT2RP2002606//PROTEIN TRANSPORT PROTEIN SEC2.//0.00034:98:
31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P17065

F-NT2RP2002609//HYPOTHETICAL 52.0 KD PROTEIN IN CLB6-SPT6 INTERGENIC
REGION.//0.00022:79:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53264

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F-NT2RP2002618//PROTEIN ARGININE N-METHYLTRANSFERASE 1 (EC 2.1.1.-)//6.2e-37:
180:44//RATTUS NORVEGICUS (RAT)//Q63009

5 F-NT2RP2002621//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3)
(FRAGMENT)//0.98:37:35//LEMUR CATTAL (RING-TAILED LEMUR)//Q34879

10 F-NT2RP2002643//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACTOR
ICP34.5)//0.042:77:32//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN MGH-10)//P37319

F-NT2RP2002672//PROTEIN Q300//0.0018:41:43//MUS MUSCULUS (MOUSE)//Q02722

15 F-NT2RP2002701//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I//3.6e-
17:100:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09701

20 F-NT2RP2002706//IMMEDIATE-EARLY PROTEIN IE180//0.00027:139:33//PSEUDORABIES
VIRUS (STRAIN KAPLAN) (PRV)//P33479

25 F-NT2RP2002710//SH3-BINDING PROTEIN 3BP-1//6.9e-09:96:40//MUS MUSCULUS
(MOUSE)//P55194

F-NT2RP2002727//TUBERIN (TUBEROUS SCLEROSIS 2 HOMOLOG PROTEIN)//3.6e-20:
160:36//RATTUS NORVEGICUS (RAT)//P49816

30 F-NT2RP2002736

F-NT2RP2002740

35 F-NT2RP2002741//RHO1 GDP-GTP EXCHANGE PROTEIN 2//2.0e-07:178:
28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P51862

40 F-NT2RP2002750//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//1.6e-09:43:72//HOMO
SAPIENS (HUMAN)//P39191

45 F-NT2RP2002752//LOW CALCIUM RESPONSE LOCUS PROTEIN T//0.95:33:39//YERSINIA
PSEUDOTUBERCULOSIS//Q00932

F-NT2RP2002753//ENDOGLUCANASE EG-1 PRECURSOR (EC 3.2.1.4) (ENDO-1,4-BETA-
GLUCANASE) (CELLULASE)//0.71:78:33//TRICHODERMA LONGIBRACHIATUM//Q12714

50 F-NT2RP2002769//50 KD SPICULE MATRIX PROTEIN PRECURSOR//0.44:76:
32//STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN)//P11994

55 F-NT2RP2002778

F-NT2RP2002800//CRAMBIN//0.99:20:50//CRAMBE ABYSSINICA (ABYSSINIAN CRAMBE)
//P01542

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- 5 F-NT2RP2002839//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7)
[CONTAINS: BASIC PEPTIDE P-F] (FRAGMENT)//0.010:87:31//HOMO SAPIENS (HUMAN)
//P02812
- 10 F-NT2RP2002857//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33)
//0.00018:57:45//RATTUS NORVEGICUS (RAT)//P04474
- 15 F-NT2RP2002862//HYPOTHETICAL 27.1 KD PROTEIN UFD4-CAP1 INTERGENIC
REGION//7.2e-27:140:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P33201
- 20 F-NT2RP2002880//DNA REPAIR PROTEIN RAD32//0.83:67:28//SCHIZOSACCHAROMYCES
POMBE (FISSION YEAST)//Q09683
- 25 F-NT2RP2002891//HOMEBOX PROTEIN DLX-2 (DLX-5) (FRAGMENT)//0.99:70:24//RATTUS
NORVEGICUS (RAT)//Q64204
- 30 F-NT2RP2002925//ALPHA-1D ADRENERGIC RECEPTOR (ALPHA 1D-ADRENOCEPTOR)
(ALPHA-1A ADRENERGIC RECEPTOR)//0.31:48:43//HOMO SAPIENS (HUMAN)//P25100
- 35 F-NT2RP2002928//CELL DIVISION CONTROL PROTEIN 40//2.8e-26:142:
42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40968
- 40 F-NT2RP2002929//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN
D2013.2 IN CHROMOSOME II//2.0e-31:186:35//CAENORHABDITIS ELEGANS//Q18964
- 45 F-NT2RP2002939//ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHATE-
LYASE) (CA(2+)-INHIBITABLE ADENYLYL CYCLASE)//0.0022:98:39//CANIS FAMILIARIS
(DOG)//P30803
- 50 F-NT2RP2002954//U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A')//0.0019:
107:30//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//P43333
- 55 F-NT2RP2002959//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19)
(UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2)//2.8e-11:33:
81//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT),
AND XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P51669
- 60 F-NT2RP2002979
- 65 F-NT2RP2002980//30S RIBOSOMAL PROTEIN S10//1.1e-09:98:36//MYCOPLASMA
CAPRICOLUM//P10129
- 70 F-NT2RP2002986//RING CANAL PROTEIN (KELCH PROTEIN)//1.1e-19:141:
39//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q04652

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F-NT2RP2002987!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.3e-07:78:47//HOMO SAPIENS (HUMAN).//P39192

5 F-NT2RP2002993//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT).//8.0e-77:165:85//RATTUS NORVEGICUS (RAT).//O54888

10 F-NT2RP2003000!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.8e-19:62:64//HOMO SAPIENS (HUMAN).//P39194

15 F-NT2RP2003034//HYPOTHETICAL PROTEIN HI1458.//1.0:42:35//HAEMOPHILUS INFLUENZAE.//P44204

20 F-NT2RP2003073!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/0.0051:16:87//HOMO SAPIENS (HUMAN).//P39189

F-NT2RP2003099

25 F-NT2RP2003108//BASIC PROLINE-RICH PEPTIDE IB-1.//0.84:47:34//HOMO SAPIENS (HUMAN).//P04281

F-NT2RP2003117

30 F-NT2RP2003121//HYPOTHETICAL 96.7 KD PROTEIN IN STE2-FRS2 INTERGENIC REGION.//9.0e-08:99:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43572

35 F-NT2RP2003125//TRANSCRIPTION REGULATOR PROTEIN BACH2 (BTB AND CNC HOMOLOG 2).//9.2e-08:134:28//MUS MUSCULUS (MOUSE).//P97303

F-NT2RP2003129

40 F-NT2RP2003137//UBIQUITIN.//3.4e-06:70:30//NEUROSPORA CRASSA.//P13117

45 F-NT2RP2003157//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II.//7.8e-13:84:40//CAENORHABDITIS ELEGANS.//Q09217

F-NT2RP2003158//26S PROTEASOME REGULATORY SUBUNIT S3 (PROTEASOME SUBUNIT P58).//3.1e-65:155:84//HOMO SAPIENS (HUMAN).//O43242

50 F-NT2RP2003161//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.0011:59:42//MUS MUSCULUS (MOUSE).//P05142

55 F-NT2RP2003164//ZYXIN.//0.0037:85:36//MUS MUSCULUS (MOUSE).//Q62523

F-NT2RP2003165!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.2e-24:77:64//HOMO SAPIENS (HUMAN).//P39194

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F-NT2RP2003177//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.55:38:39//DROSOPHILA
 MELANOGASTER (FRUIT FLY).//Q01643
 5
 F-NT2RP2003194//HYPOTHETICAL 12.5 KD PROTEIN ZK637.2 IN CHROMOSOME III.//2.3e-
 14:87:37//CAENORHABDITIS ELEGANS.//P30629
 10 F-NT2RP2003206//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3).//1.0:100:
 28//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH AMERICAN OPOSSUM).//P41306
 15 F-NT2RP2003228//DNA REPLICATION LICENSING FACTOR MCM4 (CDC21 HOMOLOG)
 (P1-CDC21).//9.3e-82:211:81//HOMO SAPIENS (HUMAN).//P33991
 F-NT2RP2003230//SEC14 CYTOSOLIC FACTOR
 (PHOSPHATIDYLINOSITOL/PHOSPHATIDYLCHOLINE TRANSFER PROTEIN) (PI/PC TP)
 20 .//1.0:51:31//CANDIDA GLABRATA (YEAST) (TORULOPSIS GLABRATA).//P53989
 F-NT2RP2003237//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//5.1e-44:66:84//HOMO
 SAPIENS (HUMAN).//P39194
 25 F-NT2RP2003243//M PROTEIN, SEROTYPE 5 PRECURSOR.//0.027:204:
 23//STREPTOCOCCUS PYOGENES.//P02977
 30 F-NT2RP2003265//BP4A PROTEIN.//0.95:35:34//BRASSICA NAPUS (RAPE).//P41505
 F-NT2RP2003272//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
 (FRAGMENT).//5.5e-06:78:35//BRASSICA NAPUS (RAPE).//P40603
 35 F-NT2RP2003277//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1)
 (UP-FRAMESHIFT SUPPRESSOR 1).//1.9e-19:145:43//SACCHAROMYCES CEREVISIAE
 (BAKER'S YEAST).//P30771
 40 F-NT2RP2003280
 F-NT2RP2003286//RNA 3'-TERMINAL PHOSPHATE CYCLASE (EC 6.5.1.4) (RNA-3'-
 45 PHOSPHATE CYCLASE) (RNA CYCLASE).//2.1e-32:137:42//SACCHAROMYCES CEREVISIAE
 (BAKER'S YEAST).//Q08096
 F-NT2RP2003293//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.7e-12:
 50 175:33//HOMO SAPIENS (HUMAN).//P51522
 F-NT2RP2003295//PTB-ASSOCIATED SPLICING FACTOR (PSF).//0.055:44:45//HOMO
 SAPIENS (HUMAN).//P23246
 55 F-NT2RP2003297

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F-NT2RP2003307//KINESIN LIGHT CHAIN (KLC).//2.0e-18:87:49//RATTUS NORVEGICUS (RAT).//P37285

5 F-NT2RP2003308//CROOKED NECK PROTEIN.//2.1e-91:244:67//DROSOPHILA MELANOGASTER (FRUIT FLY).//P17886

10 F-NT2RP2003329//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III.//5.8e-57:186:55//CAENORHABDITIS ELEGANS.//P34284

15 F-NT2RP2003339//SHORT NEUROTOXIN 1 (NEUROTOXIN ALPHA).//0.98:11:72//DENDROASPIS POLYLEPIS POLYLEPIS (BLACK MAMBA).//P01416

F-NT2RP2003347//60S RIBOSOMAL PROTEIN L38.//0.83:42:33//OSTERTAGIA OSTERTAGI.//O61570

20 F-NT2RP2003367//SYNERGISTIC-TYPE VENOM PROTEIN C9S3, CHAIN 1.//1.0:37:35//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA).//P01408

25 F-NT2RP2003391//MRNA TRANSPORT REGULATOR MTR10.//3.3e-11:229:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q99189

30 F-NT2RP2003393//PROTOCHLOROPHYLLIDE REDUCTASE CHLB SUBUNIT (EC 1.3.1.33) (NADPH- PROTOCHLOROPHYLLIDE OXIDOREDUCTASE CHLB SUBUNIT) (FRAGMENT) .//0.94:29:34//ARAUCARIA HETEROPHYLLA.//P37843

F-NT2RP2003394

35 F-NT2RP2003401//60 KD CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN).//0.95:125:28//THERMUS AQUATICUS (SUBSP. THERMOPHILUS).//P45746

40 F-NT2RP2003433//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//9.8e-78:178:84//RATTUS NORVEGICUS (RAT).//P38378

F-NT2RP2003445

45 F-NT2RP2003446//HYPOTHETICAL PROTEIN E-115.//0.00030:106:33//HUMAN ADENOVIRUS TYPE 2.//P03290

50 F-NT2RP2003456//PHOTOSYSTEM II REACTION CENTRE M PROTEIN.//1.0:27:51//MARCHANTIA POLYMORPHA (LIVERWORT).//P12168

55 F-NT2RP2003466//LINOLEOYL-COA DESATURASE (EC 1.14.99.25) (DELTA(6)-DESATURASE).//6.7e-06:108:32//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//Q08871

F-NT2RP2003480//TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2) (CBF-2) (T-14-6).//7.2e-15:38:50//GALLUS GALLUS (CHICKEN).//Q98937

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- F-NT2RP2003499//5E5 ANTIGEN.//0.090:114:32//RATTUS NORVEGICUS (RAT).//Q63003
- 5 F-NT2RP2003506//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//2.0e-11:
91:43//SUS SCROFA (PIG).//P04175
- F-NT2RP2003511//PARAMYOSIN, SHORT FORM (MIMIPARAMYOSIN).//0.0020:108:
10 25//DROSOPHILA MELANOGASTER (FRUIT FLY).//P35416
- F-NT2RP2003513//PTB-ASSOCIATED SPLICING FACTOR (PSF).//1.2e-05:96:36//HOMO
15 SAPIENS (HUMAN).//P23246
- F-NT2RP2003517//HYPOTHETICAL 12.9 KD PROTEIN CY49.27.//0.0059:22:
31//MYCOBACTERIUM TUBERCULOSIS.//Q10696
- 20 F-NT2RP2003522//HYPOTHETICAL 10.0 KD PROTEIN.//1.0:65:30//THERMOPROTEUS
TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19283
- F-NT2RP2003533//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//8.7e-18:94:54//HOMO
25 SAPIENS (HUMAN).//P08547
- F-NT2RP2003543//SYNAPSINS IA AND IB.//0.045:101:35//RATTUS NORVEGICUS (RAT)
30 .//P09951
- F-NT2RP2003559//ITBA2 PROTEIN (DXS9879E).//0.98:37:37//HOMO SAPIENS (HUMAN)
35 .//Q14657
- F-NT2RP2003564//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A))
(RO(SS-A)).//6.4e-35:175:44//HOMO SAPIENS (HUMAN).//P19474
- F-NT2RP2003567//HYPOTHETICAL 11.2 KD PROTEIN T18D3.7 IN CHROMOSOME X.//0.72:
40 82:34//CAENORHABDITIS ELEGANS.//Q22544
- F-NT2RP2003581//HOMEBOX PROTEIN OTX1.//0.90:61:37//MUS MUSCULUS (MOUSE)
45 .//P80205
- F-NT2RP2003596//ELONGATION FACTOR P (EF-P).//0.83:61:32//MYCOPLASMA
GENITALIUM.//P47272
- 50 F-NT2RP2003604//ALPHA-CATENIN.//1.5e-11:152:33//DROSOPHILA MELANOGASTER
(FRUIT FLY).//P35220
- F-NT2RP2003629//PHOSPHOLIPASE A2 ALPHA (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2-
55 ACYLHYDROLASE).//0.97:85:27//CROTALUS ADAMANTEUS (EASTERN DIAMONDBACK
RATTLESNAKE).//P00623

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- F-NT2RP2003643//ACYLNEURAMINATE CYTIDYLYLTRANSFERASE (EC 2.7.7.43) (CMP-N-ACETYLNEURAMINIC ACID SYNTHETASE) (CMP-NEUNAC SYNTHETASE) (CMP-SIALIC ACID SYNTHETASE).//3.9e-12:84:40//NEISSERIA MENINGITIDIS.//Q57385
- 5 F-NT2RP2003668//!!!! ALU-SUBFAMILY SX WARNING ENTRY !!!!!/5.0e-33:74:81//HOMO SAPIENS (HUMAN).//P39195
- 10 F-NT2RP2003687//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.7e-05:40:67//HOMO SAPIENS (HUMAN).//P39188
- 15 F-NT2RP2003691//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.5e-37:56:67//HOMO SAPIENS (HUMAN).//P39194
- F-NT2RP2003702//HYPOTHETICAL OXIDOREDUCTASE IN INLA 5'REGION (EC 1.-.-) (ORFA).//1.3e-07:98:37//LISTERIA MONOCYTOGENES.//P25145
- 20 F-NT2RP2003704//GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (EC 2.3.2.2) (GAMMA- GLUTAMYLTRANSFERASE 5) (GGT-REL).//0.66:23:52//HOMO SAPIENS (HUMAN).//P36269
- 25 F-NT2RP2003706//GLUTAMYL AMINOPEPTIDASE (EC 3.4.11.7) (EAP) (AMINOPEPTIDASE A) (APA) (DIFFERENTIATION ANTIGEN GP160).//1.2e-22:187:35//HOMO SAPIENS (HUMAN).//Q07075
- 30 F-NT2RP2003713//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 6 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 6) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 6) (DEUBIQUITINATING ENZYME 6) (PROTO-ONCOGENE TRE-2).//2.7e-06:119:34//HOMO SAPIENS (HUMAN).//P35125
- 35 F-NT2RP2003714//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//6.7e-27:68:75//HOMO SAPIENS (HUMAN).//Q05481
- 40 F-NT2RP2003727//HYPOTHETICAL PROTEIN MG007 HOMOLOG.//0.64:110:30//MYCOPLASMA PNEUMONIAE.//P75105
- 45 F-NT2RP2003737//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//1.2e-72:147:90//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), AND XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P51669
- 50 F-NT2RP2003751//EXTRACELLULAR GLOBIN PRECURSOR.//0.67:68:30//PSEUDOTERRANOVA DECIPIENS (COD WORM).//P26914
- 55 F-NT2RP2003760//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//1.0e-98:235:82//BOS TAURUS (BOVINE).//P53620

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F-NT2RP2003764//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.011:69:34//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10341

5 F-NT2RP2003769//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:33:36//EQUUS CABALLUS (HORSE).//P48663

10 F-NT2RP2003770//PHOSPHATE REGULON SENSOR PROTEIN PHOR (EC 2.7.3.-) (FRAGMENT).//0.029:35:42//PSEUDOMONAS AERUGINOSA.//P23621

15 F-NT2RP2003777//HYPOTHETICAL 82 KD AVIRULENCE PROTEIN IN AVRBS3 REGION.//0.041:67:34//XANTHOMONAS CAMPESTRIS (PV. VESICATORIA).//P14728

F-NT2RP2003781//HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II.//4.7e-54:204:47//CAENORHABDITIS ELEGANS.//Q09201

20 F-NT2RP2003793//PSEUDO-HEVEIN (MINOR HEVEIN).//0.61:30:36//HEVEA BRASILIENSIS (PARA RUBBER TREE).//P80359

25 F-NT2RP2003825//ENDOTHELIN-1 PRECURSOR (ET-1) (FRAGMENT).//1.0:35:37//CANIS FAMILIARIS (DOG).//P13206

30 F-NT2RP2003840//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//2.5e-05:80:38//CAENORHABDITIS ELEGANS.//Q11076

F-NT2RP2003857//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17).//0.54:28:50//ESCHERICHIA COLI.//P05834

35 F-NT2RP2003859//DROSOCIN PRECURSOR.//1.0:37:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//P36193

F-NT2RP2003871

40

F-NT2RP2003885//CUTICLE PROTEIN 32 (LM-32) (LM-ACP 32) (FRAGMENT).//1.0:28:50//LOCUSTA MIGRATORIA (MIGRATORY LOCUST).//P11736

45 F-NT2RP2003912//SERINE/THREONINE-PROTEIN KINASE NEK1 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 1).//4.8e-110:268:80//MUS MUSCULUS (MOUSE).//P51954

50 F-NT2RP2003952//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//0.00024:92:31//RATTUS NORVEGICUS (RAT).//O09175

55 F-NT2RP2003968//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//9.2e-05:101:36//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437

F-NT2RP2003976//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!1.7e-21:62:62//HOMO

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SAPIENS (HUMAN).//P39188

5 F-NT2RP2003981//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS8.//2.7e-08:
165:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39702

F-NT2RP2003984//UNC-87 PROTEIN.//0.75:71:28//CAENORHABDITIS ELEGANS.//P37806

10 F-NT2RP2003986/////ALU SUBFAMILY SP WARNING ENTRY !!!!!5.3e-19:47:70//HOMO
SAPIENS (HUMAN).//P39193

15 F-NT2RP2003988/////ALU SUBFAMILY SX WARNING ENTRY !!!!!2.2e-18:80:58//HOMO
SAPIENS (HUMAN).//P39195

20 F-NT2RP2004013//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B
TRANSCRIPTION FACTOR 3).//1.0e-52:141:77//HOMO SAPIENS (HUMAN).//P20290

F-NT2RP2004014//MACROPHAGE INFLAMMATORY PROTEIN-2-ALPHA (MIP2-ALPHA)
(CINC-2-ALPHA).//0.99:45:26//RATTUS NORVEGICUS (RAT).//Q10746

25 F-NT2RP2004041//SYNAPSINS IA AND IB.//0.0022:51:37//BOS TAURUS (BOVINE).//P17599

30 F-NT2RP2004042//CRUSTACEAN HYPERGLYCEMIC HORMONE PRECURSOR (CHH)
(FRAGMENT).//1.0:49:28//PENAEUS VANNAMEI (PENOEID SHRIMP) (EUROPEAN WHITE
SHRIMP).//Q26181

35 F-NT2RP2004066//CALDESMON (CDM).//2.9e-05:175:21//GALLUS GALLUS (CHICKEN)
.//P12957

F-NT2RP2004081//CADMIUM-METALLOTHIONEIN (CD-MT).//0.93:59:23//HELIX POMATIA
(ROMAN SNAIL) (EDIBLE SNAIL).//P33187

40 F-NT2RP2004098//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1)
.//4.6e-09:121:30//HOMO SAPIENS (HUMAN).//Q15404

45 F-NT2RP2004124//NONHISTONE CHROMOSOMAL PROTEIN HMG-17.//0.068:63:
31//GALLUS GALLUS (CHICKEN).//P02314

50 F-NT2RP2004142//HYPOTHETICAL 59.1 KD PROTEIN IN VPS15-YMC2 INTERGENIC
REGION.//7.9e-05:94:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38262

F-NT2RP2004152//LAMIN L(I).//0.25:167:19//XENOPUS LAEVIS (AFRICAN CLAWED FROG)
.//P09010

55 F-NT2RP2004165//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC
REGION.//0.0014:124:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214

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F-NT2RP2004170//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.012:125:30//MUS MUSCULUS (MOUSE).//P05143

5 F-NT2RP2004172//HYPOTHETICAL 105.7 KD PROTEIN IN TPK3-PIR1 INTERGENIC REGION.//4.1e-26:214:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36051

10 F-NT2RP2004187//ZINC FINGER PROTEIN 174.//3.7e-12:76:47//HOMO SAPIENS (HUMAN) .//Q15697

15 F-NT2RP2004194//HYPOTHETICAL 10.5 KD PROTEIN C31A2.13C IN CHROMOSOME I.//0.0013:92:23//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09730

F-NT2RP2004196//METALLOTHIONEIN 10-II (MT-10-II).//0.92:36:36//MYTILUS EDULIS (BLUE MUSSEL).//P80247

20 F-NT2RP2004207//MALE ACCESSORY GLAND SECRETORY PROTEIN 355A PRECURSOR.//0.92:62:35//DROSOPHILA SIMULANS (FRUIT FLY).//P33737

25 F-NT2RP2004226//66 KD STRESS PROTEIN (P66).//0.030:113:26//PHYSARUM POLYCEPHALUM (SLIME MOLD).//P90587

30 F-NT2RP2004232//PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU).//2.0e-48:211:51//HOMO SAPIENS (HUMAN).//Q15139

F-NT2RP2004239//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT PW212 PRECURSOR.//0.00038:111:36//TRITICUM AESTIVUM (WHEAT).//P08489

35 F-NT2RP2004240//METALLOTHIONEIN-II (MT-II) (METALLOTHIONEIN-LIKE PROTEIN) (MT-CE).//1.0:39:28//CAENORHABDITIS ELEGANS.//P17512

40 F-NT2RP2004242//RAS-RELATED PROTEIN RGP1 (GTP-BINDING REGULATORY PROTEIN RGP1).//0.0036:64:28//ORYZA SATIVA (RICE).//P25766

45 F-NT2RP2004245//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:21:42//PONGO PYGMAEUS PYGMAEUS (BORNEAN ORANGUTAN).//P92896

F-NT2RP2004270//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//0.00023:118:33//NEPHILA CLAVIPES (ORB SPIDER).//P46804

50 F-NT2RP2004300//PROBABLE E4 PROTEIN.//0.18:77:40//HUMAN PAPILLOMAVIRUS TYPE 8.//P06425

55 F-NT2RP2004316

F-NT2RP2004321//HYPOTHETICAL 10.8 KD PROTEIN SSR2439.//1.0:50:28//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//Q01904

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5 F-NT2RP2004339//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/5.0e-33:84:77//HOMO
SAPIENS (HUMAN).//P39195

10 F-NT2RP2004347//HYPOTHETICAL 40.9 KD PROTEIN F33H1.3 FROM CHROMOSOME
II./0.78:96:30//CAENORHABDITIS ELEGANS.//Q09556

15 F-NT2RP2004364//MINOR OUTER CAPSID PROTEIN (NS26) (NONSTRUCTURAL PROTEIN
VP9)./0.059:143:30//BOVINE ROTAVIRUS (STRAIN UK).//P04515

20 F-NT2RP2004365//EAMZP30-47 PROTEIN (FRAGMENT)./0.27:38:39//EIMERIA
ACERVULINA.//P21959

25 F-NT2RP2004366//GLYCOPROTEIN L PRECURSOR./0.64:71:28//MAREK'S DISEASE
HERPESVIRUS (STRAIN GA) (MDHV).//P52510

30 F-NT2RP2004373//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR (HISTIDINE-PROLINE
RICH GLYCOPROTEIN) (HPRG) (FRAGMENT)./0.59:50:40//ORYCTOLAGUS CUNICULUS
(RABBIT).//Q28640

35 F-NT2RP2004389//HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III./4.0e-
16:89:43//CAENORHABDITIS ELEGANS.//P34388

40 F-NT2RP2004392

45 F-NT2RP2004396//SINGLE-STRANDED NUCLEIC ACID-BINDING PROTEIN./0.42:89:
29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P10080

50 F-NT2RP2004399//SOMATOTROPIN PRECURSOR (GROWTH HORMONE)./1.0:72:
34//MESOCRICETUS AURATUS (GOLDEN HAMSTER).//P37886

55 F-NT2RP2004400

F-NT2RP2004412//SPERM PROTAMINE P1./0.24:38:31//NOTORYCTES TYPHLOPS
(MARSUPIAL MOLE).//P42143

F-NT2RP2004425//SUPPRESSOR PROTEIN SRP40./0.0087:197:22//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST).//P32583

F-NT2RP2004463//ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR)
(ALPHA-2AAR)./1.3e-05:121:37//MUS MUSCULUS (MOUSE).//Q01338

F-NT2RP2004476//NICKEL-SENSITIVE T-TYPE CALCIUM CHANNEL ALPHA-1 SUBUNIT
(RBE-II)./0.20:68:36//RATTUS NORVEGICUS (RAT).//Q07652

F-NT2RP2004490//FOS-RELATED ANTIGEN 1./0.94:59:33//HOMO SAPIENS (HUMAN)

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//P15407

- 5 F-NT2RP2004512//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3)
(FRAGMENTS)//1.0:37:32//PISASTER OCHRACEUS (SEA STAR)//P24998
- 10 F-NT2RP2004523//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.1e-15:57:71//HOMO
SAPIENS (HUMAN)//P39194
- 15 F-NT2RP2004538//KINESIN-LIKE PROTEIN KIF1A (AXONAL TRANSPORTER OF SYNAPTIC
VESICLES)//1.2e-48:121:60//HOMO SAPIENS (HUMAN)//Q12756
- 20 F-NT2RP2004551//HYPOTHETICAL 7.6 KD PROTEIN (ORF 65)//1.0:20:50//EUGLENA
GRACILIS//P32095
- 25 F-NT2RP2004568//PUTATIVE ATP-DEPENDENT RNA HELICASE C30D11.03//5.2e-07:150:
30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09903
- 30 F-NT2RP2004580//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.7e-37:100:78//HOMO
SAPIENS (HUMAN)//P39192
- 35 F-NT2RP2004587//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC
REGION//8.2e-06:150:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53214
- 40 F-NT2RP2004594//HYPOTHETICAL 45.3 KD PROTEIN C09F5.7 IN CHROMOSOME II//0.84:
105:24//CAENORHABDITIS ELEGANS//Q09458
- 45 F-NT2RP2004600//MYRISTOYLATED ALANINE-RICH C-KINASE SUBSTRATE (MARCKS)
//0.17:127:29//RATTUS NORVEGICUS (RAT)//P30009
- 50 F-NT2RP2004602//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-05:50:58//HOMO
SAPIENS (HUMAN)//P39188
- 55 F-NT2RP2004614//HYPOTHETICAL 11.6 KD PROTEIN//1.0:68:33//VACCINIA VIRUS (STRAIN
COPENHAGEN)//P20561
- 60 F-NT2RP2004655//GLYCINE-RICH RNA-BINDING PROTEIN 7//7.0e-05:70:
42//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//Q03250
- 65 F-NT2RP2004664//HYPOTHETICAL 104.0 KD PROTEIN C32A11.03C IN CHROMOSOME
I//0.30:78:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10328
- 70 F-NT2RP2004675
- 75 F-NT2RP2004681
- 80 F-NT2RP2004689//HYPOTHETICAL 78.3 KD PROTEIN IN RAM2-ATP7 INTERGENIC

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REGION.//0.021:179:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P34243

- 5 F-NT2RP2004709//HYPOTHETICAL PROTEIN MJ0647.//0.90:39:43//METHANOCOCCUS
JANNASCHII.//Q58063
- 10 F-NT2RP2004710//GAR2 PROTEIN.//0.085:60:30//SCHIZOSACCHAROMYCES POMBE
(FISSION YEAST).//P41891
- F-NT2RP2004736//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!4.4e-15:97:49//HOMO
SAPIENS (HUMAN).//P39188
- 15 F-NT2RP2004743//MALE SPECIFIC SPERM PROTEIN MST87F.//0.43:24:41//DROSOPHILA
MELANOGASTER (FRUIT FLY).//P08175
- 20 F-NT2RP2004767//36.4 KD PROLINE-RICH PROTEIN.//0.0051:88:27//LYCOPERSICON
ESCULENTUM (TOMATO).//Q00451
- 25 F-NT2RP2004768//SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH
KINASE 1).//9.0e-29:166:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38692
- F-NT2RP2004775
- 30 F-NT2RP2004791//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA
LIGASE) (LEURS).//7.4e-60:226:53//CAENORHABDITIS ELEGANS.//Q09996
- 35 F-NT2RP2004799//SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR
(EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA).//2.2e-42:133:
57//NEOCALLIMASTIX FRONTALIS (RUMEN FUNGUS).//P53587
- 40 F-NT2RP2004802//HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3'REGION.//0.018:86:
32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38898
- F-NT2RP2004816//H<BETA>58 PROTEIN.//1.0e-68:145:93//MUS MUSCULUS (MOUSE)
//P40336
- 45 F-NT2RP2004841//DSRD PROTEIN.//0.83:33:39//ARCHAEOGLOBUS FULGIDUS.//P70742
- 50 F-NT2RP2004861//KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIA3A.//0.0072:41:39//OVIS
ARIES (SHEEP).//P02443
- F-NT2RP2004897//METALLOTHIONEIN-LIKE PROTEIN 1.//0.99:41:41//CASUARINA GLAUCA
(SWAMP OAK).//Q39511
- 55 F-NT2RP2004933//DEATH-ASSOCIATED PROTEIN KINASE 1 (EC 2.7.1.-) (DAP KINASE 1)
//8.4e-34:102:67//HOMO SAPIENS (HUMAN).//P53355

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F-NT2RP2004936//HIGH POTENTIAL IRON-SULFUR PROTEIN, ISOZYME 2 (HIPIP 2).//0.87:36:33//ECTOTHIORHODOSPIRA VACUOLATA.//P38524

5 F-NT2RP2004959//STEM CELL FACTOR PRECURSOR (SCF) (MAST CELL GROWTH FACTOR) (MGF) (C-KIT LIGAND).//1.0:69:28//CANIS FAMILIARIS (DOG).//Q06220

10 F-NT2RP2004961//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946) (FRAGMENT).//2.1e-21:73:58//HOMO SAPIENS (HUMAN).//Q06730

F-NT2RP2004962//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//0.17:28:57//HOMO SAPIENS (HUMAN).//P39189

15 F-NT2RP2004967//HYPOTHETICAL 7.3 KD PROTEIN.//0.76:41:31//THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19301

20 F-NT2RP2004978//SPERMATID-SPECIFIC PROTEIN T2 [CONTAINS: SPERM PROTAMINE SP2].//0.44:40:45//SEPIA OFFICINALIS (COMMON CUTTLEFISH).//P80002

F-NT2RP2004982

25 F-NT2RP2004985//HYPOTHETICAL PROTEIN KIAA0144.//1.2e-51:204:57//HOMO SAPIENS (HUMAN).//Q14157

30 F-NT2RP2004999//LONG NEUROTOXIN 1 (ALPHA-BUNGAROTOXIN) (BGTX).//0.23:73:26//BUNGARUS MULTICINCTUS (MANY-BANDED KRAIT).//P01378

35 F-NT2RP2005000//ATPASE STABILIZING FACTOR 15 KD PROTEIN.//0.12:37:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P16965

F-NT2RP2005001//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.90:54:31//HOMO SAPIENS (HUMAN).//P22531

40 F-NT2RP2005003//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR.//1.6e-30:78:56//MUS MUSCULUS (MOUSE).//P15533

45 F-NT2RP2005012//NPL1 PROTEIN (SEC63 PROTEIN).//0.00024:94:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P14906

50 F-NT2RP2005018//GAG POLYPROTEIN (CORE POLYPROTEIN) [CONTAINS: CORE PROTEINS P19, P10] (FRAGMENT).//1.0:91:28//AVIAN ENDOGENOUS ROUS-ASSOCIATED VIRUS-0 (EV-2) (AVIAN RETROVIRUS RAV-0).//P06937

F-NT2RP2005020

55 F-NT2RP2005022//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//4.9e-11:106:35//PODOSPORA ANSERINA.//Q00808

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F-NT2RP2005031

5 F-NT2RP2005037//ANTI-SILENCING PROTEIN 1.//2.2e-32:117:55//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST).//P32447

10 F-NT2RP2005038//DNA NUCLEOTIDYLEXOTRANSFERASE (EC 2.7.7.31) (TERMINAL
ADDITION ENZYME) (TERMINAL DEOXYNUCLEOTIDYLTRANSFERASE) (TERMINAL
TRANSFERASE).//9.3e-28:187:40//AMBYSTOMA MEXICANUM (AXOLOTL).//O57486

15 F-NT2RP2005108//CUTICLE COLLAGEN 2.//0.33:62:38//CAENORHABDITIS
ELEGANS.//P17656

20 F-NT2RP2005116//PUTATIVE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 ALPHA
SUBUNIT (EIF-3 ALPHA).//4.0e-54:161:63//CAENORHABDITIS ELEGANS.//P34466

F-NT2RP2005126//CHLOROPLAST 50S RIBOSOMAL PROTEIN L27 (FRAGMENT).//0.23:46:
39//PLEUROCHRYYSIS HAPTONEMOFERA.//P41552

25 F-NT2RP2005139//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.016:43:37//BOS
TAURUS (BOVINE).//P25508

30 F-NT2RP2005140//HYPOTHETICAL 7.4 KD PROTEIN YCF33.//0.96:51:39//GUILLARDIA
THETA (CRYPTOMONAS PHI).//O78517

F-NT2RP2005144//TUBBY PROTEIN.//5.6e-08:66:45//MUS MUSCULUS (MOUSE).//P50586

35 F-NT2RP2005147

40 F-NT2RP2005159//PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN
PRECURSOR.//0.94:57:29//NICOTIANA TABACUM (COMMON TOBACCO), AND SPINACIA
OLERACEA (SPINACH).//P12164

45 F-NT2RP2005162//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC
REGION.//1.2e-33:139:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38821

F-NT2RP2005168//HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U)
.//2.8e-33:102:61//HOMO SAPIENS (HUMAN).//Q00839

50 F-NT2RP2005204//DNA DAMAGE TOLERANCE PROTEIN RHC31 (RAD31 HOMOLOG)
.//3.9e-28:141:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06624

55 F-NT2RP2005227

F-NT2RP2005239//TRNA SPLICING PROTEIN SPL1.//2.0e-38:117:64//CANDIDA ALBICANS
(YEAST).//P87185

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- 5 F-NT2RP2005254//OMEGA-AGATOXIN IB (OMEGA-AGA-IB) (FRAGMENT).//0.26:29:48//AGELENOPSIS APERTA (FUNNEL-WEB SPIDER).//P15970
- F-NT2RP2005270//HOMEBOX PROTEIN HOX-A4 (CHOX-1.4).//0.037:82:34//GALLUS GALLUS (CHICKEN).//P17277
- 10 F-NT2RP2005276//LONG-CHAIN-FATTY-ACID-COA LIGASE 4 (EC 6.2.1.3) (LONG-CHAIN ACYL-COA SYNTHETASE 4) (LACS 4).//2.0e-59:174:61//RATTUS NORVEGICUS (RAT).//O35547
- 15 F-NT2RP2005287//ZINC FINGER PROTEIN 26 (ZINC FINGER PROTEIN KOX20) (FRAGMENT).//1.5e-05:27:70//HOMO SAPIENS (HUMAN).//P17031
- 20 F-NT2RP2005288//PROBABLE RUBREDOXIN HUPI.//1.0:42:28//RHIZOBIUM LEGUMINOSARUM (BIOVAR VICIAE).//P28151
- F-NT2RP2005289//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.1e-21:75:70//HOMO SAPIENS (HUMAN).//P39193
- 25 F-NT2RP2005293//TRANSLATION INITIATION FACTOR IF-2.//0.58:170:24//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//P55972
- 30 F-NT2RP2005315//CUTICLE COLLAGEN 7 (FRAGMENT).//0.091:65:38//CAENORHABDITIS ELEGANS.//P18832
- 35 F-NT2RP2005325//CHROMOGRANIN A PRECURSOR (CGA) (PITUITARY SECRETORY PROTEIN I) (SP-I) [CONTAINS: PANCREASTATIN; WE-14].//9.5e-09:98:39//HOMO SAPIENS (HUMAN).//P10645
- 40 F-NT2RP2005336//HYPOTHETICAL 68.7 KD PROTEIN IN STB1-MCK1 INTERGENIC REGION.//0.00011:124:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P42846
- F-NT2RP2005344//PROBABLE CALCIUM-TRANSPORTING ATPASE 4 (EC 3.6.1.38).//4.7e-21:92:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12675
- 45 F-NT2RP2005354
- 50 F-NT2RP2005358//MYOSIN IC HEAVY CHAIN.//0.012:91:39//ACANTHAMOEBA CASTELLANII (AMOEB).//P10569
- F-NT2RP2005360//ACROSIN PRECURSOR (EC 3.4.21.10).//0.0022:73:36//ORYCTOLAGUS CUNICULUS (RABBIT).//P48038
- 55 F-NT2RP2005393//HYPOTHETICAL 25.9 KD PROTEIN AH6.3 IN CHROMOSOME II.//0.00085:135:28//CAENORHABDITIS ELEGANS.//Q09202

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5 F-NT2RP2005407//SQUALENE MONOOXYGENASE (EC 1.14.99.7) (SQUALENE EPOXIDASE) (SE)//0.96:109:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32476
 F-NT2RP2005436//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN)//0.0011:54:42//ZEA MAYS (MAIZE)//P14918
 10 F-NT2RP2005441//PROLINE-RICH PROTEIN MP-2 PRECURSOR//0.039:182:29//MUS MUSCULUS (MOUSE)//P05142
 F-NT2RP2005453
 15 F-NT2RP2005457//NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-B14.5B) (CI-B14.5B)//4.0e-10:124:37//BOS TAURUS (BOVINE) //Q02827
 20 F-NT2RP2005464//HYPOTHETICAL 9.5 KD PROTEIN//0.96:42:33//VACCINIA VIRUS (STRAIN COPENHAGEN)//P20553
 25 F-NT2RP2005465//MITOCHONDRIAL CARRIER PROTEIN RIM2//4.6e-09:92:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38127
 F-NT2RP2005472//HYPOTHETICAL PROTEIN BB0129//0.76:80:32//BORRELIA BURGDOFFER (LYME DISEASE SPIROCHETE)//O51155
 30 F-NT2RP2005476//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!1.0e-31:39:89//HOMO SAPIENS (HUMAN)//P39193
 35 F-NT2RP2005490//METALLOTHIONEIN-II (MT-II)//0.14:27:33//SCYLLA SERRATA (MUD CRAB)//P02806
 40 F-NT2RP2005491//DNA-DIRECTED RNA POLYMERASE SUBUNIT I (EC 2.7.7.6)//0.95:45:31//METHANOCOCCUS JANNASCHII//Q58785
 F-NT2RP2005495//HYPOTHETICAL 10.8 KD PROTEIN IN GP30-RIII INTERGENIC REGION//0.99:68:30//BACTERIOPHAGE T4//Q02407
 45 F-NT2RP2005496//ZINC FINGER PROTEIN 135//1.4e-54:120:59//HOMO SAPIENS (HUMAN) //P52742
 50 F-NT2RP2005498//PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55) //9.5e-76:146:86//RATTUS NORVEGICUS (RAT)//P36876
 55 F-NT2RP2005501//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35)

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(LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-31) (GALACTOSIDE-BINDING PROTEIN)
(GALBP).//0.025:70:40//HOMO SAPIENS (HUMAN).//P17931

5 F-NT2RP2005509//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//1.0:166:27//GALLUS
GALLUS (CHICKEN).//P02457

10 F-NT2RP2005520//CHROMOSOME ASSEMBLY PROTEIN XCAP-E.//7.9e-45:118:
79//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P50533

F-NT2RP2005525//50S RIBOSOMAL PROTEIN L11.//1.0:47:27//BORRELIA BURGDORFERI
(LYME DISEASE SPIROCHETE).//O51354

15 F-NT2RP2005531//PROTEIN-TYROSINE PHOSPHATASE MEG1 (EC 3.1.3.48) (PTPASE-
MEG1) (MEG).//9.8e-13:84:45//HOMO SAPIENS (HUMAN).//P29074

20 F-NT2RP2005539//RING CANAL PROTEIN (KELCH PROTEIN).//4.9e-10:90:
33//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

25 F-NT2RP2005540//NUCLEOTIDE BINDING PROTEIN EXPZ.//0.36:119:21//BACILLUS
SUBTILIS.//P39115

F-NT2RP2005549//HYPOTHETICAL 32.0 KD PROTEIN C16C10.10 IN CHROMOSOME
III.//6.0e-39:179:46//CAENORHABDITIS ELEGANS.//Q09253

30 F-NT2RP2005555

F-NT2RP2005557//HYPOTHETICAL 23.7 KD PROTEIN C13G6.14 IN CHROMOSOME I.//4.9e-
06:90:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09790

35 F-NT2RP2005581

40 F-NT2RP2005600//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.014:37:40//HOMO
SAPIENS (HUMAN).//P02811

45 F-NT2RP2005605//GONADOLIBERIN I PRECURSOR (LHRH I) (LUTEINIZING HORMONE
RELEASING HORMONE I) (GONADOTROPIN RELEASING HORMONE I) (GNRH I)
(LULIBERIN I) (FRAGMENT).//0.64:26:42//MACACA MULATTA (RHESUS MACAQUE).//P55247

50 F-NT2RP2005620//HYPOTHETICAL 45.1 KD PROTEIN IN RPS5-ZMS1 INTERGENIC
REGION.//8.7e-31:138:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47160

F-NT2RP2005622//NEUROTOXIN-LIKE PROTEIN STR1 (ANATOXIN AAH STR1).//0.39:22:
40//ANDROCTONUS AUSTRALIS HECTOR (SAHARA SCORPION).//P80950

55 F-NT2RP2005635//HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC
REGION.//5.8e-43:144:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38795

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F-NT2RP2005637//VPU PROTEIN (U ORF PROTEIN)//0.91:33:45//CHIMPANZEE
 IMMUNODEFICIENCY VIRUS (SIV(CPZ)) (CIV)//P17286
 5
 F-NT2RP2005640//METALLOTHIONEIN-LIKE PROTEIN LSC54//0.63:41:31//BRASSICA
 NAPUS (RAPE)//P43402
 10 F-NT2RP2005645
 F-NT2RP2005651//OCTAMER-BINDING TRANSCRIPTION FACTOR 3A (OCT-3A) (OCT-4)
 //0.0023:50:42//HOMO SAPIENS (HUMAN)//Q01860
 15 F-NT2RP2005654//HYPOTHETICAL 48.6 KD PROTEIN IN BET1-PAN1 INTERGENIC
 REGION//6.1e-16:76:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40564
 20 F-NT2RP2005669//METALLOTHIONEIN-II (MT-II)//0.76:16:50//SCYLLA SERRATA (MUD
 CRAB)//P02806
 F-NT2RP2005675//PUTATIVE ORAL CANCER SUPPRESSOR (DELETED IN ORAL
 25 CANCER-1)//6.5e-26:116:54//MESOCRICETUS AURATUS (GOLDEN HAMSTER)//P49119
 F-NT2RP2005683//HYPOTHETICAL PROTEIN HI0275//0.17:50:40//HAEMOPHILUS
 INFLUENZAE//P43975
 30 F-NT2RP2005690//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C
 REDUCTASE)//1.3e-16:75:30//PISUM SATIVUM (GARDEN PEA)//Q04708
 35 F-NT2RP2005694//HYPOTHETICAL PROTEIN KIAA0032//9.6e-11:135:34//HOMO SAPIENS
 (HUMAN)//Q15034
 F-NT2RP2005701//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS:
 40 PEPTIDE P-D] (FRAGMENT)//0.084:158:32//HOMO SAPIENS (HUMAN)//P10161
 F-NT2RP2005712//METALLOTHIONEIN-II (MT-II)//0.19:14:50//STENELLA COERULEOALBA
 (STRIPED DOLPHIN)//P14425
 45 F-NT2RP2005719//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT)//1.0:36:41//ORYCTOLAGUS
 CUNICULUS (RABBIT)//P02456
 50 F-NT2RP2005722//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT)//7.8e-37:131:62//HOMO
 SAPIENS (HUMAN)//P16415
 55 F-NT2RP2005723//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//0.98:23:60//HOMO
 SAPIENS (HUMAN)//P39192
 F-NT2RP2005726//HYPOTHETICAL PROTEIN TP0375//0.98:30:43//TREPONEMA

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PALLIDUM.//O83390

- 5 F-NT2RP2005732//PERIOD CLOCK PROTEIN (FRAGMENT).//0.41:20:55//DROSOPHILA ROBUSTA (FRUIT FLY).//Q03296
- 10 F-NT2RP2005741//SMR1 PROTEIN PRECURSOR (VCS-ALPHA 1).//0.38:58:36//RATTUS NORVEGICUS (RAT).//P13432
- 15 F-NT2RP2005748//ZINC FINGER PROTEIN KOX23 (FRAGMENT).//0.026:19:68//HOMO SAPIENS (HUMAN).//P17034
- 20 F-NT2RP2005752//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.//0.90:101:31//HOMO SAPIENS (HUMAN).//P02461
- 25 F-NT2RP2005753//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.50:22:59//HOMO SAPIENS (HUMAN).//P30808
- 30 F-NT2RP2005763//PUTATIVE ATP-DEPENDENT RNA HELICASE STE13.//4.7e-14:108:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09181
- 35 F-NT2RP2005767//NONHISTONE CHROMOSOMAL PROTEIN 6B.//4.1e-08:65:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P11633
- 40 F-NT2RP2005773//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).//1.2e-14:65:61//HOMO SAPIENS (HUMAN).//P32322
- 45 F-NT2RP2005775//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP).//1.3e-103:199:90//ORYCTOLAGUS CUNICULUS (RABBIT).//P42675
- 50 F-NT2RP2005781//SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1 / PRP-3) (PRP-2 / PRP-4) (PIF-F / PIF-S) (PROTEIN A / PROTEIN C) [CONTAINS: PEPTIDE P-C].//0.090:73:36//HOMO SAPIENS (HUMAN).//P02810
- 55 F-NT2RP2005784//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).//3.5e-06:79:37//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).//P08393
- 60 F-NT2RP2005804//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//1.8e-07:43:55//OWENIA FUSIFORMIS.//P21260
- 65 F-NT2RP2005812//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//6.3e-14:143:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40004
- 70 F-NT2RP2005815//FERROCHELATASE (EC 4.99.1.1) (PROTOHEME FERRO-LYASE) (HEME

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SYNTHETASE).//0.0017:123:37//MYCOBACTERIUM AVIUM.//O07401

5 F-NT2RP2005835//SHP1 PROTEIN.//1.2e-08:135:26//SACCHAROMYCES CEREVISIAE
(BAKER'S YEAST).//P34223

10 F-NT2RP2005841//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.23:28:
53//HOMO SAPIENS (HUMAN).//P22532

F-NT2RP2005853//HYPOTHETICAL 8.5 KD PROTEIN IN ASIA-MOTA INTERGENIC
REGION.//0.99:33:48//BACTERIOPHAGE T4.//P22917

15 F-NT2RP2005857//CHROMOSOME ASSEMBLY PROTEIN XCAP-C.//8.6e-84:235:
66//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P50532

20 F-NT2RP2005859//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.017:60:
40//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643

25 F-NT2RP2005868//ATP SYNTHASE B' CHAIN PRECURSOR (EC 3.6.1.34) (SUBUNIT II)
.//0.28:121:28//SPINACIA OLERACEA (SPINACH).//P31853

30 F-NT2RP2005886//MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH)
[CONTAINS: LINKER HISTONE PROTEINS ALPHA, BETA, DELTA AND GAMMA].//0.80:130:
28//TETRAHYMENA THERMOPHILA.//P40631

F-NT2RP2005890

35 F-NT2RP2005901//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.35:18:
44//DROSOPHILA YAKUBA (FRUIT FLY).//P03933

40 F-NT2RP2005908//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.0e-28:61:65//HOMO
SAPIENS (HUMAN).//P39194

F-NT2RP2005933//PERIOD CLOCK PROTEIN (P230) (FRAGMENT).//1.7e-11:85:
49//ACETABULARIA MEDITERRANEA (MERMAID'S WINE GLASS).//P12347

45 F-NT2RP2005942//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE
ADENYLYLTRANSFERASE).//7.2e-59:216:58//BOS TAURUS (BOVINE).//P25500

50 F-NT2RP2005980//HYPOTHETICAL 11.5 KD PROTEIN IN RSP8A-AST1 INTERGENIC
REGION.//1.0:49:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38185

55 F-NT2RP2006023//DNA REPAIR PROTEIN RECN (RECOMBINATION PROTEIN N)
(FRAGMENT).//1.0:40:45//VIBRIO CHOLERAEE.//P52118

F-NT2RP2006038//HYPOTHETICAL 30.2 KD PROTEIN C02F5.4 IN CHROMOSOME III.//4.0e-
11:90:34//CAENORHABDITIS ELEGANS.//P34281

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5 F-NT2RP2006043//LAMININ BETA-1 CHAIN VARIANT (LAMININ BETA-1-2 CHAIN
(FRAGMENT)).//0.00067:73:38//GALLUS GALLUS (CHICKEN).//Q01636

10 F-NT2RP2006052//METALLOTHIONEIN-I (MT-I).//0.19:31:38//CERCOPITHECUS AETHIOPS
(GREEN MONKEY) (GRIVET).//P02797

15 F-NT2RP2006069//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENTS).//1.0:66:34//RATTUS
NORVEGICUS (RAT).//P02466

20 F-NT2RP2006071//RESTIN.//0.40:156:29//GALLUS GALLUS (CHICKEN).//O42184

25 F-NT2RP2006098//HYPOTHETICAL 21.7 KD PROTEIN IN TUP1-ABP1 INTERGENIC
REGION.//0.99:95:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25651

30 F-NT2RP2006100//LONG NEUROTOXIN 4 (ALPHA-NEUROTOXIN).//0.94:43:
34//OPHIOPHAGUS HANNAH (KING COBRA) (NAJA HANNAH).//P80156

35 F-NT2RP2006103//50S RIBOSOMAL PROTEIN L32.//0.40:36:38//SYNECHOCYSTIS SP.
(STRAIN PCC 6803).//P73014

40 F-NT2RP2006106//CUTICLE COLLAGEN 1.//0.28:85:29//CAENORHABDITIS
ELEGANS.//P08124

45 F-NT2RP2006141//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//1.9e-
08:57:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09701

50 F-NT2RP2006166

55 F-NT2RP2006184//HYPOTHETICAL 11.2 KD PROTEIN IN CSGC-MDOG INTERGENIC
REGION PRECURSOR.//0.95:87:26//ESCHERICHIA COLI.//P75917

F-NT2RP2006186//MICROTUBULE-ASSOCIATED PROTEIN 2.//0.088:124:33//MUS
MUSCULUS (MOUSE).//P20357

F-NT2RP2006196//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/4.0e-05:49:61//HOMO
SAPIENS (HUMAN).//P39193

F-NT2RP2006200//PROCOLLAGEN ALPHA 2(V) CHAIN PRECURSOR.//0.0013:205:
32//HOMO SAPIENS (HUMAN).//P05997

F-NT2RP2006219//GONADAL PROTEIN GDL.//3.5e-18:158:37//DROSOPHILA
MELANOGASTER (FRUIT FLY).//P22468

F-NT2RP2006237//FIBRINOGEN- AND IG-BINDING PROTEIN PRECURSOR (MRP
PROTEIN).//0.79:103:28//STREPTOCOCCUS PYOGENES.//P30141

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- 5 F-NT2RP2006238//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//4.7e-07:127:39//MUS MUSCULUS (MOUSE).//P05143
- 10 F-NT2RP2006258//PROBABLE E5 PROTEIN.//0.78:47:34//RHESUS PAPILLOMAVIRUS TYPE 1 (RHPV 1).//P24834
- 15 F-NT2RP2006261//PENAEIDIN-3A PRECURSOR (P3-A).//0.61:35:40//PENAEUS VANNAMEI (PENOEID SHRIMP) (EUROPEAN WHITE SHRIMP).//P81058
- 20 F-NT2RP2006275//ELECTROMOTOR NEURON-ASSOCIATED PROTEIN 2 (FRAGMENT) .//1.2e-28:59:57//TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).//P14401
- 25 F-NT2RP2006312//HIGH-MOBILITY-GROUP PROTEIN (NONHISTONE CHROMOSOMAL PROTEIN).//1.6e-06:53:35//TETRAHYMENA PYRIFORMIS.//P40625
- 30 F-NT2RP2006320//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).//0.90:24:41//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BH5 ISOLATE) (HIV-1).//P04612
- 35 F-NT2RP2006321//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//0.0051:25:76//HOMO SAPIENS (HUMAN).//P39193
- 40 F-NT2RP2006323//WISKOTT-ALDRICH SYNDROME PROTEIN (WASP).//0.84:33:39//HOMO SAPIENS (HUMAN).//P42768
- 45 F-NT2RP2006333//MYOTOXIN 3 PRECURSOR (CROTAMINE 3).//0.56:37:40//CROTALUS DURISSUS TERRIFICUS (SOUTH AMERICAN RATTLESNAKE).//P24333
- 50 F-NT2RP2006334//SUCCINYL-COA LIGASE [GDP-FORMING], ALPHA-CHAIN 3 PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, ALPHA CHAIN 3).//0.00097:46:41//TRICHOMONAS VAGINALIS.//P53401
- 55 F-NT2RP2006365//NONSPECIFIC LIPID-TRANSFER PROTEIN 4.3 PRECURSOR (LTP 4.3) .//0.18:75:29//HORDEUM VULGARE (BARLEY).//Q42842
- 60 F-NT2RP2006393//OMEGA-CONOTOXIN MVIIC PRECURSOR (FRAGMENT).//0.82:15:66//CONUS MAGUS (MAGUS CONE).//P37300
- 65 F-NT2RP2006436//ANTERIOR-RESTRICTED HOMEBOX PROTEIN (RATHKE POUCH HOMEBOX).//1.4e-08:50:50//MUS MUSCULUS (MOUSE).//Q61658
- 70 F-NT2RP2006441//METALLOTHIONEIN-LIKE PROTEIN 1.//0.99:22:54//MIMULUS GUTTATUS (SPOTTED MONKEY FLOWER) (YELLOW MONKEY FLOWER).//P20238
- 75 F-NT2RP2006454//SPERM PROTAMINE P1.//0.60:47:36//TACHYGLOSSUS ACULEATUS

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ACULEATUS (AUSTRALIAN ECHIDNA).//P35311

F-NT2RP2006456

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F-NT2RP2006464//PHOTOSYSTEM I IRON-SULFUR CENTER (PHOTOSYSTEM I SUBUNIT VII) (9 KD POLYPEPTIDE) (PSI-C).//0.91:79:30//SYNECHOCOCCUS SP. (STRAIN PCC 7002) (AGMENELLUM QUADRUPLICATUM).//P31087

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F-NT2RP2006467//PUTATIVE CUTICLE COLLAGEN F55C10.3.//0.15:53:35//CAENORHABDITIS ELEGANS.//Q21184

15

F-NT2RP2006472//HYPOTHETICAL 19 KD PROTEIN (ORF 167).//0.33:98:26//MARCHANTIA POLYMORPHA (LIVERWORT).//P12202

F-NT2RP2006534

20

F-NT2RP2006554//ANTI-SIGMA F FACTOR ANTAGONIST (STAGE II SPORULATION PROTEIN AA).//0.91:50:34//BACILLUS SPHAERICUS.//O32723

25

F-NT2RP2006565//SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 1 (SCAMP 37).//6.0e-66:93:96//RATTUS NORVEGICUS (RAT).//P56603

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F-NT2RP2006571//CYTOCHROME P450 2B10 (EC 1.14.14.1) (CYP1B10) (TESTOSTERONE 16-ALPHA HYDROXYLASE) (P450-16-ALPHA) (CLONE PF3/46).//4.5e-40:138:57//MUS MUSCULUS (MOUSE).//P12791

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F-NT2RP2006573//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//0.53:46:39//BOS TAURUS (BOVINE).//P02318

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F-NT2RP2006598//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.3e-12:44:77//HOMO SAPIENS (HUMAN).//P39195

F-NT2RP3000002//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.4e-19:60:63//HOMO SAPIENS (HUMAN).//P39192

45

F-NT2RP3000031//HYPOTHETICAL 89.8 KD PROTEIN F41H10.6 IN CHROMOSOME IV.//2.1e-39:210:42//CAENORHABDITIS ELEGANS.//Q20296

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F-NT2RP3000046//POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF.//1.4e-25:149:44//PSEUDOMONAS PUTIDA.//P25755

55

F-NT2RP3000047//NPL4 PROTEIN.//4.7e-48:275:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33755

F-NT2RP3000050//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//3.2e-72:232:59//HOMO SAPIENS (HUMAN).//P51522

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- 5 F-NT2RP3000055//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.26:57:36//DROSOPHILA
MELANOGASTER (FRUIT FLY).//Q01643
- 10 F-NT2RP3000068//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC
REGION.//0.0014:66:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47170
- 15 F-NT2RP3000072//HYPOTHETICAL 6.7 KD PROTEIN IN NOHA-CSPI INTERGENIC
REGION.//0.95:49:30//ESCHERICHIA COLI.//P77695
- 20 F-NT2RP3000080//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.1e-17:64:68//HOMO
SAPIENS (HUMAN).//P39188
- 25 F-NT2RP3000085//BIOTIN CARBOXYLASE (EC 6.3.4.14) (A SUBUNIT OF ACETYL-COA
CARBOXYLASE (EC 6.4.1.2)) (ACC).//4.4e-43:169:51//BACILLUS SUBTILIS.//P49787
- 30 F-NT2RP3000092//CELL DIVISION CONTROL PROTEIN 1.//0.00016:103:
31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40986
- 35 F-NT2RP3000109//ACYL CARRIER PROTEIN HOMOLOG (ACP).//0.76:83:28//MYCOPLASMA
GENITALIUM.//P47529
- 40 F-NT2RP3000134
- 45 F-NT2RP3000142//GAR2 PROTEIN.//0.00098:241:20//SCHIZOSACCHAROMYCES POMBE
(FISSION YEAST).//P41891
- 50 F-NT2RP3000149//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.0014:33:36//PONGO
PYGMAEUS ABELII (SUMATRAN ORANGUTAN).//P92694
- 55 F-NT2RP3000186//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/8.3e-15:36:83//HOMO
SAPIENS (HUMAN).//P39188
- F-NT2RP3000197//HYPOTHETICAL 6.0 KD PROTEIN IN THI12 5'REGION.//0.91:21:
52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53820
- F-NT2RP3000207//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-
ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//0.026:209:
27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640
- F-NT2RP3000220//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)
.//1.0:26:42//HOMO SAPIENS (HUMAN).//P30808
- F-NT2RP3000233//RING CANAL PROTEIN (KELCH PROTEIN).//2.1e-42:249:
39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

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F-NT2RP3000235//HOMEBOX PROTEIN H40 (FRAGMENT).//0.55:45:40//APIS MELLIFERA (HONEYBEE).//P15858

5 F-NT2RP3000247//HYPOTHETICAL PROTEIN KIAA0218.//1.7e-82:123:69//HOMO SAPIENS (HUMAN).//Q93075

10 F-NT2RP3000251//SERINE PROTEINASE STUBBLE (EC 3.4.21.-) (STUBBLE-STUBBLOID PROTEIN).//1.0:53:33//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q05319

15 F-NT2RP3000252//HYPOTHETICAL 40 KD GTP-BINDING PROTEIN IN RIBOSOMAL PROTEIN GENE CLUSTER 5'REGION.//2.2e-06:96:32//HALOBACTERIUM CUTIRUBRUM.//P17103

20 F-NT2RP3000255//HISTONE H1.1 (FRAGMENT).//0.95:71:33//BOS TAURUS (BOVINE).//P02253

F-NT2RP3000267//HYPOTHETICAL 21.1 KD PROTEIN IN SSR-SERA INTERGENIC REGION (O182).//0.38:77:33//ESCHERICHIA COLI.//P09160

25 F-NT2RP3000299//MYOSIN IC HEAVY CHAIN.//1.2e-11:147:34//ACANTHAMOEBA CASTELLANII (AMOEBA).//P10569

30 F-NT2RP3000312//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.64:216:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214

35 F-NT2RP3000320//TRANSLATION INITIATION FACTOR IF-2.//5.2e-05:184:22//AQUIFEX AEOLICUS.//O67825

F-NT2RP3000324//HYPOTHETICAL PROTEIN HI1036.//0.69:64:35//HAEMOPHILUS INFLUENZAE.//P44097

40 F-NT2RP3000333//WIR1A PROTEIN.//0.35:51:41//TRITICUM AESTIVUM (WHEAT).//Q01482

45 F-NT2RP3000341//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//2.1e-30:57:80//HOMO SAPIENS (HUMAN).//P39189

F-NT2RP3000348

50 F-NT2RP3000350//HYPOTHETICAL 40 KD GTP-BINDING PROTEIN IN RIBOSOMAL PROTEIN GENE CLUSTER 5'REGION.//0.0011:77:35//HALOBACTERIUM CUTIRUBRUM.//P17103

55 F-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//1.2e-97:222:84//BOS TAURUS (BOVINE).//P08760

F-NT2RP3000361//PRE-MRNA SPLICING FACTOR PRP6.//2.2e-08:128:

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28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P19735

5 F-NT2RP3000366//RAS-RELATED PROTEIN RAB-18//2.1e-107:206:99//MUS MUSCULUS
(MOUSE)//P35293

10 F-NT2RP3000393//HOMEODOMAIN PROTEIN HOX-C4 (HOX-3E) (CP19)//0.0023:36:52//HOMO
SAPIENS (HUMAN)//P09017

F-NT2RP3000397//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAF BOX
PROTEIN 13)//5.5e-27:116:44//MUS MUSCULUS (MOUSE)//O35286

15 F-NT2RP3000403//PRE-MRNA PROCESSING PROTEIN PRP40//0.00044:67:
34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P33203

20 F-NT2RP3000418//RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE
TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE]//2.2e-16:228:34//MUS MUSCULUS
(MOUSE)//P11369

25 F-NT2RP3000433//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.7e-17:79:55//HOMO
SAPIENS (HUMAN)//P39188

F-NT2RP3000439//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC
REGION//9.8e-10:201:26//ESCHERICHIA COLI//P37908

30 F-NT2RP3000441//PROTEIN-EXPORT MEMBRANE PROTEIN SECY HOMOLOG//0.91:48:
35//MYCOBACTERIUM LEPRAE//P38388

35 F-NT2RP3000449//HOMEODOMAIN PROTEIN HOX-B8 (HOX-2.4) (FRAGMENT)//1.0:42:
33//GALLUS GALLUS (CHICKEN)//P23681

40 F-NT2RP3000451

F-NT2RP3000456//COLLAGEN ALPHA 1(I) CHAIN

45 (FRAGMENTS)//0.00018:178:36//RATTUS NORVEGICUS (RAT)//P02454

F-NT2RP3000484//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF)
//0.098:40:27//BOS TAURUS (BOVINE)//P37359

50 F-NT2RP3000487//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)//0.00037:16:
81//VOLVOX CARTERI//P21997

55 F-NT2RP3000512

F-NT2RP3000526//HYPOTHETICAL NIN REGION PROTEIN ORF56//0.51:37:
43//BACTERIOPHAGE LAMBDA//P03769

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- 5 F-NT2RP3000527//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.0e-16:234:30//HOMO SAPIENS (HUMAN).//P51522
- 10 F-NT2RP3000531//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//3.4e-15:192:30//HOMO SAPIENS (HUMAN).//P15151
- 15 F-NT2RP3000542//CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) (FRAGMENT).//0.60:51:39//ASTERINA PECTINIFERA (STARFISH).//P11958
- 20 F-NT2RP3000561//HYPOTHETICAL ATP-BINDING PROTEIN MJ0423.//0.79:53:32//METHANOCOCCUS JANNASCHII.//Q57866
- 25 F-NT2RP3000562//ACCESSORY GLAND PEPTIDE PRECURSOR (PARAGONIAL PEPTIDE B).//0.99:26:34//DROSOPHILA MAURITIANA (FRUIT FLY), AND DROSOPHILA SIMULANS (FRUIT FLY).//O18666
- 30 F-NT2RP3000578//HYPOTHETICAL 49.8 KD PROTEIN IN RPL14B-GPA1 INTERGENIC REGION.//1.5e-26:127:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38755
- 35 F-NT2RP3000582
- 40 F-NT2RP3000584//METALLOTHIONEIN-II (MT-II).//0.28:27:29//MUS MUSCULUS (MOUSE).//P02798
- 45 F-NT2RP3000590//UVS-2 PROTEIN.//4.8e-10:113:33//NEUROSPORA CRASSA.//P33288
- 50 F-NT2RP3000592//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//0.00087:178:31//HOMO SAPIENS (HUMAN).//O00268
- 55 F-NT2RP3000596//YEMANUCLEIN-ALPHA.//1.8e-05:98:34//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25992
- 60 F-NT2RP3000599//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//0.00095:90:37//HOMO SAPIENS (HUMAN).//Q15428
- 65 F-NT2RP3000603//5E5 ANTIGEN.//1.0e-09:181:34//RATTUS NORVEGICUS (RAT).//Q63003
- 70 F-NT2RP3000605//STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (STEROL REGULATORY ELEMENT-BINDING TRANSCRIPTION FACTOR 1).//0.00098:76:34//HOMO SAPIENS (HUMAN).//P36956
- 75 F-NT2RP3000622//HYPOTHETICAL PROTEIN MG096 HOMOLOG 5 (P02_ORF427).//0.15:52:36//MYCOPLASMA PNEUMONIAE.//P75277
- 80 F-NT2RP3000624//HYPOTHETICAL PROTEIN KIAA0256.//5.4e-16:222:31//HOMO SAPIENS

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(HUMAN).//Q93073

F-NT2RP3000628

5

F-NT2RP3000632//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10)
./2.0e-16:52:63//MUS MUSCULUS (MOUSE).//Q61967

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F-NT2RP3000644//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/6.7e-40:102:79//HOMO
SAPIENS (HUMAN).//P39194

15

F-NT2RP3000661//HYPOTHETICAL 139.1 KD PROTEIN C08B11.3 IN CHROMOSOME
II./6.0e-08:83:36//CAENORHABDITIS ELEGANS.//Q09441

20

F-NT2RP3000665//HOMEODOMAIN PROTEIN PROPHET OF PIT-1 (PROP-1) (PITUITARY
SPECIFIC HOMEODOMAIN FACTOR).//0.13:48:35//HOMO SAPIENS (HUMAN).//O75360

F-NT2RP3000685//HYPOTHETICAL 33.5 KD PROTEIN IN CAT1 5'REGION (ORFY).//0.26:
202:23//CLOSTRIDIUM KLUYVERI.//P38943

25

F-NT2RP3000690//INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE
PHOSPHO- HYDROLASE) (PPASE).//0.99:131:26//SACCHAROMYCES CEREVISIAE (BAKER'S
YEAST).//P00817

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F-NT2RP3000736//HYPOTHETICAL 28.7 KD PROTEIN IN RNR3-ARC15 INTERGENIC
REGION.//3.5e-27:211:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40516

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F-NT2RP3000739//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME
I.//6.0e-23:114:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10149

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F-NT2RP3000742//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE
PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-
DELTA-1) (PLC-III).//6.7e-12:85:36//RATTUS NORVEGICUS (RAT).//P10688

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F-NT2RP3000753//CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER
PROTEIN B) (S-LAYER PROTEIN 1).//0.00011:208:28//CLOSTRIDIUM
THERMOCELLUM.//Q06852

50

F-NT2RP3000759//ADP-RIBOSYLATION FACTOR 6.//8.1e-28:141:38//GALLUS GALLUS
(CHICKEN).//P26990

F-NT2RP3000815//CYTOCHROME C-551 (C551) (CYTOCHROME C8).//0.24:45:
37//PSEUDOMONAS DENITRIFICANS.//P00103

55

F-NT2RP3000825//ALPHA-LACTALBUMIN (LACTOSE SYNTHASE B PROTEIN (EC 2.4.1.22))
./0.82:51:39//MACROPUS RUFOGRISEUS (RED-NECKED WALLABY).//P07458

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F-NT2RP3000826//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS)//0.025:79:37//BOS TAURUS (BOVINE)//P25508

5 F-NT2RP3000836//HYPOTHETICAL PROTEIN IN KSGA 3'REGION (ORF L5) (FRAGMENT)
//0.85:36:47//MYCOPLASMA CAPRICOLUM//P43040

10 F-NT2RP3000841//UDP-GLUCURONOSYLTRANSFERASE 1-7 PRECURSOR,
MICROSOMAL (EC 2.4.1.17) (UDPGT) (UGT1*7) (UGT1-07) (UGT1.7) (UGT1A7) (UGTP4)
(FRAGMENT)//1.0:70:34//MUS MUSCULUS (MOUSE)//Q62452

15 F-NT2RP3000845//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-)
//5.2e-72:247:61//HOMO SAPIENS (HUMAN)//P27448

20 F-NT2RP3000847//HYPOTHETICAL PROTEIN KIAA0161//0.037:55:30//HOMO SAPIENS
(HUMAN)//P50876

F-NT2RP3000850/////ALU SUBFAMILY SQ WARNING ENTRY !!!!!//7.4e-31:90:75//HOMO
SAPIENS (HUMAN)//P39194

25 F-NT2RP3000852//HYDROPHOBIC SEED PROTEIN (HPS)//0.33:23:69//GLYCINE MAX
(SOYBEAN)//P24337

30 F-NT2RP3000859//IMMEDIATE-EARLY PROTEIN//3.6e-07:189:25//HERPESVIRUS SAIMIRI
(STRAIN 11)//Q01042

F-NT2RP3000865

35 F-NT2RP3000868//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE ISOFORM (FRAGMENT)
//1.4e-09:232:28//GALLUS GALLUS (CHICKEN)//P29616

40 F-NT2RP3000869//CUTICLE COLLAGEN 2//4.5e-08:58:46//CAENORHABDITIS
ELEGANS//P17656

45 F-NT2RP3000875//HOMEBOX PROTEIN CDX-2 (CAUDAL-TYPE HOMEBOX PROTEIN 2)
//0.90:62:37//MUS MUSCULUS (MOUSE)//P43241

F-NT2RP3000901//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS)//0.99:124:33//BOS
TAURUS (BOVINE)//P02453

50 F-NT2RP3000904

55 F-NT2RP3000917//DHP1 PROTEIN//6.5e-60:229:55//SCHIZOSACCHAROMYCES POMBE
(FISSION YEAST)//P40848

F-NT2RP3000919//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME
I//2.4e-19:159:34//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10149

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- 5 F-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A//3.7e-48:73:98//HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT).//P39027
- F-NT2RP3000980//COPA/INCA PROTEIN (REPA3 PROTEIN).//0.24:19:47//ESCHERICHIA COLI.//P13946
- 10 F-NT2RP3000994//MATERNAL EFFECT PROTEIN STAUFEN.//1.4e-10:78:48//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25159
- 15 F-NT2RP3001004//HYPOTHETICAL 7.6 KD PROTEIN B0563.8 IN CHROMOSOME X.//0.70:50:32//CAENORHABDITIS ELEGANS.//Q11084
- F-NT2RP3001007
- 20 F-NT2RP3001055//N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG.//1.3e-05:138:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P36416
- 25 F-NT2RP3001057//ZINC FINGER PROTEIN 45 (BRC1744).//4.0e-28:141:51//HOMO SAPIENS (HUMAN).//Q02386
- F-NT2RP3001081//HYPOTHETICAL 46.4 KD PROTEIN T16H12.5 IN CHROMOSOME III.//3.8e-08:144:29//CAENORHABDITIS ELEGANS.//P34568
- 30 F-NT2RP3001084//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//3.4e-06:217:32//NEPHILA CLAVIPES (ORB SPIDER).//P46804
- 35 F-NT2RP3001096//SYNAPTONEMAL COMPLEX PROTEIN SC65.//1.1e-30:244:33//RATTUS NORVEGICUS (RAT).//Q64375
- 40 F-NT2RP3001107//ARYLSULFATASE F (EC 3.1.6.-) (ASF) (FRAGMENT).//0.041:47:44//HOMO SAPIENS (HUMAN).//P54793
- F-NT2RP3001109
- 45 F-NT2RP3001111//MALE SPECIFIC SPERM PROTEIN MST84DC.//0.17:28:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01644
- 50 F-NT2RP3001113//INVOLUCRIN.//0.00036:192:23//MUS MUSCULUS (MOUSE).//P48997
- F-NT2RP3001115
- 55 F-NT2RP3001116//AMINOPEPTIDASE G (EC 3.4.11.-) (FRAGMENT).//0.99:29:51//STREPTOMYCES LIVIDANS.//Q54340
- F-NT2RP3001119//COLLAGEN ALPHA 4(IV) CHAIN (FRAGMENT).//0.0015:73:39//BOS

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TAURUS (BOVINE).//Q29442

5 F-NT2RP3001120//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//1.3e-57:229:52//HOMO
SAPIENS (HUMAN).//P16415

10 F-NT2RP3001126//HYPOTHETICAL 91.2 KD PROTEIN IN RPS4B-SCH9 INTERGENIC
REGION.//2.8e-07:83:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38888

F-NT2RP3001133//CALCIUM BINDING PROTEIN.//2.0e-08:171:32//DICTYOSTELIUM
DISCOIDEUM (SLIME MOLD).//P35085

15 F-NT2RP3001140//F-SPONDIN PRECURSOR.//2.0e-147:244:97//RATTUS NORVEGICUS
(RAT).//P35446

20 F-NT2RP3001147//TROPOMYOSIN 2 (TMII).//0.11:159:23//SCHISTOSOMA MANSONI (BLOOD
FLUKE).//P42638

F-NT2RP3001150//OCTAPEPTIDE-REPEAT PROTEIN T2.//6.2e-09:163:25//MUS MUSCULUS
(MOUSE).//Q06666

25 F-NT2RP3001155//DNA POLYMERASE ALPHA-BINDING PROTEIN (POB1/CTF4 PROTEIN)
(CHROMOSOME REPLICATION PROTEIN CHL15).//4.1e-05:244:23//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST).//Q01454

30 F-NT2RP3001176//LEUKOSIALIN PRECURSOR (LEUCOCYTE SIALOGLYCOPROTEIN)
(SIALOPHORIN) (CD43) (LY 48) (B CELL DIFFERENTIATION ANTIGEN LP-3).//0.21:136:
26//MUS MUSCULUS (MOUSE).//P15702

35 F-NT2RP3001214//SAP1 PROTEIN.//0.058:133:30//SACCHAROMYCES CEREVISIAE
(BAKER'S YEAST).//P39955

40 F-NT2RP3001216//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I) (FRAGMENT).//2.1e-08:
137:33//HOMO SAPIENS (HUMAN).//P35663

45 F-NT2RP3001221//GAMMA-BUTYROBETAINE,2-OXOGLUTARATE DIOXYGENASE (EC
1.14.11.1) (GAMMA-BUTYROBETAINE HYDROXYLASE).//4.2e-05:131:26//PSEUDOMONAS
SP. (STRAIN AK-1).//P80193

50 F-NT2RP3001232//HYPOTHETICAL PROTEIN PRECURSOR IN CS5 3'REGION
(FRAGMENT).//0.75:57:31//ESCHERICHIA COLI.//P33792

F-NT2RP3001236//TRANSFORMING PROTEIN MAF.//0.017:136:30//AVIAN
MUSCULOAPONEUROTIC FIBROSARCOMA VIRUS AS42.//P23091

55 F-NT2RP3001239//ELECTROMOTOR NEURON-ASSOCIATED PROTEIN 1 (FRAGMENT)
.//4.2e-55:221:49//TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).//P14400

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F-NT2RP3001245

5 F-NT2RP3001253//TROPOMYOSIN 2, MUSCLE THORACIC ISOFORM (TROPOMYOSIN I)
./0.0042:142:24//DROSOPHILA MELANOGASTER (FRUIT FLY)//P09491

10 F-NT2RP3001260//COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR./0.0011:89:43//HOMO
SAPIENS (HUMAN)//P53420

15 F-NT2RP3001268//ZINC FINGER PROTEIN 45 (BRC1744)./9.0e-29:194:44//HOMO SAPIENS
(HUMAN)//Q02386

F-NT2RP3001272//HYPOTHETICAL 75.2 KD PROTEIN C13F4.08C IN CHROMOSOME
I./8.2e-17:183:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10199

20 F-NT2RP3001274//SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5)
(PROTEIN PHOSPHATASE T) (PPT) (FRAGMENT)./1.7e-09:78:39//MUS MUSCULUS
(MOUSE)//Q60676

25 F-NT2RP3001281//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/7.7e-08:38:71//HOMO
SAPIENS (HUMAN)//P39188

30 F-NT2RP3001297//HYPOTHETICAL PROTEIN KIAA0281 (HA6725)./2.2e-57:159:70//HOMO
SAPIENS (HUMAN)//Q92556

35 F-NT2RP3001307//SPERM PROTAMINE P1./0.21:46:39//ORNITHORHYNCHUS ANATINUS
(DUCKBILL PLATYPUS)//P35307

F-NT2RP3001318

40 F-NT2RP3001325//ENHANCER OF RUDIMENTARY HOMOLOG./1.0:73:24//BRACHYDANIO
RERIO (ZEBRAFISH) (ZEBRA DANIO)//Q98874

45 F-NT2RP3001338//ZINC FINGER PROTEIN 29 (ZINC FINGER PROTEIN KOX26)
(FRAGMENT)./0.0021:56:35//HOMO SAPIENS (HUMAN)//P17037

F-NT2RP3001339//CITRON PROTEIN./3.6e-06:90:33//MUS MUSCULUS (MOUSE)//P49025

50 F-NT2RP3001340//HYPOTHETICAL PROTEIN UL61./7.2e-11:202:34//HUMAN
CYTOMEGALOVIRUS (STRAIN AD169)//P16818

55 F-NT2RP3001355//TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE
TRANSPORT PROTEIN) (CTP) (TRICARBOXYLATE CARRIER PROTEIN)./7.7e-16:129:
33//HOMO SAPIENS (HUMAN)//P53007

F-NT2RP3001356//RAS-RELATED PROTEIN RABA (FRAGMENT)./0.00041:66:

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28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P34141

F-NT2RP3001374

5

F-NT2RP3001383//PTB-ASSOCIATED SPLICING FACTOR (PSF).//2.5e-06:190:32//HOMO SAPIENS (HUMAN).//P23246

10

F-NT2RP3001384//CHORION PROTEIN S15.//0.00079:94:37//DROSOPHILA VIRILIS (FRUIT FLY).//P13424

15

F-NT2RP3001392//VPU PROTEIN (ORF-X PROTEIN) (UPX PROTEIN).//1.0:22:45//CAPRINE ARTHRITIS ENCEPHALITIS VIRUS (CAEV).//P31834

20

F-NT2RP3001396//HYPOTHETICAL 8.1 KD PROTEIN (ORF4).//1.0:37:32//STRAWBERRY MILD YELLOW EDGE-ASSOCIATED VIRUS (SMYEA).//Q00848

F-NT2RP3001398//KRUEPPEL-RELATED ZINC FINGER PROTEIN 2 (HKR2 PROTEIN) (FRAGMENT).//1.9e-08:45:37//HOMO SAPIENS (HUMAN).//P10073

25

F-NT2RP3001399//SSU72 PROTEIN.//7.3e-18:84:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53538

30

F-NT2RP3001407//SCY1 PROTEIN.//1.5e-08:143:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53009

35

F-NT2RP3001420//HYPOTHETICAL 7.9 KD PROTEIN.//0.25:41:26//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20542

F-NT2RP3001426//DNAJ PROTEIN.//7.5e-15:78:43//HAEMOPHILUS INFLUENZAE.//P43735

40

F-NT2RP3001427//WERNER SYNDROME HELICASE.//3.6e-13:159:33//HOMO SAPIENS (HUMAN).//Q14191

45

F-NT2RP3001428//NUCLEOPROTEIN TPR.//1.8e-53:117:99//HOMO SAPIENS (HUMAN).//P12270

F-NT2RP3001432//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.96:52:21//TARSUS SYRICHIA (TARSIER).//Q36151

50

F-NT2RP3001447//HYPOTHETICAL 5.5 KD PROTEIN IN REPLICATION ORIGIN REGION (ORF1).//0.96:45:35//ESCHERICHIA COLI.//P14505

55

F-NT2RP3001449//HOMEODOMAIN PROTEIN SAX-1 (CHOX-3) (FRAGMENT).//0.0043:53:43//GALLUS GALLUS (CHICKEN).//P19601

F-NT2RP3001453//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.0048:65:

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40//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643

5 F-NT2RP3001457//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS28.//0.55:
121:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q02767

10 F-NT2RP3001459//MYOSIN IC HEAVY CHAIN.//0.10:126:34//ACANTHAMOEBA CASTELLANII
(AMOEBA).//P10569

F-NT2RP3001472//NONHISTONE CHROMOSOMAL PROTEIN 6A.//3.0e-14:87:
43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P11632

15 F-NT2RP3001490//METALLOTHIONEIN-LIKE PROTEIN LSC54.//1.0:39:35//BRASSICA
NAPUS (RAPE).//P43402

20 F-NT2RP3001495//UBIQUITIN-PROTEIN LIGASE RSP5 (EC 6.3.2.-).//3.3e-14:148:
35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39940

25 F-NT2RP3001497//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.13:44:38//BOS
TAURUS (BOVINE).//P25508

30 F-NT2RP3001527//SPERM PROTAMINE P1.//0.35:29:37//DIDELPHIS MARSUPIALIS
VIRGINIANA (NORTH AMERICAN OPOSSUM), AND MONODELPHIS DOMESTICA (SHORT-
TAILED GREY OPOSSUM).//P35305

F-NT2RP3001529//HYPOTHETICAL 43.3 KD GTP-BINDING PROTEIN IN DACB-RPMA
INTERGENIC REGION.//3.3e-21:125:37//ESCHERICHIA COLI.//P42641

35 F-NT2RP3001538//HNF3/FH TRANSCRIPTION FACTOR GENESIS (WINGED HELIX
PROTEIN CWH-3).//0.13:53:39//GALLUS GALLUS (CHICKEN).//P79772

40 F-NT2RP3001554//ELECTROMOTOR NEURON-ASSOCIATED PROTEIN 2 (FRAGMENT)
.//2.3e-48:137:52//TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).//P14401

45 F-NT2RP3001580//GERM CELL-LESS PROTEIN.//8.2e-18:100:42//DROSOPHILA
MELANOGASTER (FRUIT FLY).//Q01820

F-NT2RP3001587//UBIQUITIN-ACTIVATING ENZYME E1-LIKE (POLYMERASE-INTERACTING
PROTEIN 2).//2.0e-47:188:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P52488

50 F-NT2RP3001589//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//7.4e-41:87:80//HOMO
SAPIENS (HUMAN).//P39193

55 F-NT2RP3001607//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:49:
32//DICENTRARCHUS LABRAX (EUROPEAN SEA BASS).//Q36362

F-NT2RP3001608//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//0.0013:

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177:25//ZEA MAYS (MAIZE)//P14918

5 F-NT2RP3001621//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.84:29:37//DROSOPHILA
MELANOGASTER (FRUIT FLY)//Q01645

F-NT2RP3001629//RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1 (P21-RAC1)
(FRAGMENTS).//0.91:57:24//CAVIA PORCELLUS (GUINEA PIG)//P80236

10 F-NT2RP3001634//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//8.9e-11:73:54//HOMO
SAPIENS (HUMAN)//P39189

15 F-NT2RP3001642//HYPOTHETICAL PROTEIN KIAA0210.//1.1e-12:117:29//HOMO SAPIENS
(HUMAN)//Q92609

20 F-NT2RP3001646//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.0092:69:34//ORGYIA
PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV)//O10341

F-NT2RP3001671//RING CANAL PROTEIN (KELCH PROTEIN).//0.0042:55:41//DROSOPHILA
MELANOGASTER (FRUIT FLY)//Q04652

25 F-NT2RP3001672

30 F-NT2RP3001676//GTP-BINDING PROTEIN LEPA (FRAGMENT).//1.2e-15:56:
62//PSEUDOMONAS FLUORESCENS.//P26843

F-NT2RP3001678//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//0.054:187:
31//NEPHILA CLAVIPES (ORB SPIDER).//P46804

35 F-NT2RP3001679//HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III.//1.5e-
07:63:44//CAENORHABDITIS ELEGANS.//P34679

40 F-NT2RP3001688//GLUCOAMYLASE S1 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-
GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE) (GAI).//1.0:83:
28//SACCHAROMYCES DIASTATICUS (YEAST).//P04065

45 F-NT2RP3001690//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//0.021:247:
24//HOMO SAPIENS (HUMAN).//P12883

50 F-NT2RP3001698

F-NT2RP3001708//TWISTED GASTRULATION PROTEIN PRECURSOR.//7.7e-12:73:
43//DROSOPHILA MELANOGASTER (FRUIT FLY).//P54356

55 F-NT2RP3001712//CEC-1 PROTEIN.//1.9e-07:121:29//CAENORHABDITIS
ELEGANS.//P34618

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- F-NT2RP3001716//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.89:54:40//DROSOPHILA SIMULANS (FRUIT FLY).//P13729
- 5 F-NT2RP3001724//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1).//7.5e-41:164:48//HOMO SAPIENS (HUMAN).//O14646
- 10 F-NT2RP3001727//HYPOTHETICAL 37.7 KD PROTEIN ZK686.3 IN CHROMOSOME III.//1.5e-51:240:41//CAENORHABDITIS ELEGANS.//P34669
- F-NT2RP3001730//SEPTIN 2 HOMOLOG (FRAGMENT).//2.4e-122:267:86//HOMO SAPIENS (HUMAN).//Q14141
- 15 F-NT2RP3001739//INTESTINAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER).//0.99:63:34//RATTUS NORVEGICUS (RAT).//P70545
- 20 F-NT2RP3001752//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/4.0e-21:60:85//HOMO SAPIENS (HUMAN).//P39193
- F-NT2RP3001753//HYPOTHETICAL PROTEIN KIAA0127.//7.9e-12:83:44//HOMO SAPIENS (HUMAN).//Q14140
- 25 F-NT2RP3001764//DUAL SPECIFICITY PROTEIN PHOSPHATASE 6 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE PYST1).//7.7e-25:146:36//HOMO SAPIENS (HUMAN).//Q16828
- 30 F-NT2RP3001777//SERINE/THREONINE-PROTEIN KINASE STE20 HOMOLOG (EC 2.7.1.-) //0.0096:204:25//CANDIDA ALBICANS (YEAST).//Q92212
- 35 F-NT2RP3001782//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.91:34:44//PONGO PYGMAEUS ABELII (SUMATRAN ORANGUTAN).//P92694
- 40 F-NT2RP3001792//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M) //1.8e-33:159:53//HOMO SAPIENS (HUMAN).//P52272
- 45 F-NT2RP3001799//LIGHT-HARVESTING PROTEIN B800/830/1020, ALPHA-2 CHAIN (EHS-ALPHA-2) (ANTENNA PIGMENT PROTEIN, ALPHA-2 CHAIN).//0.14:46:28//ECTOTHIORHODOSPIRA HALOCHLORIS.//P80103
- F-NT2RP3001819//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR.//0.00030:77:36//HOMO SAPIENS (HUMAN).//P08123
- 50 F-NT2RP3001844//OCTAMER-BINDING TRANSCRIPTION FACTOR 1 (OTF-1) (NF-A1) (FRAGMENT).//0.99:43:34//MACROPUS EUGENII (TAMMAR WALLABY).//Q28466
- 55 F-NT2RP3001854//FIBRINOGEN- AND IG-BINDING PROTEIN PRECURSOR (MRP PROTEIN).//9.3e-10:213:24//STREPTOCOCCUS PYOGENES.//P30141

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- 5 F-NT2RP3001855//HOMEBOX PROTEIN PKNOX1 (HOMEBOX PROTEIN PREP-1)//2.6e-61:220:60//HOMO SAPIENS (HUMAN)//P55347
- 5 F-NT2RP3001857//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1//1.0e-13:213:24//PODOSPORA ANSERINA//Q00808
- 10 F-NT2RP3001896//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66)//0.074:124:34//HOMO SAPIENS (HUMAN)//Q15428
- 15 F-NT2RP3001898//REGULATORY PROTEIN E2//0.36:131:29//CANINE ORAL PAPILLOMAVIRUS (COPV)//Q89420
- 20 F-NT2RP3001915//CHITIN BIOSYNTHESIS PROTEIN CHS5 (CAL3 PROTEIN)//0.0021:237:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q12114
- 20 F-NT2RP3001926//HYPOTHETICAL 14.0 KD PROTEIN IN RPL15B-GCR3 INTERGENIC REGION//1.0:63:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q03880
- 25 F-NT2RP3001929//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.4e-14:35:60//HOMO SAPIENS (HUMAN)//P39195
- 30 F-NT2RP3001931//HYPOTHETICAL 59.3 KD PROTEIN IN TAP42-ARP9 INTERGENIC REGION//0.86:162:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q05040
- 35 F-NT2RP3001938//GLYCOPROTEIN GP50//0.0036:54:40//PSEUDORABIES VIRUS (STRAIN RICE) (PRV)//P07645
- 35 F-NT2RP3001943//33.2 KD PROTEIN IN DIND-RPH INTERGENIC REGION (ORF X)//1.0:113:27//ESCHERICHIA COLI//P23839
- 40 F-NT2RP3001944//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III//4.1e-56:208:47//CAENORHABDITIS ELEGANS//Q09251
- 45 F-NT2RP3001969//PUFF II/9-2 PROTEIN PRECURSOR//0.0078:149:26//SCIARA COPROPHILA (FUNGUS GNAT)//P22312
- 50 F-NT2RP3001989//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE)//1.0:41:31//MUS MUSCULUS (MOUSE)//P02319
- 50 F-NT2RP3002002//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.2e-44:69:79//HOMO SAPIENS (HUMAN)//P39195
- 55 F-NT2RP3002004//TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2)//0.00024:45:40//MUS MUSCULUS (MOUSE)//Q61345

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- 5 F-NT2RP3002007//TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN)
(NEURONECTIN) (GMEM) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-
EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C).//0.21:115:28//HOMO
SAPIENS (HUMAN).//P24821
- 10 F-NT2RP3002014//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III.//1.7e-
25:139:48//CAENORHABDITIS ELEGANS.//Q09232
- 15 F-NT2RP3002033//ACTIVATOR OF APOPTOSIS HAKIRI (NEURONAL DEATH PROTEIN
DP5).//0.14:65:41//HOMO SAPIENS (HUMAN).//O00198
- 20 F-NT2RP3002045//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2
ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE
ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT).//8.1e-108:192:98//MUS MUSCULUS
(MOUSE).//P17427
- 25 F-NT2RP3002054//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.046:
176:31//STREPTOMYCES FRADIAE.//P20186
- 30 F-NT2RP3002056//140 KD NUCLEOLAR PHOSPHOPROTEIN (NOPP140).//1.4e-07:245:
25//RATTUS NORVEGICUS (RAT).//P41777
- 35 F-NT2RP3002057//SMALL HYDROPHOBIC PROTEIN.//1.0:12:66//SIMIAN VIRUS 5 (STRAIN
W3) (SV5).//P07577
- 40 F-NT2RP3002062//PROTEASE A INHIBITOR 3 (PROTEINASE INHIBITOR I(A)3).//1.0:49:
32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P01094
- 45 F-NT2RP3002063//ACYL CARRIER PROTEIN (ACP).//0.99:38:31//HAEMOPHILUS
INFLUENZAE.//P43709
- 50 F-NT2RP3002081//HYPOTHETICAL 100.5 KD PROTEIN C1B9.04 IN CHROMOSOME I.//5.8e-
35:253:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10429
- 55 F-NT2RP3002097//HYPOTHETICAL 98.1 KD PROTEIN IN SPX19-GCR2 INTERGENIC
REGION.//6.2e-06:99:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40164
- F-NT2RP3002102//HYPOTHETICAL 7.4 KD PROTEIN.//0.68:34:47//THERMOPROTEUS
TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19302
- F-NT2RP3002108//HYPOTHETICAL 105.5 KD PROTEIN R13F6.10 IN CHROMOSOME
III.//7.9e-19:179:34//CAENORHABDITIS ELEGANS.//Q21986
- 55 F-NT2RP3002142//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.6e-17:37:75//HOMO
SAPIENS (HUMAN).//P39188

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- F-NT2RP3002146//CUTICLE COLLAGEN 40.//0.00034:90:37//CAENORHABDITIS ELEGANS.//P34804
- 5 F-NT2RP3002147//SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR (ALLELE S) .//0.011:166:28//HOMO SAPIENS (HUMAN).//P10163
- 10 F-NT2RP3002151//G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG (GTP-BINDING PROTEIN GST1-HS).//4.8e-11:60:53//HOMO SAPIENS (HUMAN).//P15170
- 15 F-NT2RP3002163//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//0.028:191:29//HOMO SAPIENS (HUMAN).//O00268
- F-NT2RP3002165//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP.//2.3e-131:223:91//MUS MUSCULUS (MOUSE).//Q02614
- 20 F-NT2RP3002166//D-ALANYL CARRIER PROTEIN (DCP).//1.0:65:33//LACTOBACILLUS CASEI.//P55153
- 25 F-NT2RP3002173//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.4e-26:114:62//HOMO SAPIENS (HUMAN).//P39194
- F-NT2RP3002181//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.25:31:38//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645
- 30 F-NT2RP3002244//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//0.069:16:62//OVIS ARIES (SHEEP), AND CAPRA HIRCUS (GOAT).//P04102
- 35 F-NT2RP3002248//MICROFIBRILLAR-ASSOCIATED PROTEIN 1 (ASSOCIATED MICROFIBRIL PROTEIN) (AMF).//0.0079:187:24//GALLUS GALLUS (CHICKEN).//P55080
- 40 F-NT2RP3002255//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//4.6e-10:168:34//MUS MUSCULUS (MOUSE).//P05143
- 45 F-NT2RP3002273//SCD6 PROTEIN.//1.5e-11:160:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P45978
- F-NT2RP3002276//PROBABLE E4 PROTEIN.//0.91:54:29//HUMAN PAPILLOMAVIRUS TYPE 16.//P06922
- 50 F-NT2RP3002303//HYPOTHETICAL 30.2 KD PROTEIN C4D7.04C IN CHROMOSOME I.//1.7e-42:191:43//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14171
- 55 F-NT2RP3002304
- F-NT2RP3002330//NNP-1 PROTEIN.//0.52:140:18//MUS MUSCULUS (MOUSE).//P56183

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F-NT2RP3002343//5E5 ANTIGEN.//0.0056:189:30//RATTUS NORVEGICUS (RAT).//Q63003

5 F-NT2RP3002351//NAD-DEPENDENT METHYLENETETRAHYDROFOLATE
DEHYDROGENASE (EC 1.5.1.15) / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE
(EC 3.5.4.9) MITOCHONDRIAL PRECURSOR.//1.0e-66:196:68//HOMO SAPIENS (HUMAN)
./P13995

10 F-NT2RP3002352//PRESYNAPTIC PROTEIN SAP102 (SYNAPSE-ASSOCIATED PROTEIN
102) (NEUROENDOCRINE-DLG) (NE-DLG).//0.79:173:27//HOMO SAPIENS (HUMAN)
./Q92796

15 F-NT2RP3002377//PUTATIVE HELICASE YGR271W.//1.0e-56:216:44//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST).//P53327

20 F-NT2RP3002399//MINICHROMOSOME MAINTENANCE PROTEIN 6.//1.4e-19:136:
31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53091

F-NT2RP3002402//EBNA-6 NUCLEAR PROTEIN (EBNA-3C) (EBNA-4B).//0.74:107:
36//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03204

25 F-NT2RP3002455//DNAJ PROTEIN (FRAGMENT).//5.6e-06:57:42//AGROBACTERIUM
TUMEFACIENS.//P50018

30 F-NT2RP3002484//HYPOTHETICAL 46.5 KD PROTEIN C12B10.04 IN CHROMOSOME
I.//0.00032:52:48//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10438

35 F-NT2RP3002501//HYPOTHETICAL 34.9 KD PROTEIN IN FRE2-JEN1 INTERGENIC
REGION.//9.4e-42:209:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36007

F-NT2RP3002512//HYPOTHETICAL 37.4 KD PROTEIN IN GPM1-MCR1 INTERGENIC
REGION.//7.7e-32:162:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36059

40 F-NT2RP3002529//PUTATIVE VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN
C2G11.03C.//2.1e-45:241:43//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09805

45 F-NT2RP3002545

F-NT2RP3002549//HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III.//2.8e-
41:161:52//CAENORHABDITIS ELEGANS.//Q10010

50 F-NT2RP3002566//IMMEDIATE-EARLY PROTEIN IE180.//0.56:130:24//PSEUDORABIES
VIRUS (STRAIN KAPLAN) (PRV).//P33479

55 F-NT2RP3002587

F-NT2RP3002590

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- 5 F-NT2RP3002602//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1)
(THIOREDOXIN- RELATED GLYCOPROTEIN 1).//0.00091:111:28//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST).//P17967
- 10 F-NT2RP3002603//HYPOTHETICAL 14.2 KD PROTEIN IN BLAB 3'REGION.//1.0:65:
40//STREPTOMYCES CACAOI.//P33654
- 15 F-NT2RP3002628//DNAJ-LIKE PROTEIN SLR0093.//2.4e-17:101:44//SYNECHOCYSTIS SP.
(STRAIN PCC 6803).//P50027
- 20 F-NT2RP3002631//METALLOTHIONEIN-IB (MT-1B).//0.092:36:33//HOMO SAPIENS (HUMAN)
.//P07438
- 25 F-NT2RP3002650//DUALIN.//3.0e-21:184:37//GALLUS GALLUS (CHICKEN).//Q90830
- 30 F-NT2RP3002659//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR.//0.00016:223:
33//HOMO SAPIENS (HUMAN).//P08123
- 35 F-NT2RP3002660//40S RIBOSOMAL PROTEIN S27A.//0.16:72:31//CAENORHABDITIS
ELEGANS.//P37165
- 40 F-NT2RP3002663//OXYSTEROL-BINDING PROTEIN.//5.4e-23:168:41//HOMO SAPIENS
(HUMAN).//P22059
- 45 F-NT2RP3002671//HYPOTHETICAL 124.5 KD PROTEIN IN SKO1-RPL44A INTERGENIC
REGION.//6.0e-38:203:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53893
- 50 F-NT2RP3002682//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.25:
63:31//ARTEMIA SALINA (BRINE SHRIMP).//P19049
- 55 F-NT2RP3002687//HYPOTHETICAL 30.4 KD PROTEIN IN LEF3-IAP2 INTERGENIC
REGION.//0.029:60:36//AUTOGRAPHIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS
(ACMPV).//P41469
- F-NT2RP3002688//KINESIN-LIKE PROTEIN KIF1B.//5.3e-61:130:88//MUS MUSCULUS
(MOUSE).//Q60575
- F-NT2RP3002701//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//7.4e-05:
109:33//MUS MUSCULUS (MOUSE).//P15265
- F-NT2RP3002713//PROBABLE ATP-DEPENDENT RNA HELICASE DDX10 (DEAH BOX
PROTEIN 10).//0.77:70:32//HOMO SAPIENS (HUMAN).//Q13206
- F-NT2RP3002763//HYPOTHETICAL 11.3 KD PROTEIN C2C6.07 IN CHROMOSOME I.//6.7e-
11:66:40//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14056

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- 5 F-NT2RP3002770//COLLAGEN ALPHA 1(IX) CHAIN (FRAGMENT).//0.33:87:34//MUS MUSCULUS (MOUSE).//Q05722
- 5 F-NT2RP3002785//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//9.7e-36:187:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24371
- 10 F-NT2RP3002799//!!!! ALU SUBFAMILY J WARNING ENTRY!!!!//5.6e-08:41:73//HOMO SAPIENS (HUMAN).//P39188
- 15 F-NT2RP3002810//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//0.0034:35:65//HOMO SAPIENS (HUMAN).//P39193
- 20 F-NT2RP3002818//MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B).//3.2e-17:148:37//MUS MUSCULUS (MOUSE).//P27790
- 25 F-NT2RP3002861//HYPOTHETICAL 70.2 KD PROTEIN IN GSH1-CHS6 INTERGENIC REGION.//1.7e-05:95:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P42951
- 25 F-NT2RP3002869//TRYPSIN INHIBITOR II (BDTI-II).//0.97:23:39//BRYONIA DIOICA (RED BRYONY).//P11968
- 30 F-NT2RP3002876//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33) .//0.00017:140:31//RATTUS NORVEGICUS (RAT).//P04474
- 35 F-NT2RP3002877//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.5e-06:55:60//HOMO SAPIENS (HUMAN).//P39194
- 40 F-NT2RP3002909//P53-BINDING PROTEIN 53BP2 (BCL2-BINDING PROTEIN) (BBP).//4.6e-08:129:38//HOMO SAPIENS (HUMAN).//Q13625
- 40 F-NT2RP3002911//HYPOTHETICAL PROTEIN C18.//0.99:26:50//SWINEPOX VIRUS (STRAIN KASZA) (SPV).//P32217
- 45 F-NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-23:113:47//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
- 50 F-NT2RP3002953//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//0.55:116:27//DROSOPHILA MELANOGASTER (FRUIT FLY).//P33450
- 50 F-NT2RP3002955//HYPOTHETICAL 16.5 KD PROTEIN IN BLTR-SPOIIIIC INTERGENIC REGION.//0.87:67:37//BACILLUS SUBTILIS.//P54445
- 55 F-NT2RP3002969//LONG-CHAIN-FATTY-ACID-COA LIGASE 4 (EC 6.2.1.3) (LONG-CHAIN ACYL-COA SYNTHETASE 4) (LACS 4).//6.7e-56:189:59//HOMO SAPIENS (HUMAN).//O60488

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F-NT2RP3002972//HYPOTHETICAL 73.0 KD PROTEIN IN CLA4-MID1 INTERGENIC REGION.//0.0028:147:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48566

5 F-NT2RP3002978//PROBABLE E5 PROTEIN.//0.15:55:36//HUMAN PAPILLOMAVIRUS TYPE 51.//P26553

10 F-NT2RP3002985//METALLOTHIONEIN (MT).//0.0031:49:42//PLEURONECTES PLATESSA (PLAICE).//P07216

15 F-NT2RP3002988//NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR (MOTCH PROTEIN).//1.0:111:29//MUS MUSCULUS (MOUSE).//Q01705

F-NT2RP3003008//HYPOTHETICAL 54.7 KD PROTEIN F37A4.1 IN CHROMOSOME III.//0.96:112:25//CAENORHABDITIS ELEGANS.//P41879

20 F-NT2RP3003032

F-NT2RP3003059//HYPOTHETICAL 52.3 KD PROTEIN C56F8.06C IN CHROMOSOME I PRECURSOR.//9.7e-27:216:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10254

30 F-NT2RP3003061//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//3.7e-25:167:34//HOMO SAPIENS (HUMAN).//P16157

F-NT2RP3003068//SERYL-TRNA SYNTHETASE (EC 6.1.1.11) (SERINE-TRNA LIGASE) (SERRS) (FRAGMENT).//0.074:82:39//SULFOLOBUS SOLFATARICUS.//O33780

35 F-NT2RP3003071//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//0.0085:128:30//HOMO SAPIENS (HUMAN).//P50552

40 F-NT2RP3003078//SPERM ACROSOMAL PROTEIN FSA-ACR.1 PRECURSOR (FRAGMENT).//0.028:165:31//VULPES VULPES (RED FOX).//P53353

45 F-NT2RP3003101//TETRACYCLINE RESISTANCE PROTEIN, CLASS C (TETA(C)).//1.0e-14:243:25//ESCHERICHIA COLI.//P02981

F-NT2RP3003121//SUPPRESSOR PROTEIN SRP40.//7.4e-05:143:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583

50 F-NT2RP3003133//65 KD YES-ASSOCIATED PROTEIN (YAP65).//0.024:61:42//GALLUS GALLUS (CHICKEN).//P46936

55 F-NT2RP3003138//KINESIN-LIKE PROTEIN KIF4.//1.1e-118:151:93//MUS MUSCULUS (MOUSE).//P33174

F-NT2RP3003139//ATP-BINDING CASSETTE TRANSPORTER ABC1.//1.0:70:

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30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q92337

5 F-NT2RP3003145//MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (HMFG)
(BREAST EPITHELIAL ANTIGEN BA46) (MFGM).//2.0e-12:121:37//HOMO SAPIENS (HUMAN)
//Q08431

10 F-NT2RP3003150

F-NT2RP3003157//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//4.0e-79:
260:54//HOMO SAPIENS (HUMAN).//P51522

15 F-NT2RP3003185//TROPOMYOSIN.//0.077:122:27//SCHIZOSACCHAROMYCES POMBE
(FISSION YEAST).//Q02088

20 F-NT2RP3003193//ZINC FINGER PROTEIN 135.//7.2e-91:239:65//HOMO SAPIENS (HUMAN)
//P52742

F-NT2RP3003197//HYPOTHETICAL 28.1 KD PROTEIN IN SIPU-PBPC INTERGENIC
25 REGION.//1.3e-07:117:34//BACILLUS SUBTILIS.//P42966

F-NT2RP3003203//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME
I.//9.9e-23:132:39//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10149

30 F-NT2RP3003204//RAS-LIKE PROTEIN RASB.//0.92:103:27//DICTYOSTELIUM DISCOIDEUM
(SLIME MOLD).//P32252

F-NT2RP3003210//VERY HYPOTHETICAL 13.2 KD PROTEIN IN PTC3-SAS3 INTERGENIC
35 REGION.//0.23:106:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38190

F-NT2RP3003212//SUPPRESSOR PROTEIN SRP40.//0.019:171:23//SACCHAROMYCES
40 CEREVISIAE (BAKER'S YEAST).//P32583

F-NT2RP3003230//CORONIN-LIKE PROTEIN P57.//8.3e-74:183:73//BOS TAURUS (BOVINE)
//Q92176

45 F-NT2RP3003242//STANNIOCALCIN PRECURSOR.//1.4e-21:127:37//HOMO SAPIENS
(HUMAN).//P52823

50 F-NT2RP3003251//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR.//3.1e-
51:198:52//MUS MUSCULUS (MOUSE).//P15533

F-NT2RP3003264//E6 PROTEIN.//1.0:31:41//HUMAN PAPILLOMAVIRUS TYPE 48.//Q80920

55 F-NT2RP3003278//45.8 KD PROTEIN IN SHM1-MRPL37 INTERGENIC REGION.//8.6e-07:80:
33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38344

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F-NT2RP3003282//DYNAMIN 2 (DYNAMIN UDNM)//8.0e-108:226:88//MUS MUSCULUS (MOUSE)//P39054

5 F-NT2RP3003290//BIOH PROTEIN//0.0055:107:30//ESCHERICHIA COLI//P13001

F-NT2RP3003301//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-)//1.3e-69:200:55//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//O64948

10

F-NT2RP3003302//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//6.4e-69:102:66//HOMO SAPIENS (HUMAN)//P08547

15 F-NT2RP3003311//MYOSIN II HEAVY CHAIN, NON MUSCLE//0.18:225:26//ACANTHAMOEBA CASTELLANII (AMOEBA)//P05659

20 F-NT2RP3003313//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT)//0.0014:142:33//HOMO SAPIENS (HUMAN)//P10162

F-NT2RP3003327//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52)//8.8e-18:94:43//MUS MUSCULUS (MOUSE)//Q62191

25

F-NT2RP3003330//HYPOTHETICAL PROTEIN KIAA0176 (FRAGMENT)//1.3e-20:123:44//HOMO SAPIENS (HUMAN)//Q14681

30 F-NT2RP3003344//HYPOTHETICAL 8.8 KD PROTEIN IN ICDC-MINE INTERGENIC REGION//1.0:28:42//ESCHERICHIA COLI//P75991

35 F-NT2RP3003346//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!//6.9e-26:74:78//HOMO SAPIENS (HUMAN)//P39191

F-NT2RP3003353//HYPOTHETICAL 52.4 KD PROTEIN R08D7.2 IN CHROMOSOME III//3.7e-10:118:33//CAENORHABDITIS ELEGANS//P30641

40

F-NT2RP3003377//PUTATIVE CUTICLE COLLAGEN F09G8.6//1.5e-05:102:37//CAENORHABDITIS ELEGANS//P34391

45 F-NT2RP3003384

F-NT2RP3003385//SKD3 PROTEIN//5.1e-83:210:69//MUS MUSCULUS (MOUSE)//Q60649

50 F-NT2RP3003403

F-NT2RP3003409//SOX-22 PROTEIN//0.042:173:28//HOMO SAPIENS (HUMAN)//O15370

55 F-NT2RP3003411//PROBABLE E3 PROTEIN//0.17:91:31//BOVINE PAPILLOMAVIRUS TYPE 2//P11300

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- F-NT2RP3003427//HOLOTRICIN 3 PRECURSOR.//0.012:36:41//HOLOTRICHIA
DIOMPHALIA.//Q25055
- 5 F-NT2RP3003433
- F-NT2RP3003464//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC
REGION.//0.0042:110:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214
- 10 F-NT2RP3003490
- F-NT2RP3003491//10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES) (HEAT
SHOCK 10 KD PROTEIN).//0.99:49:34//LEPTOSPIRA INTERROGANS.//P35472
- 15 F-NT2RP3003500//SCY1 PROTEIN.//6.8e-14:192:26//SACCHAROMYCES CEREVISIAE
(BAKER'S YEAST).//P53009
- 20 F-NT2RP3003543//COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR.//0.0026:175:30//HOMO
SAPIENS (HUMAN).//P29400
- 25 F-NT2RP3003552//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.19:21:47//BOS TAURUS
(BOVINE).//P20072
- F-NT2RP3003555//HYPOTHETICAL 32.6 KD PROTEIN IN MET30-PIG2 INTERGENIC
REGION.//7.3e-27:159:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40529
- 30 F-NT2RP3003564//RNA REPLICASE POLYPROTEIN (EC 2.7.7.48).//1.0:99:30//TURNIP
YELLOW MOSAIC VIRUS.//P10358
- 35 F-NT2RP3003572//PUTATIVE CUTICLE COLLAGEN F09G8.6.//0.33:128:
32//CAENORHABDITIS ELEGANS.//P34391
- 40 F-NT2RP3003576//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//7.1e-28:58:77//HOMO
SAPIENS (HUMAN).//P39195
- F-NT2RP3003589//RAS-RELATED PROTEIN RAB-10.//5.4e-54:114:94//CANIS FAMILIARIS
(DOG).//P24409
- 45 F-NT2RP3003621//COAGULATION FACTOR XII PRECURSOR (EC 3.4.21.38) (HAGEMAN
FACTOR) (HAF).//2.0e-15:89:40//HOMO SAPIENS (HUMAN).//P00748
- 50 F-NT2RP3003625//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.99:22:50//DROSOPHILA
MELANOGASTER (FRUIT FLY).//Q01645
- 55 F-NT2RP3003656//HOMEBOX PROTEIN OTX3 (ZOTX3).//0.30:111:25//BRACHYDANIO
RERIO (ZEBRAFISH) (ZEBRA DANIO).//Q90267

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- F-NT2RP3003659//HYPOTHETICAL 49.8 KD PROTEIN IN RPL14B-GPA1 INTERGENIC REGION.//1.1e-20:127:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38755
- 5 F-NT2RP3003665//PENAEIDIN-3C PRECURSOR (P3-C).//0.34:52:34//PENAEUS VANNAMEI (PENOEID SHRIMP) (EUROPEAN WHITE SHRIMP).//P81060
- 10 F-NT2RP3003672//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7).//8.7e-15:146:42//HOMO SAPIENS (HUMAN).//P14209
- 15 F-NT2RP3003680//HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION.//4.3e-25:159:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43601
- F-NT2RP3003686//NONHISTONE CHROMOSOMAL PROTEIN HMG-17.//0.067:63:31//GALLUS GALLUS (CHICKEN).//P02314
- 20 F-NT2RP3003701//F-SPONDIN PRECURSOR.//1.8e-13:193:27//RATTUS NORVEGICUS (RAT).//P35446
- 25 F-NT2RP3003716//SLIT PROTEIN PRECURSOR.//1.3e-12:150:34//DROSOPHILA MELANOGASTER (FRUIT FLY).//P24014
- 30 F-NT2RP3003726//INSERTION ELEMENT IS136 HYPOTHETICAL 16.9 KD PROTEIN).//0.47:109:28//AGROBACTERIUM TUMEFACIENS.//P05680
- F-NT2RP3003746//HYPOTHETICAL 7.7 KD PROTEIN IN FIXX 3'REGION (ORF1).//0.57:34:38//AZORHIZOBIUM CAULINODANS.//P26486
- 35 F-NT2RP3003795//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//4.3e-10:40:90//HOMO SAPIENS (HUMAN).//P39195
- 40 F-NT2RP3003799//MATING-TYPE PHEROMONE BBP1(3) PRECURSOR.//0.75:60:36//SCHIZOPHYLLUM COMMUNE (BRACKET FUNGUS).//P78744
- 45 F-NT2RP3003800//PROTO-ONCOGENE TYROSINE-PROTEIN KINASE SRC (EC 2.7.1.112) (P60-SRC).//4.2e-51:72:95//GALLUS GALLUS (CHICKEN).//P00523
- F-NT2RP3003805//HYPOTHETICAL 32.1 KD PROTEIN IN DBP7-GCN3 INTERGENIC REGION.//0.00069:160:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36121
- 50 F-NT2RP3003809//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENTS).//0.028:135:35//GALLUS GALLUS (CHICKEN).//P12105
- 55 F-NT2RP3003819//C-HORDEIN (PCP387) (FRAGMENT).//0.0026:90:33//HORDEUM VULGARE (BARLEY).//P06472
- F-NT2RP3003825//PHOSPHATIDYLCHOLINE TRANSFER PROTEIN (PC-TP).//5.6e-20:174:

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31//BOS TAURUS (BOVINE).//P02720

5 F-NT2RP3003828//ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHATE-
LYASE) (CA(2+)-INHIBITABLE ADENYLYL CYCLASE).//0.0017:111:38//CANIS FAMILIARIS
(DOG).//P30803

10 F-NT2RP3003831//ENDONUCLEASE G PRECURSOR (EC 3.1.30.-) (ENDO G).//1.1e-37:187:
42//MUS MUSCULUS (MOUSE).//O08600

15 F-NT2RP3003833//HYPOTHETICAL 6.4 KD PROTEIN IN INTE-PIN INTERGENIC
REGION.//1.0:38:39//ESCHERICHIA COLI.//P75979

F-NT2RP3003842

20 F-NT2RP3003846//RETINAL DEGENERATION B PROTEIN (PROBABLE CALCIUM
TRANSPORTER RDGB).//0.61:54:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//P43125

25 F-NT2RP3003870//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.83:51:37//DROSOPHILA
MELANOGASTER (FRUIT FLY).//Q01643

F-NT2RP3003876//PROTEIN TRANSPORT PROTEIN SEC2.//0.0017:151:
27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P17065

30 F-NT2RP3003914//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE
PRECURSOR (EC 2.4.1.-) (DUGT).//3.3e-23:76:64//DROSOPHILA MELANOGASTER (FRUIT
FLY).//Q09332

35 F-NT2RP3003918//VESICLE-ASSOCIATED MEMBRANE PROTEIN/SYNAPTOBREVIN
BINDING PROTEIN (VAP-33).//5.5e-45:127:69//APLYSIA CALIFORNICA (CALIFORNIA SEA
HARE).//Q16943

40 F-NT2RP3003932

45 F-NT2RP3003989//PREPROTEIN TRANSLOCASE SECE SUBUNIT.//0.96:46:
32//THERMOTOGA MARITIMA.//P35874

F-NT2RP3003992//NUCLEAR LOCALIZATION SEQUENCE BINDING PROTEIN (P67)
.//0.0011:170:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P27476

50 F-NT2RP3004013//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA
ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1).//3.6e-21:134:45//RATTUS
NORVEGICUS (RAT).//P51400

55 F-NT2RP3004016//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC
REGION.//0.00021:64:40//AUTOGRAPHIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS
(ACMNPV).//P41479

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F-NT2RP3004041//SPERM PROTAMINE P1.//0.0028:43:46//ORNITHORHYNCHUS
 ANATINUS (DUCKBILL PLATYPUS).//P35307
 5
 F-NT2RP3004051//MICROBIAL COLLAGENASE PRECURSOR (EC 3.4.24.3) (120 KD
 COLLAGENASE).//0.0079:194:24//CLOSTRIDIUM PERFRINGENS.//P43153
 10
 F-NT2RP3004070//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.4e-11:51:72//HOMO
 SAPIENS (HUMAN).//P39188
 F-NT2RP3004078//DNA BINDING PROTEIN RFX2.//2.7e-114:243:87//MUS MUSCULUS
 15 (MOUSE).//P48379
 F-NT2RP3004093//HYPOTHETICAL 32.3 KD PROTEIN IN RHSE-NARV INTERGENIC
 REGION (ORFB).//8.0e-13:111:41//ESCHERICHIA COLI.//P37757
 20
 F-NT2RP3004095//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.5e-17:72:65//HOMO
 SAPIENS (HUMAN).//P39188
 25
 F-NT2RP3004110//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.6e-10:51:72//HOMO
 SAPIENS (HUMAN).//P39195
 F-NT2RP3004125//ZINC FINGER PROTEIN 75.//1.1e-28:118:47//HOMO SAPIENS (HUMAN)
 30 .//P51815
 F-NT2RP3004145//AEROLYSIN REGULATORY PROTEIN.//0.012:45:33//AEROMONAS
 SOBRIA.//P09165
 35
 F-NT2RP3004148//METALLOTHIONEIN-I (MT-1).//0.055:18:50//COLUMBA LIVIA (DOMESTIC
 PIGEON).//P15786
 40
 F-NT2RP3004155//UBIQUINONE BIOSYNTHESIS PROTEIN COQ7 HOMOLOG.//1.7e-82:178:
 89//RATTUS NORVEGICUS (RAT).//Q63619
 F-NT2RP3004189//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.7e-11:215:
 45 24//PODOSPORA ANSERINA.//Q00808
 F-NT2RP3004206//CROOKED NECK PROTEIN.//3.8e-101:241:73//DROSOPHILA
 MELANOGASTER (FRUIT FLY).//P17886
 50
 F-NT2RP3004207//CUTICLE COLLAGEN 12 PRECURSOR.//0.13:130:
 33//CAENORHABDITIS ELEGANS.//P20630
 55
 F-NT2RP3004209//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15)
 (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4)
 (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//6.5e-16:

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207:29//HOMO SAPIENS (HUMAN).//Q13107

5 F-NT2RP3004215//PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT.//1.0:69:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P35179

10 F-NT2RP3004242//HYPOTHETICAL 30.2 KD PROTEIN ZK632.12 IN CHROMOSOME III.//1.1e-64:191:63//CAENORHABDITIS ELEGANS.//P34657

F-NT2RP3004246//RING3 PROTEIN (KIAA9001).//0.060:101:28//HOMO SAPIENS (HUMAN).//P25440

15 F-NT2RP3004253//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//1.1e-07:184:35//BOS TAURUS (BOVINE).//P02453

20 F-NT2RP3004258//SUPPRESSOR PROTEIN SRP40.//4.9e-08:98:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583

25 F-NT2RP3004262//DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40).//1.6e-63:210:61//HOMO SAPIENS (HUMAN).//P25685

F-NT2RP3004282//HYPOTHETICAL PROTEIN F44G4.1 IN CHROMOSOME II (FRAGMENT).//1.6e-29:177:38//CAENORHABDITIS ELEGANS.//P54073

30 F-NT2RP3004332//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).//0.030:118:36//CRICETULUS GRISEUS (CHINESE HAMSTER).//P11414

35 F-NT2RP3004334

40 F-NT2RP3004341//ALPHA-INTERNEXIN (ALPHA-INX).//0.91:110:26//MUS MUSCULUS (MOUSE).//P46660

F-NT2RP3004348//HYPOTHETICAL 105.3 KD PROTEIN C01G6.5 IN CHROMOSOME III.//0.60:198:24//CAENORHABDITIS ELEGANS.//P46012

45 F-NT2RP3004349//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.0e-37:60:76//HOMO SAPIENS (HUMAN).//P39193

50 F-NT2RP3004378//HYPOTHETICAL 18.8 KD PROTEIN IN GNTR-GGT INTERGENIC REGION (O162).//0.0026:76:28//ESCHERICHIA COLI.//P46854

55 F-NT2RP3004399//LEUCINE-RICH PRIMARY RESPONSE PROTEIN 1 (FOLLICLE-STIMULATING HORMONE PRIMARY RESPONSE PROTEIN).//4.4e-109:212:96//HOMO SAPIENS (HUMAN).//Q92674

F-NT2RP3004424//JTV-1 PROTEIN.//4.5e-18:60:70//HOMO SAPIENS (HUMAN).//Q13155 F-

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NT2RP3004428//METALLOTHIONEIN-A (MTA)//0.0010:36:47//STRONGYLOCENTROTUS
PURPURATUS (PURPLE SEA URCHIN)//P04734

- 5 F-NT2RP3004451//MYOSIN IC HEAVY CHAIN//0.00072:113:34//ACANTHAMOEBA
CASTELLANII (AMOEBIA)//P10569
- 10 F-NT2RP3004454//VERPROLIN//3.3e-07:156:29//SACCHAROMYCES CEREVISIAE
(BAKER'S YEAST)//P37370
- 15 F-NT2RP3004466//HYPOTHETICAL PROTEIN F-215//0.0013:125:32//HUMAN ADENOVIRUS
TYPE 2//P03291
- 20 F-NT2RP3004472//GERM CELL-LESS PROTEIN//7.3e-33:170:40//DROSOPHILA
MELANOGASTER (FRUIT FLY)//Q01820
- 25 F-NT2RP3004475//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131)//8.4e-54:
214:46//HOMO SAPIENS (HUMAN)//P98171
- 30 F-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35//3.9e-
47:199:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P34110
- 35 F-NT2RP3004490//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
//0.0013:121:33//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P17437
- 40 F-NT2RP3004498//HYPOTHETICAL 43.5 KD PROTEIN IN COTD-KDUD INTERGENIC
REGION PRECURSOR//0.066:87:35//BACILLUS SUBTILIS//P50840
- 45 F-NT2RP3004503//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.0e-34:102:69//HOMO
SAPIENS (HUMAN)//P39194
- 50 F-NT2RP3004504//SUPPRESSOR PROTEIN SRP40//0.64:93:34//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST)//P32583
- 55 F-NT2RP3004507//MOB1 PROTEIN (MPS1 BINDER 1)//2.2e-16:90:42//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST)//P40484
- F-NT2RP3004527
- F-NT2RP3004534//S-PHASE ENTRY CYCLIN 6//0.38:148:22//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST)//P32943
- F-NT2RP3004539//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR
(IGFBP-1) (IBP-1) (IGF-BINDING PROTEIN 1)//0.38:89:38//RATTUS NORVEGICUS (RAT)

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//P21743

5 F-NT2RP3004544//CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 2
(CYTADHERENCE ACCESSORY PROTEIN 2)//0.0024:200:24//MYCOPLASMA
PNEUMONIAE//P75471

10 F-NT2RP3004566//GASTRULA ZINC FINGER PROTEIN XLCGF17.1 (FRAGMENT)//4.6e-25:
126:43//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P18713

F-NT2RP3004569//ANKYRIN//8.3e-07:150:28//MUS MUSCULUS (MOUSE)//Q02357

15 F-NT2RP3004572//TRANSCRIPTION INITIATION FACTOR TFIID 150 KD SUBUNIT (TAFII-
150) (TAFII150)//1.6e-70:247:54//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q24325

20 F-NT2RP3004578//CENTROMERIC PROTEIN E (CENP-E PROTEIN)//1.5e-10:210:
26//HOMO SAPIENS (HUMAN)//Q02224

F-NT2RP3004594//P54 PROTEIN PRECURSOR//0.0044:230:24//ENTEROCOCCUS
25 FAECIUM (STREPTOCOCCUS FAECIUM)//P13692

F-NT2RP3004617//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR//1.5e-
14:113:34//MUS MUSCULUS (MOUSE)//P15533

30 F-NT2RP3004618//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME
III//4.5e-08:149:30//CAENORHABDITIS ELEGANS//P34681

35 F-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEIN)
//1.0e-24:75:48//DROSOPHILA MELANOGASTER (FRUIT FLY)//P54352

F-NT2RP3004670//CUTICLE COLLAGEN 21/0.00090:159:29//CAENORHABDITIS
40 ELEGANS//P17656

F-NT2RP4000008//CHLORINE CHANNEL PROTEIN P64//4.0e-79:243:62//BOS TAURUS
(BOVINE)//P35526

45 F-NT2RP4000023

F-NT2RP4000035//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.6e-06:46:67//HOMO
50 SAPIENS (HUMAN)//P39194

F-NT2RP4000049//CALDESMON (CDM)//0.41:63:34//GALLUS GALLUS (CHICKEN)//P12957

55 F-NT2RP4000051//DUALIN//2.3e-23:195:37//GALLUS GALLUS (CHICKEN)//Q90830

F-NT2RP4000078//RING CANAL PROTEIN (KELCH PROTEIN)//1.2e-24:182:
31//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q04652

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- F-NT2RP4000102//XPAR7 PROTEIN.//1.0:54:33//BACILLUS LICHENIFORMIS.//Q99166
- 5 F-NT2RP4000109//SLIT PROTEIN PRECURSOR.//1.9e-60:230:46//DROSOPHILA
MELANOGASTER (FRUIT FLY).//P24014
- 10 F-NT2RP4000111//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD
SUBUNIT (CPSF 100 KD SUBUNIT).//1.4e-91:157:100//BOS TAURUS (BOVINE).//Q10568
- F-NT2RP4000129//5E5 ANTIGEN.//0.00072:124:37//RATTUS NORVEGICUS (RAT).//Q63003
- 15 F-NT2RP4000147//ZINC FINGER PROTEIN GCS1.//1.5e-26:119:43//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST).//P35197
- 20 F-NT2RP4000150
- F-NT2RP4000151//HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III.//4.2e-
31:180:47//CAENORHABDITIS ELEGANS.//P32740
- 25 F-NT2RP4000159//SPORE COAT PROTEIN SP96.//0.84:107:28//DICTYOSTELIUM
DISCOIDEUM (SLIME MOLD).//P14328
- 30 F-NT2RP4000167//HYPOTHETICAL 98.1 KD PROTEIN IN SPX19-GCR2 INTERGENIC
REGION.//2.4e-08:133:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40164
- 35 F-NT2RP4000185//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118
PROTEIN).//5.4e-05:143:32//HERBES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).//P28284
- F-NT2RP4000210//PAIRED AMPHIPATHIC HELIX PROTEIN.//1.8e-40:258:
35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P22579
- 40 F-NT2RP4000212//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).//1.4e-20:104:
40//APLYSIA CALIFORNICA (CALIFORNIA SEA HARE).//P15287
- 45 F-NT2RP4000214//FERREDOXIN.//1.0:19:42//MOORELLA THERMOACETICA (CLOSTRIDIUM
THERMOACETICUM).//P00203
- 50 F-NT2RP4000218//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.7e-15:48:60//HOMO
SAPIENS (HUMAN).//P39188
- F-NT2RP4000243//DUALIN.//5.8e-78:192:70//GALLUS GALLUS (CHICKEN).//Q90830
- 55 F-NT2RP4000246//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//3.1e-83:207:
76//MUS MUSCULUS (MOUSE).//Q03173
- F-NT2RP4000259//GLUTATHIONE PEROXIDASE 2 (EC 1.11.1.9).//5.5e-29:153:

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43//HELIANTHUS ANNUUS (COMMON SUNFLOWER).//O23968

5 F-NT2RP4000263//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.98:42:40//BOS TAURUS
(BOVINE).//P20072

10 F-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME
I.//3.5e-71:209:66//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87115

F-NT2RP4000312//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1)
.//8.9e-22:166:37//HOMO SAPIENS (HUMAN).//Q15404

15 F-NT2RP4000321//VERPROLIN.//0.00018:260:28//SACCHAROMYCES CEREVISIAE
(BAKER'S YEAST).//P37370

20 F-NT2RP4000323//ANTHOPLEURIN B (TOXIN AP-B).//0.42:15:46//ANTHOPLEURA
XANTHOGRAMMICA (GIANT GREEN SEA ANEMONE).//P01531

F-NT2RP4000355//HYPOTHETICAL 90.9 KD PROTEIN IN GCN20-CMK1 INTERGENIC
REGION.//0.75:125:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43596

25 F-NT2RP4000360//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25)
(FRAGMENT).//0.27:92:33//RATTUS NORVEGICUS (RAT).//P10164

30 F-NT2RP4000367//HYPOTHETICAL 7.3 KD PROTEIN IN 100 KD PROTEIN REGION.//0.99:
52:32//HUMAN ADENOVIRUS TYPE 41.//P23691

35 F-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR
(MRF-1).//4.1e-40:163:52//HOMO SAPIENS (HUMAN).//O75570

F-NT2RP4000376//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//4.2e-59:125:
80//RATTUS NORVEGICUS (RAT).//P54319

40 F-NT2RP4000381//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT
PROTEIN) (NF-H).//0.00058:194:30//MUS MUSCULUS (MOUSE).//P19246

45 F-NT2RP4000398//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.2e-45:153:39//HOMO
SAPIENS (HUMAN).//Q99676

50 F-NT2RP4000415//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC
REGION PRECURSOR.//0.00066:201:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)
.//P47179

55 F-NT2RP4000417//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-
MANNOSIDASE 1B).//1.8e-25:196:40//MUS MUSCULUS (MOUSE).//P39098

F-NT2RP4000424//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.0e-15:72:61//HOMO

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SAPIENS (HUMAN).//P39195

5 F-NT2RP4000448//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//7.0e-23:63:82//HOMO
SAPIENS (HUMAN).//P39192

10 F-NT2RP4000449//REGULATORY PROTEIN SIR2 (SILENT INFORMATION REGULATOR 2)
.//1.3e-41:102:45//KLUYVEROMYCES LACTIS (YEAST).//P33294

F-NT2RP4000455//HOMEBOX PROTEIN SAX-1 (CHOX-3) (FRAGMENT).//0.00014:92:
30//GALLUS GALLUS (CHICKEN).//P19601

15 F-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 7 (EC 3.1.2.15)
(UBIQUITIN THIOLESTERASE 7) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 7)
(DEUBIQUITINATING ENZYME 7) (HERPESVIRUS ASSOCIATED UBIQUITIN-SPECIFIC
20 PROTEASE).//1.0e-29:218:38//HOMO SAPIENS (HUMAN).//Q93009

F-NT2RP4000480//TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE
REGULATORY PROTEIN ALGR3).//0.049:117:29//PSEUDOMONAS AERUGINOSA.//P15276

25 F-NT2RP4000481//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//2.3e-05:152:
23//CAENORHABDITIS ELEGANS.//Q09475

30 F-NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1).//2.3e-48:172:52//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST).//P40484

F-NT2RP4000500//HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III.//1.3e-
23:165:35//CAENORHABDITIS ELEGANS.//P34535

35 F-NT2RP4000515//PHOSPHODIESTERASE I (EC 3.1.4.1) (5'-EXONUCLEASE) (5'-
NUCLEOTIDE PHOSPHODIESTERASE) (FRAGMENT).//1.0:48:37//BOS TAURUS (BOVINE)
40 .//P15396

F-NT2RP4000517//METALLOTHIONEIN-LIKE PROTEIN TYPE 2.//1.0:41:36//VICIA FABA
(BROAD BEAN).//Q41657

45 F-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1.//1.1e-11:93:
36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P45818

50 F-NT2RP4000519//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.68:55:40//BOS
TAURUS (BOVINE).//P25508

F-NT2RP4000524//IGA FC RECEPTOR PRECURSOR (BETA ANTIGEN) (B ANTIGEN).//0.37:
187:24//STREPTOCOCCUS AGALACTIAE.//P27951

55 F-NT2RP4000528//NPL4 PROTEIN.//2.1e-45:305:36//SACCHAROMYCES CEREVISIAE
(BAKER'S YEAST).//P33755

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- 5 F-NT2RP4000541//HOMEBOX PROTEIN CHOX-1 (FRAGMENT)//0.23:28:50//GALLUS GALLUS (CHICKEN)//P13544
- 10 F-NT2RP4000556//HYPOTHETICAL 34.1 KD PROTEIN C40H1.4 IN CHROMOSOME III//4.3e-14:174:34//CAENORHABDITIS ELEGANS//Q03574
- 15 F-NT2RP4000560//HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III//2.1e-19:155:36//CAENORHABDITIS ELEGANS//P34679
- 20 F-NT2RP4000588//HYPOTHETICAL PROTEIN E-115//0.014:64:35//HUMAN ADENOVIRUS TYPE 2//P03290
- 25 F-NT2RP4000614//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN)//2.7e-27:188:44//GALLUS GALLUS (CHICKEN)//P30352
- 30 F-NT2RP4000638//EARLY NODULIN 55-1 PRECURSOR (N-55-1) (FRAGMENT)//0.55:40:40//GLYCINE MAX (SOYBEAN)//Q05544
- 35 F-NT2RP4000648//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2,4e-06:31:74//HOMO SAPIENS (HUMAN)//P39188
- 40 F-NT2RP46000657//HYPOTHETICAL PROTEIN MJ1065//2.5e-40:237:40//METHANOCOCCUS JANNASCHII//Q58465
- 45 F-NT2RP4000704
- 50 F-NT2RP4000713//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556//4.0e-07:134:40//STREPTOMYCES FRADIAE//P20186
- 55 F-NT2RP4000724//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE]//1.1e-62:109:88//HOMO SAPIENS (HUMAN)//P10266
- 60 F-NT2RP4000728//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR//0.0033:190:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32323
- 65 F-NT2RP4000737//PTB-ASSOCIATED SPLICING FACTOR (PSF)//1.0e-05:114:34//HOMO SAPIENS (HUMAN)//P23246
- 70 F-NT2RP4000739//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//1.0:20:50//ANAS PLATYRHYNCHOS (DOMESTIC DUCK)//P50655
- 75 F-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION//0.0013:67:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53915

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- 5 F-NT2RP4000787//POLLEN SPECIFIC PROTEIN SF3.//1.3e-13:79:39//HELIANTHUS ANNUUS (COMMON SUNFLOWER).//P29675
- 10 F-NT2RP4000817//SUPPRESSOR PROTEIN SRP40.//1.3e-05:255:21//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583
- 15 F-NT2RP4000833
- F-NT2RP4000837//MALE SPECIFIC SPERM PROTEIN MST54DB.//0.18:38:44//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643
- 20 F-NT2RP4000839//TRANSCRIPTION INITIATION FACTOR TFIID 90 KD SUBUNIT (TAFII-90) .//0.026:38:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38129
- F-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//2.8e-64:229:53//RATTUS NORVEGICUS (RAT).//O09175
- 25 F-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//3.6e-84:174:54//HOMO SAPIENS (HUMAN).//P16415
- 30 F-NT2RP4000878//MYELOID UPREGULATED PROTEIN.//8.2e-88:227:74//MUS MUSCULUS (MOUSE).//O35682
- F-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME E1 (A1S9 PROTEIN).//9.1e-55:268:43//HOMO SAPIENS (HUMAN).//P22314
- 35 F-NT2RP4000907//BDNF / NT-3 GROWTH FACTORS RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKB TYROSINE KINASE) (GP145-TRKB) (TRK-B).//5.4e-10:220:25//HOMO SAPIENS (HUMAN).//Q16620
- 40 F-NT2RP4000915//60S ACIDIC RIBOSOMAL PROTEIN P2 (FRAGMENT).//0.46:23:60//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P51407
- 45 F-NT2RP4000918//METHYL-ACCEPTING CHEMOTAXIS PROTEIN TLPB.//0.00010:148:32//BACILLUS SUBTILIS.//P39217
- 50 F-NT2RP4000925//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//3.5e-27:220:36//HOMO SAPIENS (HUMAN).//Q06828
- 55 F-NT2RP4000927//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).//0.64:75:37//BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA).//P29128
- F-NT2RP4000928//PHOSPHATIDATE CYTIDYLTRANSFERASE (EC 2.7.7.41) (CDP-DIGLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-

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DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE)
(CDP-DAG SYNTHASE).//3.1e-104:263:66//HOMO SAPIENS (HUMAN).//Q92903

5 F-NT2RP4000929//HYPOTHETICAL 22.2 KD PROTEIN IN NSR1-TIF4631 INTERGENIC
REGION.//0.93:107:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53288

10 F-NT2RP4000955//PUTATIVE CUTICLE COLLAGEN F09G8.6.//2.0e-05:102:
37//CAENORHABDITIS ELEGANS.//P34391

F-NT2RP4000973//HYPOTHETICAL 48.6 KD PROTEIN IN BET1-PAN1 INTERGENIC
15 REGION.//2.3e-17:78:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40564

F-NT2RP4000975//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS:
PEPTIDE P-D] (FRAGMENT).//0.0041:142:33//HOMO SAPIENS (HUMAN).//P10162

20 F-NT2RP4000979//HYPOTHETICAL 14.5 KD PROTEIN.//0.77:106:33//VACCINIA VIRUS
(STRAIN COPENHAGEN).//P20517

25 F-NT2RP4000984//HYPOTHETICAL 124.8 KD PROTEIN C29E4.4 IN CHROMOSOME
III.//0.90:94:25//CAENORHABDITIS ELEGANS.//P34343

F-NT2RP4000989//ANTHOPLEURIN B (TOXIN AP-B).//0.76:41:41//ANTHOPLEURA
30 XANTHOGRAMMICA (GIANT GREEN SEA ANEMONE).//P01531

F-NT2RP4000996//PROTEIN Q300.//0.00024:41:53//MUS MUSCULUS (MOUSE).//Q02722

35 F-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE I135 KD POLYPEPTIDE (EC 2.7.7.6)
(RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT).//8.7e-
115:261:82//RATTUS NORVEGICUS (RAT).//O54888

40 F-NT2RP4001004//EC PROTEIN HOMOLOG 2 (FRAGMENT).//0.50:61:34//ARABIDOPSIS
THALIANA (MOUSE-EAR CRESS).//Q42377

F-NT2RP4001006//HYPOTHETICAL 43.5 KD PROTEIN IN COTD-KDUD INTERGENIC
45 REGION PRECURSOR.//0.010:152:29//BACILLUS SUBTILIS.//P50840

F-NT2RP4001010//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-
50 ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.9e-05:247:
25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640

F-NT2RP4001029//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-
55 BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1).//1.1e-14:175:31//DROSOPHILA
MELANOGASTER (FRUIT FLY).//P13002

F-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA
LIGASE) (LEURS).//1.5e-74:272:55//CAENORHABDITIS ELEGANS.//Q09996

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- 5 F-NT2RP4001057//HYPOTHETICAL 62.2 KD PROTEIN ZK652.6 IN CHROMOSOME
III.//0.0064:76:38//CAENORHABDITIS ELEGANS.//P34664
- F-NT2RP4001064//DUALIN.//2.5e-24:199:38//GALLUS GALLUS (CHICKEN).//Q90830
- 10 F-NT2RP4001078//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-
135) (TAFII135) (TAFII-130) (TAFII130).//0.11:139:38//HOMO SAPIENS (HUMAN).//O00268
- 15 F-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA2+-
ATPASE).//1.5e-22:242:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P13586
- F-NT2RP4001080//POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTB) (HETEROGENEOUS
NUCLEAR RIBONUCLEOPROTEIN I) (HNRNP I).//1.7e-82:178:69//SUS SCROFA (PIG)
//Q29099
- 20 F-NT2RP4001086//LEUCINE-RICH ACIDIC NUCLEAR PROTEIN.//0.00039:141:26//RATTUS
NORVEGICUS (RAT).//P49911
- 25 F-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA
ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1).//9.9e-07:79:43//HOMO SAPIENS
(HUMAN).//P78563
- 30 F-NT2RP4001100//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC
REGION.//4.4e-16:207:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40032
- 35 F-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//8.1e-115:
224:99//RATTUS NORVEGICUS (RAT).//P38378
- F-NT2RP4001122//TIPD PROTEIN.//7.5e-11:129:31//DICTYOSTELIUM DISCOIDEUM (SLIME
MOLD).//O15736
- 40 F-NT2RP4001126//TRICHOHYALIN.//1.4e-19:257:28//OVIS ARIES (SHEEP).//P22793
- 45 F-NT2RP4001138//PUTATIVE F420-DEPENDENT NADP REDUCTASE (EC 1.-.-.-).//0.00010:
204:25//METHANOCOCCUS JANNASCHII.//Q58896
- 50 F-NT2RP4001143//HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC
REGION.//4.5e-34:168:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43616
- F-NT2RP4001148//SOF1 PROTEIN.//2.4e-41:158:41//SACCHAROMYCES CEREVISIAE
(BAKER'S YEAST).//P33750
- 55 F-NT2RP4001149//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//1.3e-08:106:
41//VOLVOX CARTERI.//P21997

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F-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//3.6e-24:194:32//GALLUS GALLUS (CHICKEN).//P35331

5 F-NT2RP4001159//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2).//0.0056:117:25//PLASMODIUM FALCIPARUM (ISOLATE K1 / THAILAND).//Q03643

10 F-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//5.9e-24:184:34//BRASSICA OLERACEA (CAULIFLOWER).//P52178

15 F-NT2RP4001206//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2).//0.0029:117:26//PLASMODIUM FALCIPARUM (ISOLATE K1 / THAILAND).//Q03643

F-NT2RP4001207//CHROMOSOME SEGREGATION PROTEIN CSE1.//1.0e-07:144:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33307

20 F-NT2RP4001210//DERMORPHIN 1 PRECURSOR [CONTAINS: DELTORPHIN (DERMENKEPHALIN); DERMORPHIN].//0.019:130:30//PHYLLOMEDUSA SAUVAGEI (SAUVAGE'S LEAF FROG).//P05422

25 F-NT2RP4001213//ZINC FINGER PROTEIN 177.//3.2e-28:176:39//HOMO SAPIENS (HUMAN).//Q13360

30 F-NT2RP4001219//DISULFIDE ISOMERASE MPD1 PRECURSOR (EC 5.3.4.1).//2.4e-13:108:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12404

35 F-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN).//2.7e-56:242:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-NT2RP4001235//REGULATORY PROTEIN E2.//0.0080:100:38//HUMAN PAPILLOMAVIRUS TYPE 25.//P36787

40 F-NT2RP4001256//CUTICLE COLLAGEN 1.//0.014:104:31//CAENORHABDITIS ELEGANS.//P08124

45 F-NT2RP4001260//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17).//0.00077:16:68//ESCHERICHIA COLI.//P05834

F-NT2RP4001274//HISTONE H1.M6.1.//0.98:65:35//TRYPANOSOMA CRUZI.//P40273

50 F-NT2RP4001276//ELAV PROTEIN.//0.00054:134:33//DROSOPHILA VIRILIS (FRUIT FLY).//P23241

55 F-NT2RP4001313//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//0.014:71:35//NICOTIANA TABACUM (COMMON TOBACCO).//P13983

F-NT2RP4001315//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS9.//2.3e-12:

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190:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P54787

5 F-NT2RP4001336//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1//0.0037:108:
31//PODOSPORA ANSERINA//Q00808

F-NT2RP4001339//HYPOTHETICAL PROTEIN MJ0810//1.2e-09:150:34//METHANOCOCCUS
JANNASCHII//Q58220

10 F-NT2RP4001343//HYPOTHETICAL 85.2 KD PROTEIN F52C9.3 IN CHROMOSOME III//1.4e-
18:244:27//CAENORHABDITIS ELEGANS//Q10123

15 F-NT2RP4001345//PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR
(EC 2.3.1.43) (LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-
CHOLESTEROL ACYLTRANSFERASE) (FRAGMENT)//4.0e-49:212:50//GALLUS GALLUS
(CHICKEN)//P53760

20 F-NT2RP4001351//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1//5.7e-11:229:
26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P25386

25 F-NT2RP4001353//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1)
//0.00088:84:28//HOMO SAPIENS (HUMAN)//Q15404

30 F-NT2RP4001372//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC
PROTEIN)//1.0e-22:222:30//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q08180

35 F-NT2RP4001373//OV-17 ANTIGEN PRECURSOR (IMMUNODOMINANT HYPODERMAL
ANTIGEN)//0.51:92:26//ONCHOCERCA VOLVULUS//P36991

F-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112)
(TYROSINE- PROTEIN KINASE 1)//3.5e-13:146:35//DICTYOSTELIUM DISCOIDEUM (SLIME
MOLD)//P18160

40 F-NT2RP4001379//HYPOTHETICAL 64.2 KD PROTEIN IN SLT2-PUT2 INTERGENIC
REGION//1.2e-14:207:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38767

45 F-NT2RP4001389//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6)
(RPB1) (FRAGMENT)//0.073:112:33//CRICETULUS GRISEUS (CHINESE HAMSTER)
//P11414

50 F-NT2RP4001407//CENTROMERIC PROTEIN E (CENP-E PROTEIN)//0.0019:233:24//HOMO
SAPIENS (HUMAN)//Q02224

55 F-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT)//6.2e-89:195:81//HOMO SAPIENS
(HUMAN)//Q14141

F-NT2RP4001433//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6)//1.5e-85:216:

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56//HOMO SAPIENS (HUMAN).//P28160

5 F-NT2RP4001442//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6)
(VERSION 1).//0.012:107:35//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P18616

F-NT2RP4001447//60S ACIDIC RIBOSOMAL PROTEIN P2 (EL12).//0.0046:69:33//ARTEMIA
SALINA (BRINE SHRIMP).//P02399

10 F-NT2RP4001474//CBP3 PROTEIN PRECURSOR.//0.0011:111:29//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST).//P21560

15 F-NT2RP4001483//2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR
(EC 1.2.4.2) (ALPHA-KETOGLUTARATE DEHYDROGENASE).//6.2e-60:146:61//HOMO
SAPIENS (HUMAN).//Q02218

20 F-NT2RP4001498//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//2.3e-
24:137:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09701

25 F-NT2RP4001502//HYPOTHETICAL 24.7 KD PROTEIN IN POM152-REC114 INTERGENIC
REGION.//6.0e-22:148:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40206

F-NT2RP4001507//CUTICLE COLLAGEN 40.//0.00029:166:31//CAENORHABDITIS
ELEGANS.//P34804

30 F-NT2RP4001524//LACTOCOCCIN A IMMUNITY PROTEIN.//0.74:96:30//LACTOCOCCUS
LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS), AND LACTOCOCCUS LACTIS
(SUBSP. CREMORIS) (STREPTOCOCCUS CREMORIS).//Q00561

35 F-NT2RP4001529//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-
BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1).//2.8e-06:79:41//DROSOPHILA
MELANOGASTER (FRUIT FLY).//P13002

40 F-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NOT1/CDC39-HMR INTERGENIC
REGION.//5.4e-34:88:46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25656

45 F-NT2RP4001551//CELL DIVISION CONTROL PROTEIN 68.//1.5e-18:243:
30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32558

50 F-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-).//0.00030:158:
24//MYCOBACTERIUM TUBERCULOSIS.//P96902

F-NT2RP4001567//IMPORTIN ALPHA-1 SUBUNIT (KARYOPHERIN ALPHA-1 SUBUNIT)
.//0.00013:147:29//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P52170

55 F-NT2RP4001568//HYPOTHETICAL PROTEIN KIAA0041 (FRAGMENT).//8.0e-22:119:
42//HOMO SAPIENS (HUMAN).//Q15057

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- 5 F-NT2RP4001571//NEUROMODULIN (AXONAL MEMBRANE PROTEIN GAP-43) (PP46) (B-50) (PROTEIN F1) (CALMODULIN-BINDING PROTEIN P-57).//0.012:167:28//BOS TAURUS (BOVINE).//P06836
- 10 F-NT2RP4001574//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//6.8e-115:208:98//BOS TAURUS (BOVINE).//P53620
- 15 F-NT2RP4001575//M-RELATED PROTEIN PRECURSOR.//0.22:184:25//STREPTOCOCCUS PYOGENES.//P16946
- 20 F-NT2RP4001592//SOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE-TRNA LIGASE) (ILERS).//7.4e-45:229:39//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P73505
- 25 F-NT2RP4001610//APOLIPOPROTEIN C-III PRECURSOR (APO-CIII).//0.41:74:28//SUS SCROFA (PIG).//P27917
- 30 F-NT2RP4001614//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//1.0:29:37//HOMO SAPIENS (HUMAN).//P02811
- 35 F-NT2RP4001634//MYOSIN HEAVY CHAIN, PERINATAL SKELETAL MUSCLE (FRAGMENT).//0.16:233:23//RATTUS NORVEGICUS (RAT).//P04462
- 40 F-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN MET18/34MS19.//4.2e-21:249:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40469
- 45 F-NT2RP4001644//MYOSIN LIGHT CHAIN KINASE (EC 2.7.1.117) (MLCK).//4.5e-18:111:44//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P25323
- 50 F-NT2RP4001656//HYPOTHETICAL 108.5 KD PROTEIN R06F6.2 IN CHROMOSOME II.//3.4e-13:175:32//CAENORHABDITIS ELEGANS.//Q09600
- 55 F-NT2RP4001677//HYPOTHETICAL 73.6 KD PROTEIN CY49.21.//0.065:66:43//MYCOBACTERIUM TUBERCULOSIS.//Q10690
- 60 F-NT2RP4001679//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.3e-36:103:72//HOMO SAPIENS (HUMAN).//P39194
- 65 F-NT2RP4001696//PHOTOSYSTEM II REACTION CENTRE J PROTEIN.//0.93:37:37//CHLORELLA VULGARIS.//P56338
- 70 F-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.//4.3e-11:128:32//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10282
- 75 F-NT2RP4001730//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//4.1e-22:201:27//DROSOPHILA MELANOGASTER (FRUIT

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FLY).//Q09332

5 F-NT2RP4001739//HOMEODOMAIN PROTEIN HOX-A10 (HOX-1H) (HOX-1.8) (PL).//1.0:67:
34//HOMO SAPIENS (HUMAN).//P31260

10 F-NT2RP4001753//ZINC FINGER PROTEIN 10 (ZINC FINGER PROTEIN KOX1) (FRAGMENT)
//1.2e-19:72:62//HOMO SAPIENS (HUMAN).//P21506

F-NT2RP4001760//BREAKPOINT CLUSTER REGION PROTEIN.//1.8e-13:179:28//HOMO
SAPIENS (HUMAN).//P11274

15 F-NT2RP4001790//ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION
FACTOR RU49).//7.9e-38:147:49//MUS MUSCULUS (MOUSE).//Q07231

20 F-NT2RP4001803//CUTICLE COLLAGEN 12 PRECURSOR.//0.40:48:39//CAENORHABDITIS
ELEGANS.//P20630

25 F-NT2RP4001822//NOVEL ANTIGEN 2 (NAG-2).//2.7e-27:173:36//HOMO SAPIENS (HUMAN)
//O14817

F-NT2RP4001823//PUTATIVE CUTICLE COLLAGEN F09G8.6.//3.3e-16:152:
42//CAENORHABDITIS ELEGANS.//P34391

30 F-NT2RP4001828//HOLIN.//0.99:33:36//BACTERIOPHAGE HP1.//P51727

35 F-NT2RP4001838//METASTASIS-ASSOCIATED PROTEIN MTA1.//1.2e-07:95:31//HOMO
SAPIENS (HUMAN).//Q13330

F-NT2RP4001841//INTESTINAL MUCIN-LIKE PROTEIN (MLP) (FRAGMENT).//0.94:141:
22//RATTUS NORVEGICUS (RAT).//P98089

40 F-NT2RP4001849//SH3-BINDING PROTEIN 3BP-1.//5.6e-52:276:45//MUS
MUSCULUS (MOUSE).//P55194

45 F-NT2RP4001861//HYPOTHETICAL 10.6 KD PROTEIN IN GALE-PEPT INTERGENIC
REGION.//0.92:39:51//BACILLUS SUBTILIS.//P55185

50 F-NT2RP4001889//HYPOTHETICAL BHLF1 PROTEIN.//0.32:97:31//EPSTEIN-BARR VIRUS
(STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181

55 F-NT2RP4001893//2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDENT
RNAASE) (RNASE L) (RIBONUCLEASE 4) (FRAGMENT).//3.6e-07:124:29//MUS MUSCULUS
(MOUSE).//Q05921

F-NT2RP4001896//HYPOTHETICAL 89.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN
PMT6-PCT1 INTERGENIC REGION.//3.9e-10:210:28//SACCHAROMYCES CEREVISIAE

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(BAKER'S YEAST).//P42935

5 F-NT2RP4001901//ACROSIN PRECURSOR (EC 3.4.21.10).//2.4e-07:53:45//ORYCTOLAGUS CUNICULUS (RABBIT).//P48038

10 F-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//3.1e-19:170:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12024

F-NT2RP4001938//ZINC FINGER PROTEIN MOK-2.//1.3e-28:72:50//MUS MUSCULUS (MOUSE).//P24399

15 F-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN- BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE) .//4.8e-14:183:30//TRITICUM AESTIVUM (WHEAT).//Q43209

20 F-NT2RP4001950//HYPOTHETICAL PROTEIN ORF-1137.//3.7e-07:115:29//MUS MUSCULUS (MOUSE).//P11260

25 F-NT2RP4001953

F-NT2RP4001966//WALL-ASSOCIATED PROTEIN PRECURSOR.//0.13:151:27//BACILLUS SUBTILIS.//Q07833

30 F-NT2RP4001975//FIBRIL-FORMING COLLAGEN ALPHA CHAIN.//0.00031:190:31//RIFTIA PACHYPTILA (TUBE WORM).//P30754

35 F-NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN).//3.5e-18:185:29//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

40 F-NT2RP4002047//GTP-BINDING PROTEIN GUF1 (GTPASE GUF1).//4.0e-49:158:65//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P46943

45 F-NT2RP4002052//HYPOTHETICAL 54.3 KD PROTEIN C23D3.03C IN CHROMOSOME I.//0.0047:148:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09844

F-NT2RP4002058//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE F56D2.6.//0.057:66:30//CAENORHABDITIS ELEGANS.//Q20875

50 F-NT2RP4002071//VERY HYPOTHETICAL 13.2 KD PROTEIN CY251.09.//0.94:45:46//MYCOBACTERIUM TUBERCULOSIS.//Q10888

55 F-NT2RP4002075//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.44:36:38//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1).//P18804

F-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)

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//2.6e-19:46:76//HOMO SAPIENS (HUMAN)//Q05481

- 5 F-NT2RP4002081//MHC CLASS II REGULATORY FACTOR RFX1 (RFX) (ENHANCER FACTOR C) (EF-C)//2.8e-05:196:31//HOMO SAPIENS (HUMAN)//P22670
- F-NT2RP4002083//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT)//0.0064:29:55//OWENIA FUSIFORMIS//P21260
- 10 F-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-)//1.1e-37:159:53//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//P38938
- 15 F-NT2RP4002791//30S RIBOSOMAL PROTEIN S20//1.0:73:26//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI)//P56027
- 20 F-NT2RP4002888//HYPOTHETICAL PROTEIN TP0352//0.98:52:26//TREPONEMA PALLIDUM//O83371
- F-NT2RP4002905//G2/MITOTIC-SPECIFIC CYCLIN S13-7 (B-LIKE CYCLIN) (FRAGMENT)//5.9e-05:138:27//GLYCINE MAX (SOYBEAN)//P25012
- 25 F-NT2RP5003459//HOMEBOX PROTEIN HOX-A3 (HOX-1.5) (MO-10)//0.027:40:40//MUS MUSCULUS (MOUSE)//P02831
- 30 F-NT2RP5003461//HYPOTHETICAL PROTEIN C22F3.14C IN CHROMOSOME I (FRAGMENT)//1.1e-12:142:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09779
- 35 F-NT2RP5003477//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1//5.3e-13:215:28//PODOSPORA ANSERINA//Q00808
- 40 F-NT2RP5003492//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)//0.0055:144:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P08640
- 45 F-NT2RP5003500//PROLINE-RICH PROTEIN MP-2 PRECURSOR//9.0e-05:103:38//MUS MUSCULUS (MOUSE)//P05142
- F-NT2RP5003506//MALE SPECIFIC SPERM PROTEIN MST87F//0.53:21:38//DROSOPHILA MELANOGASTER (FRUIT FLY)//P08175
- 50 F-NT2RP5003512//HYPOTHETICAL PROTEIN IN CYCB 3'REGION PRECURSOR (ORF2) (FRAGMENT)//0.92:49:32//PARACOCCLUS DENITRIFICANS//P29969
- 55 F-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR)//2.7e-18:165:39//PHASEOLUS AUREUS (MUNG BEAN) (VIGNA RADIATA)//P37116
- F-NT2RP5003524//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS)//6.0e-08:125:41//RATTUS

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NORVEGICUS (RAT).//P02454

5 F-NT2RP5003534//ATP SYNTHASE, SUBUNIT F (EC 3.6.1.34).//0.88:37:45//HALOBACTERIUM VOLCANII (HALOFERAX VOLCANII).//Q48331

F-OVARC1000001//GAR22 PROTEIN.//1.9e-05:41:58//HOMO SAPIENS (HUMAN).//Q99501

10 F-OVARC1000004//70 KD EXOCYST COMPLEX PROTEIN.//3.7e-08:186:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P19658

15 F-OVARC1000006//HISTONE H2A.1.//4.7e-55:117:98//RATTUS NORVEGICUS (RAT).//P02262

20 F-OVARC1000013//WD-REPEAT PROTEIN POP1.//0.00022:126:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87060

F-OVARC1000014//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//2.3e-05:220:30//GALLUS GALLUS (CHICKEN).//P02457

25 F-OVARC1000017//CUTICLE COLLAGEN DPY-13.//2.6e-05:97:30//CAENORHABDITIS ELEGANS.//P17657

30 F-OVARC1000035

F-OVARC1000058//RAS-RELATED PROTEIN RABC.//0.00015:110:24//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P34143

35 F-OVARC1000060//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.27.1) (RNASE LE).//6.8e-09:60:45//LYCOPERSICON ESCULENTUM (TOMATO).//P80022

40 F-OVARC1000068//CYTOTOXIN 4 (CARDIOTOXIN V-II-4).//1.0:27:44//NAJA MOSSAMBICA (MOZAMBIQUE COBRA).//P01452

45 F-OVARC1000071//NUCLEAR TRANSPORT FACTOR 2 (NTF-2) (PLACENTAL PROTEIN 15) (PP15).//5.2e-06:115:29//HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT).//P13662

F-OVARC1000085

50 F-OVARC1000087//HISTONE MACRO-H2A.1.//1.2e-13:174:26//RATTUS NORVEGICUS (RAT).//Q02874

55 F-OVARC1000091//OCTAPEPTIDE-REPEAT PROTEIN T2.//0.0013:137:32//MUS MUSCULUS (MOUSE).//Q06666

F-OVARC1000092//MITOCHONDRIAL RIBOSOMAL PROTEIN S7.//0.97:46:

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39//ACANTHAMOEBA CASTELLANII (AMOEBA)//P46756

5 F-OVARC1000106//HYPOTHETICAL 141.5 KD PROTEIN IN YPT53-RHO2 INTERGENIC
REGION.//0.0012:165:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53935

10 F-OVARC1000109//PROLINE RICH 33 KD EXTENSIN-RELATED PROTEIN PRECURSOR
(FRAGMENT).//0.18:35:34//DAUCUS CAROTA (CARROT)//P06600

F-OVARC1000113//HYPOTHETICAL PROTEIN C18.//1.0:26:26//SWINEPOX VIRUS (STRAIN
KASZA) (SPV)//P32217

15 F-OVARC1000114//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.6e-28:57:63//HOMO
SAPIENS (HUMAN)//P39194

20 F-OVARC1000133

F-OVARC1000139//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15)
(UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4)
25 (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//1.9e-09:
200:29//HOMO SAPIENS (HUMAN)//Q13107

F-OVARC1000145//HOMEBOX PROTEIN DLX-3.//1.0:65:30//BRACHYDANIO RERIO
30 (ZEBRAFISH) (ZEBRA DANIO)//Q01702

F-OVARC1000148//HYPHAL WALL PROTEIN 1 (CELL ELONGATION PROTEIN 2).//0.12:175:
29//CANDIDA ALBICANS (YEAST)//P46593

35 F-OVARC1000151//HYPOTHETICAL PROTEIN KIAA0161.//5.6e-20:197:30//HOMO SAPIENS
(HUMAN)//P50876

40 F-OVARC1000168//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.0030:77:38//HOMO
SAPIENS (HUMAN)//P39188

F-OVARC1000191//COLANIC ACID BIOSYNTHESIS PROTEIN WCAH.//0.95:56:
45 35//ESCHERICHIA COLI.//P32056

F-OVARC1000198//HISTONE H1.C2.//0.96:70:25//TRYPANOSOMA CRUZI.//P40268

50 F-OVARC1000209//HYPOTHETICAL 20.9 KD PROTEIN IN PLB1-HXT2 INTERGENIC
REGION.//2.5e-33:178:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q03677

F-OVARC1000212//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//1.7e-05:66:46//MUS
55 MUSCULUS (MOUSE).//P05142

F-OVARC1000240//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.8e-10:41:78//HOMO
SAPIENS (HUMAN)//P39193

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- 5 F-OVARC1000241//ENDOTHELIAL PAS DOMAIN PROTEIN 1 (EPAS-1) (HIF-1 ALPHA-LIKE FACTOR) (MHLF) (HIF-RELATED FACTOR) (HRF).//7.4e-54:177:54//MUS MUSCULUS (MOUSE).//P97481
- 10 F-OVARC1000288//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION.//2.9e-20:115:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38821
- F-OVARC1000302//CORTICOSTEROID-BINDING GLOBULIN PRECURSOR (CBG) (TRANSCORTIN).//1.0:79:25//MUS MUSCULUS (MOUSE).//Q06770
- 15 F-OVARC1000304//PROTEIN MOV-10.//1.6e-79:181:83//MUS MUSCULUS (MOUSE).//P23249
- F-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2).//6.9e-36:156:42//ASHBYA GOSSYP II (EREMOTHECIUM GOSSYP II).//Q00063
- 20 F-OVARC1000321//HYPOTHETICAL 28.1 KD PROTEIN C4F8.03 IN CHROMOSOME I.//5.2e-45:159:53//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14179
- 25 F-OVARC1000326//BASIC PROLINE-RICH PEPTIDE IB-1.//0.036:67:35//HOMO SAPIENS (HUMAN).//P04281
- 30 F-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//1.2e-16:200:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40004
- F-OVARC1000347//HYPOTHETICAL 7.6 KD PROTEIN YCF33.//0.69:41:43//CYANOPHORA PARADOXA.//P48273
- 35 F-OVARC1000384//ANTIFREEZE PEPTIDE 4 PRECURSOR.//0.98:49:34//PSEUDOPLEURONECTA AMERICANUS (WINTER FLOUNDER).//P02734
- 40 F-OVARC1000408//INTEGUMENTARY MUCIN C.1 (FIM-C.1) (FRAGMENT).//8.1e-05:115:33//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//Q05049
- 45 F-OVARC1000411//DYNACTIN, 150 KD ISOFORM (150 KD DYNEIN-ASSOCIATED POLYPEPTIDE) (DP-150) (DAP-150) (P150-GLUED).//0.00076:100:29//RATTUS NORVEGICUS (RAT).//P28023
- 50 F-OVARC1000414//HYPOTHETICAL 7.0 KD PROTEIN IN BLTR-SPOIIC INTERGENIC REGION.//1.0:46:34//BACILLUS SUBTILIS.//P54431
- 55 F-OVARC1000420//COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGEN) (FRAGMENT).//0.0028:97:37//HOMO SAPIENS (HUMAN).//P25067
- F-OVARC1000427//HYPOTHETICAL 13.9 KD PROTEIN IN PRFA-SPOIIR INTERGENIC REGION.//0.70:21:47//BACILLUS SUBTILIS.//P39150

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F-OVARC1000431

5 F-OVARC1000437//TENSIN.//9.2e-42:195:52//GALLUS GALLUS (CHICKEN).//Q04205

F-OVARC1000440//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS
 10 PROTEIN).//3.4e-31:37:97//HOMO SAPIENS (HUMAN).//P48059

F-OVARC1000442

15 F-OVARC1000443//CUTICLE COLLAGEN 2C (FRAGMENT).//0.0056:163:34//HAEMONCHUS
 CONTORTUS.//P16252

F-OVARC1000461//FIXU PROTEIN.//0.36:36:44//RHIZOBIUM LEGUMINOSARUM (BIOVAR
 20 TRIFOLII).//P42710

F-OVARC1000465//PROTEIN TRANSPORT PROTEIN SEC7.//2.4e-14:222:
 26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P11075

25 F-OVARC1000466//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//2.3e-08:29:93//HOMO
 SAPIENS (HUMAN).//P39192

30 F-OVARC1000473//DUAL SPECIFICITY PROTEIN PHOSPHATASE 7 (EC 3.1.3.48) (EC
 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE MKP-X) (FRAGMENT).//2.8e-06:96:
 36//RATTUS NORVEGICUS (RAT).//Q63340

35 F-OVARC1000479//PHOTOSYSTEM I REACTION CENTRE SUBUNIT X (PSI-K).//0.99:48:
 37//CYANIDIUM CALDARIUM (GALDIERIA SULPHURARIA).//P31567 F-OVARC1000486

40 F-OVARC1000496//HYPOTHETICAL PROTEIN MJ1213.//1.0:62:32//METHANOCOCCUS
 JANNASCHII.//Q58610

F-OVARC1000520//MEROZOITE SURFACE PROTEIN CMZ-8 (FRAGMENT).//0.0011:66:
 40//EIMERIA ACERVULINA.//P09125

45 F-OVARC1000526//PROTEIN Q300.//1.2e-05:51:43//MUS MUSCULUS (MOUSE).//Q02722

F-OVARC1000533//NEURONAL PROTEIN 3.1 (P311 PROTEIN).//0.74:43:41//HOMO
 50 SAPIENS (HUMAN).//Q16612

F-OVARC1000543//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC
 2.4.1.41) (PROTEIN- UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:
 55 POLYPEPTIDE, N- ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1).//2.3e-23:192:
 35//HOMO SAPIENS (HUMAN).//Q10472

F-OVARC1000556

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F-OVARC1000557!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.6e-08:80:47//HOMO
 SAPIENS (HUMAN).//P39188
 5
 F-OVARC1000564//VPX PROTEIN (X ORF PROTEIN) (VIRAL ACCESSORY PROTEIN).//0.45:
 32:50//HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE D194) (HIV-2).//P17760
 10
 F-OVARC1000573
 F-OVARC1000576//BETA-DEFENSIN 1 (BNDB-1).//0.47:29:41//BOS TAURUS (BOVINE)
 .//P46159
 15
 F-OVARC1000578//COLLAGEN ALPHA 1(II) CHAIN (FRAGMENTS).//0.023:96:36//BOS
 TAURUS (BOVINE).//P02459
 20
 F-OVARC1000588//MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3.//0.75:57:29//HOMO
 SAPIENS (HUMAN).//P09001
 25
 F-OVARC1000605//AUTOLYSIN PRECURSOR (EC 3.4.24.38) (GAMETE LYTIC ENZYME)
 (GLE).//0.91:134:28//CHLAMYDOMONAS REINHARDTII.//P31178
 F-OVARC1000622!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.6e-36:100:80//HOMO
 SAPIENS (HUMAN).//P39189
 30
 F-OVARC1000640//HYPOTHETICAL 8.5 KD PROTEIN YCF40 (ORF73).//0.96:34:
 38//ODONTELLA SINENSIS.//P49535
 35
 F-OVARC1000649//ANTHER-SPECIFIC PROTEIN SF18 PRECURSOR (FRAGMENT)
 .//0.0036:64:37//HELIANTHUS ANNUUS (COMMON SUNFLOWER).//P22357
 F-OVARC1000661//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENTS).//0.21:53:47//RATTUS
 NORVEGICUS (RAT).//P02466
 40
 F-OVARC1000678//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17).//1.0:17:
 58//ESCHERICHIA COLI.//P05834
 45
 F-OVARC1000679//DNA-DIRECTED RNA POLYMERASE OMEGA CHAIN (EC 2.7.7.6)
 (TRANSCRIPTASE OMEGA CHAIN) (RNA POLYMERASE OMEGA SUBUNIT).//0.096:67:
 29//ESCHERICHIA COLI.//P08374
 50
 F-OVARC1000681//PROTEIN Q300.//0.72:16:43//MUS MUSCULUS (MOUSE).//Q02722
 F-OVARC1000682//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-
 MANNOSIDASE 1B).//7.6e-70:102:99//MUS MUSCULUS (MOUSE).//P39098
 55
 F-OVARC1000689//CADMIUM-METALLOTHIONEIN (CD-MT).//0.032:30:40//HELIX POMATIA

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(ROMAN SNAIL) (EDIBLE SNAIL).//P33187

5 F-OVARC1000700//BRAIN NEURON CYTOPLASMIC PROTEIN 2.//0.17:60:40//RATTUS NORVEGICUS (RAT).//P02684

10 F-OVARC1000703//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.57:42:42//HOMO SAPIENS (HUMAN).//P02811

15 F-OVARC1000722//N-ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N-ACETYLGLUCOSAMINE (BETA 1->4)GALACTOSYLTRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANSFERASE) (GT).//1.1e-20:44:70//BOS TAURUS (BOVINE).//P08037

20 F-OVARC1000730//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III.//5.2e-29:224:36//CAENORHABDITIS ELEGANS.//Q18262

F-OVARC1000746//MATERNAL EFFECT PROTEIN STAUFEN.//6.2e-12:78:48//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25159

25 F-OVARC1000769

30 F-OVARC1000771//RAS-RELATED PROTEIN RAB-2.//1.1e-46:121:79//HOMO SAPIENS (HUMAN), AND CANIS FAMILIARIS (DOG).//P08886

F-OVARC1000781//HOMEBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC HOMEBOX PROTEIN 2).//0.81:36:52//HOMO SAPIENS (HUMAN).//P52951

35 F-OVARC1000787//40S RIBOSOMAL PROTEIN S14 (FRAGMENT).//0.96:37:48//SUS SCROFA (PIG).//Q29303

40 F-OVARC1000800//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.5e-31:47:82//HOMO SAPIENS (HUMAN).//P39189

45 F-OVARC1000802//HYPOTHETICAL 8.8 KD PROTEIN B0302.2 IN CHROMOSOME X.//0.16:55:40//CAENORHABDITIS ELEGANS.//Q10926

50 F-OVARC1000834//SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA (EC 2.7.1.-) (P68-PAK) (P21- ACTIVATED KINASE) (ALPHA-PAK) (PROTEIN KINASE MUK2).//0.87:140:31//RATTUS NORVEGICUS (RAT).//P35465

F-OVARC1000846//NUCLEOLIN (PROTEIN C23).//7.0e-07:109:30//MESOCRICETUS AURATUS (GOLDEN HAMSTER).//P08199

55 F-OVARC1000850//HYPOTHETICAL 56.2 KD PROTEIN IN ERG8-UBP8 INTERGENIC REGION.//6.9e-09:180:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04991

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- F-OVARC1000862//UBIQUITIN-CONJUGATING ENZYME E2-17.5 KD (EC 6.3.2.19)
(UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN)//0.0020:74:
28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P52490
- 5 F-OVARC1000876//MOB1 PROTEIN (MPS1 BINDER 1)//9.8e-39:154:55//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST)//P40484
- 10 F-OVARC1000883//METALLOTHIONEIN-I//0.87:38:36//CANDIDA GLABRATA (YEAST)
(TORULOPSIS GLABRATA)//P15113
- 15 F-OVARC1000885//OXIDOREDUCTASE UCPA (EC 1.-.-.)//2.8e-18:170:34//ESCHERICHIA
COLI//P37440
- 20 F-OVARC1000886//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT)//0.00033:60:45//BOS
TAURUS (BOVINE)//P02465
- F-OVARC1000890//PROBABLE E5 PROTEIN//0.92:7:71//HUMAN PAPILLOMAVIRUS TYPE
70//P50774
- 25 F-OVARC1000891//HYPOTHETICAL 8.3 KD PROTEIN (ORF5)//1.0:36:36//PARAMECIUM
TETRAURELIA//P15606
- 30 F-OVARC1000897//HYPOTHETICAL 6.1 KD PROTEIN PRECURSOR (ORF87)//1.0:34:
44//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV)//O10337
- 35 F-OVARC1000912//PUTATIVE CUTICLE COLLAGEN C09G5.4//4.0e-07:98:
35//CAENORHABDITIS ELEGANS//Q09455
- F-OVARC1000915//HYPOTHETICAL PROTEIN KIAA0288 (HA6116)//1.7e-47:115:76//HOMO
SAPIENS (HUMAN)//P56524
- 40 F-OVARC1000924//CYTOCHROME B (EC 1.10.2.2) (FRAGMENT)//0.99:54:24//BOA
CONSTRICTOR (BOA)//P92848
- 45 F-OVARC1000936//HYPOTHETICAL 7.5 KD PROTEIN IN INAA-GLPQ INTERGENIC
REGION//1.0:48:33//ESCHERICHIA COLI//P45505
- 50 F-OVARC1000937//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR//1.0:135:31//HOMO
SAPIENS (HUMAN)//P02452
- F-OVARC1000945//EARLY E1A 11 KD PROTEIN//0.087:81:24//MOUSE ADENOVIRUS TYPE
1 (MAV-1)//P12533
- 55 F-OVARC1000948
- F-OVARC1000959//HYPOTHETICAL PROTEIN MJ0933//0.99:67:28//METHANOCOCCUS

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JANNASCHII./Q58343

- 5 F-OVARC1000960///// ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.8e-32:56:75//HOMO SAPIENS (HUMAN).//P39193
- 10 F-OVARC1000964//MAMBIN (GLYCOPROTEIN IIB-IIA ANTAGONIST) (PLATELET AGGREGATION INHIBITOR) (DENDROASPIN).//1.0:30:36//DENDROASPIS JAMESONI KAIMOSAE (EASTERN JAMESON'S MAMBA).//P28375
- F-OVARC1000971
- 15 F-OVARC1000984//HYPOTHETICAL 52.3 KD PROTEIN IN MRPL10-ERG24 INTERGENIC REGION PRECURSOR.//0.093:36:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53832
- 20 F-OVARC1000996//MO25 PROTEIN.//1.9e-39:80:95//MUS MUSCULUS (MOUSE).//Q06138
- F-OVARC1000999//BRAIN-SPECIFIC HOMEODOMAIN/POU DOMAIN PROTEIN 1 (BRN-1 PROTEIN).//0.00020:50:40//HOMO SAPIENS (HUMAN).//P20264
- 25 F-OVARC1001000///// ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.4e-16:43:90//HOMO SAPIENS (HUMAN).//P39195
- 30 F-OVARC1001004//MALE SPECIFIC SPERM PROTEIN MST84DA.//0.95:33:42//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01642
- 35 F-OVARC1001010//HYPOTHETICAL PROTEIN MJ0926.//0.50:71:23//METHANOCOCCUS JANNASCHII./Q58336
- 40 F-OVARC1001011//CORTISTATIN PRECURSOR.//0.81:45:37//RATTUS NORVEGICUS (RAT).//Q62949
- F-OVARC1001032//FERREDOXIN LIKE PROTEIN.//1.0:26:46//RHIZOBIUM LEGUMINOSARUM (BIOVAR PHASEOLI).//Q05561
- 45 F-OVARC1001034//METALLOTHIONEIN-IG (MT-1G).//0.14:9:77//HOMO SAPIENS (HUMAN).//P13640
- 50 F-OVARC1001038//NUCLEOLIN (PROTEIN C23).//3.2e-07:36:80//HOMO SAPIENS (HUMAN).//P19338
- F-OVARC1001040///// ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.5e-18:45:60//HOMO SAPIENS (HUMAN).//P39194
- 55 F-OVARC1001044//BIS(5'-NUCLEOSYL)-TETRAPHOSPHATASE (SYMMETRICAL) (EC 3.6.1.41) (DIADENOSINE TETRAPHOSPHATASE).//0.88:43:39//ESCHERICHIA COLI.//P05637

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F-OVARC1001051//SERINE PROTEINASE STUBBLE (EC 3.4.21.-) (STUBBLE-STUBBLOID
 PROTEIN).//0.34:117:25//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q05319
 5
 F-OVARC1001055//PRE-B CELL ENHANCING FACTOR PRECURSOR.//1.6e-33:43:
 97//HOMO SAPIENS (HUMAN).//P43490
 10 F-OVARC1001062
 F-OVARC1001065//METHIONYL-TRNA SYNTHETASE (EC 6.1.1.10) (METHIONINE-TRNA
 LIGASE) (METRS).//0.79:76:39//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE)
 15 .//Q44951
 F-OVARC1001068//GTP-BINDING PROTEIN ERA HOMOLOG (FRAGMENT).//5.3e-15:100:
 44//BRADYRHIZOBIUM JAPONICUM.//O69162
 20 F-OVARC1001072//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.0076:41:56//HOMO
 SAPIENS (HUMAN).//P39188
 25 F-OVARC1001074//60S RIBOSOMAL PROTEIN L38.//1.0:32:40//LYCOPERSICON
 ESCULENTUM (TOMATO).//P46291
 F-OVARC1001085//HYPOTHETICAL 126.5 KD PROTEIN C13F4.06 IN CHROMOSOME
 30 I.//0.73:135:25//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10197
 F-OVARC1001092//HYPOTHETICAL 51.2 KD PROTEIN IN PET54-DIE2 INTERGENIC
 REGION.//5.6e-05:30:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P50079
 35 F-OVARC1001107//SHK1 KINASE-BINDING PROTEIN 1.//1.8e-08:52:
 51//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P78963
 40 F-OVARC1001113//DIAPHANOUS PROTEIN.//1.9e-33:218:35//DROSOPHILA
 MELANOGASTER (FRUIT FLY).//P48608
 F-OVARC1001117//GENE 7 PROTEIN.//0.68:12:50//SPIROPLASMA VIRUS 4 (SPV4).//P11339
 45 F-OVARC1001118
 F-OVARC1001129//30S RIBOSOMAL PROTEIN S17.//0.15:57:22//AQUIFEX
 50 AEOLICUS.//O66439
 F-OVARC1001154//GRANULINS PRECURSOR (ACROGRANIN).//2.3e-95:99:77//MUS
 MUSCULUS (MOUSE).//P28798
 55 F-OVARC1001161//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.//0.17:87:
 34//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P49177

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F-OVARC1001162

5 F-OVARC1001167//TRBD PROTEIN.//0.92:24:45//ESCHERICHIA COLI.//P41070

F-OVARC1001169//FRUCTOSE-1,6-BISPHOSPHATASE (EC 3.1.3.11) (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) (FRAGMENT).//0.82:35:40//MUS

10 MUSCULUS (MOUSE).//P97323

F-OVARC1001170//PROLINE-RICH PEPTIDE P-B.//0.17:27:37//HOMO SAPIENS (HUMAN) .//P02814

15 F-OVARC1001171//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!0.00023:28:75//HOMO SAPIENS (HUMAN).//P39188

20 F-OVARC1001173

F-OVARC1001176//HYPOTHETICAL BHLF1 PROTEIN.//2.7e-05:158:31//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181

25 F-OVARC1001180//UBIQUITIN-LIKE PROTEIN DSK2.//1.4e-12:208:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48510

30 F-OVARC1001188//HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//3.3e-31:129:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53215

F-OVARC1001200//HYPOTHETICAL 49.0 KD PROTEIN IN NSP1-KAR2 INTERGENIC

35 REGION.//0.018:148:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47057

F-OVARC1001232//HYPOTHETICAL PROTEIN MJ1236.//2.5e-27:141:39//METHANOCOCCUS JANNASCHII.//Q58633

40 F-OVARC1001240

F-OVARC1001243

45 F-OVARC1001244//RING3 PROTEIN (KIAA9001).//1.7e-13:37:91//HOMO SAPIENS (HUMAN) .//P25440

50 F-OVARC1001261//OCTAPEPTIDE-REPEAT PROTEIN T2.//1.3e-07:109:35//MUS MUSCULUS (MOUSE).//Q06666

F-OVARC1001268//HYPOTHETICAL 57.4 KD PROTEIN IN PILT REGION (ORF4).//0.71:43:

55 41//PSEUDOMONAS AERUGINOSA.//P24563

F-OVARC1001270//HYPOTHETICAL 9.0 KD PROTEIN IN UVSW-UVSY INTERGENIC

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REGION.//1.0:44:29//BACTERIOPHAGE T4.//P32281

5 F-OVARC1001271//HYPOTHETICAL 104.7 KD PROTEIN F23F12.8 IN CHROMOSOME III
PRECURSOR.//0.00015:188:23//CAENORHABDITIS ELEGANS.//P46504

F-OVARC1001282

10 F-OVARC1001296//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31).//0.022:101:
31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38968

15 F-OVARC1001306//HYPOTHETICAL 52.9 KD SERINE-RICH PROTEIN C11G7.01 IN
CHROMOSOME I.//0.023:134:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)
.//O13695

20 F-OVARC1001329//CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR
(CTPT).//1.3e-14:150:28//ZEA MAYS (MAIZE).//P49133

F-OVARC1001330

25 F-OVARC1001339//RIBONUCLEOPROTEIN RB97D.//0.0013:55:38//DROSOPHILA
MELANOGASTER (FRUIT FLY).//Q02926

30 F-OVARC1001341//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC
REGION.//4.9e-17:110:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40032

F-OVARC1001342

35 F-OVARC1001344//PREPROTEIN TRANSLOCASE SECE SUBUNIT.//0.99:39:
23//STAPHYLOCOCCUS CARNOSUS.//P36253

40 F-OVARC1001357//METALLOTHIONEIN.//0.99:28:42//XENOPUS LAEVIS (AFRICAN CLAWED
FROG).//Q05890

45 F-OVARC1001360//LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED
TRANSCRIPT 2).//0.86:109:31//HOMO SAPIENS (HUMAN).//P48634

F-OVARC1001369//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT).//6.7e-05:124:36//BOS
TAURUS (BOVINE).//P02465

50 F-OVARC1001372//HYPOTHETICAL 34.5 KD PROTEIN IN CLCB-CLCD INTERGENIC
REGION PRECURSOR.//0.75:33:48//PSEUDOMONAS PUTIDA, AND PSEUDOMONAS SP.
(STRAIN B13).//Q47100

55 F-OVARC1001376//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.8e-24:96:61//HOMO
SAPIENS (HUMAN).//P39188

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- F-OVARC1001381//MEMBRANE-ASSOCIATED ATPASE EPSILON CHAIN (EC 3.6.1.34) (SUL-ATPASE EPSILON).//0.96:46:39//SULFOLOBUS ACIDOCALDARIUS.//P23039
- 5 F-OVARC1001391//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.00024:189:29//HOMO SAPIENS (HUMAN).//P10162
- 10 F-OVARC1001399//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.062:18:77//HOMO SAPIENS (HUMAN).//P39195
- 15 F-OVARC1001417//HYPOTHETICAL 157.0 KD PROTEIN C38C10.5 IN CHROMOSOME III.//0.010:185:23//CAENORHABDITIS ELEGANS.//Q03570
- F-OVARC1001419//A-TYPE INCLUSION PROTEIN (ATI).//0.50:135:28//CAMELPOX VIRUS (STRAIN CP-1).//Q05482
- 20 F-OVARC1001425//COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.//0.43:85:40//HOMO SAPIENS (HUMAN).//Q03692
- 25 F-OVARC1001436//HYPOTHETICAL 11.4 KD PROTEIN (C4 PROTEIN).//0.031:100:30//TOMATO YELLOW LEAF CURL VIRUS (STRAIN AUSTRALIA) (TYLCV).//P36283
- 30 F-OVARC1001442//HOMEBOX PROTEIN HTR-A2 (FRAGMENT).//1.0:32:34//HELOBDELLA TRISERIALIS (LEECH).//P17138
- F-OVARC1001453//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF).//0.74:19:47//MUS MUSCULUS (MOUSE).//P28184
- 35 F-OVARC1001476//GTP-BINDING PROTEIN GTR2.//3.0e-12:114:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53290
- 40 F-OVARC1001480//COLLAGEN ALPHA 2(VI) CHAIN PRECURSOR.//0.00019:134:32//MUS MUSCULUS (MOUSE).//Q02788
- 45 F-OVARC1001489//HYPOTHETICAL PROTEIN HI1270.//0.98:30:43//HAEMOPHILUS INFLUENZAE.//P44149
- F-OVARC1001496//C-TERMINAL BINDING PROTEIN 2.//4.0e-65:132:100//HOMO SAPIENS (HUMAN).//P56545
- 50 F-OVARC1001506//POLYCYSTIN PRECURSOR (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE PROTEIN 1).//3.2e-70:159:94//HOMO SAPIENS (HUMAN).//P98161
- 55 F-OVARC1001525//FIBROBLAST GROWTH FACTOR INDUCIBLE PROTEIN 14 (FIN14).//1.0:36:33//MUS MUSCULUS (MOUSE).//Q61077
- F-OVARC1001542//SMALL PROLINE-RICH PROTEIN 2B (SPR-2B).//0.69:57:33//HOMO

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SAPIENS (HUMAN).//P35325

F-OVARC1001547

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F-OVARC1001555//NGG1-INTERACTING FACTOR 3.//7.6e-16:148:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53081

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F-OVARC1001577//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//8.8e-38:94:81//GALLUS GALLUS (CHICKEN).//P30352

15

F-OVARC1001600//GENE 7 PROTEIN.//0.80:38:39//SPIROPLASMA VIRUS SPV1-R8A2 B.//P15898

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F-OVARC1001610//DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE (EC 2.7.8.2) (SN-1,2- DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE) (CHOPT).//1.6e-22:122:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P17898

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F-OVARC1001611

F-OVARC1001615//HYPOTHETICAL 6.1 KD PROTEIN C03B1.10 IN CHROMOSOME X.//0.30:43:34//CAENORHABDITIS ELEGANS.//Q11116

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F-OVARC1001668//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.0e-19:45:82//HOMO SAPIENS (HUMAN).//P39192

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F-OVARC1001702//SOX-20 PROTEIN.//2.4e-28:71:83//HOMO SAPIENS (HUMAN).//O60248

F-OVARC1001703//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE NUCLEOTIDE- BINDING PROTEIN 1) (INTERFERON-GAMMA INDUCIBLE PROTEIN MAG-1) .//0.00018:88:36//MUS MUSCULUS (MOUSE).//Q01514

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F-OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B) .//2.7e-05:98:32//MUS MUSCULUS (MOUSE).//Q62267

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F-OVARC1001713//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).//4.5e-20:46:67//BOS TAURUS (BOVINE).//P07106

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F-OVARC1001726//ALPHA-AMYLASE INHIBITOR PAIM I (PIG PANCREATIC ALPHA-AMYLASE INHIBITOR OF MICROBES I).//0.59:23:56//STREPTOMYCES OLIVACEOVIRIDIS (STREPTOMYCES CORCHORUSII).//P09921

55

F-OVARC1001731//TROPOMYOSIN ALPHA CHAIN, SKELETAL MUSCLE.//2.1e-75:176:87//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//Q01173

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F-OVARC1001745//GENE 11 PROTEIN.//0.31:36:52//SPIROPLASMA VIRUS SPV1-R8A2 B.//P15902

5 F-OVARC1001762//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMINO, ACETYLTRANSFERASE 1).//2.8e-23:197:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P12945

10 F-OVARC1001766//FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PPIASE) (EC 5.2.1.8) (PROLINE ROTAMASE) (NUCLEOLAR PROLINE ISOMERASE) (FKBP-70).//2.2e-06:99:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38911

15 F-OVARC1001767//33.2 KD PROTEIN IN DIND-RPH INTERGENIC REGION (ORF X).//0.99:113:27//ESCHERICHIA COLI.//P23839

20 F-OVARC1001768

F-OVARC1001791//HYPOTHETICAL 63.3 KD PROTEIN IN MPT5-SAE2 INTERGENIC REGION.//0.090:75:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P46945

25 F-OVARC1001795//HYPOTHETICAL 7.5 KD PROTEIN IN RPBA-GP46 INTERGENIC REGION.//0.81:21:38//BACTERIOPHAGE T4.//P07878

30 F-OVARC1001802//PLECTOXIN VIII (PLT-VIII) (PLTVIII).//0.41:19:36//PLECTREURYS TRISTIS (SPIDER).//P36984

35 F-OVARC1001805//60S RIBOSOMAL PROTEIN L40 (CEP52).//0.67:24:58//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P14796

40 F-OVARC1001809//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.23:111:31//RATTUS NORVEGICUS (RAT).//P02454

F-OVARC1001812//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.99:28:42//HALICHOERUS GRYPUS (GRAY SEAL).//P38592

45 F-OVARC1001813//HYPOTHETICAL 9.9 KD PROTEIN.//0.41:36:30//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20562

50 F-OVARC1001820//HYPOTHETICAL PROTEIN ORF-1137.//0.80:58:29//MUS MUSCULUS (MOUSE).//P11260

F-OVARC1001828

55 F-OVARC1001846

F-OVARC1001861//METALLOTHIONEIN (MT).//0.18:11:54//PLEURONECTES PLATESSA

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(PLAICE).//P07216

F-OVARC1001873

5

F-OVARC1001879//HYPOTHETICAL 55.9 KD PROTEIN EEED8.6 IN CHROMOSOME II.//2.3e-05:73:31//CAENORHABDITIS ELEGANS.//Q09296

10

F-OVARC1001880//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC PEPTIDE P-F] (FRAGMENT).//2.4e-11:203:32//HOMO SAPIENS (HUMAN).//P02812

15

F-OVARC1001883//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.3e-16:86:59//HOMO SAPIENS (HUMAN).//P39188

20

F-OVARC1001900//HYPOTHETICAL 105.9 KD PROTEIN F22B7.5 IN CHROMOSOME III.//0.0053:48:47//CAENORHABDITIS ELEGANS.//P34408

F-OVARC1001901

25

F-OVARC1001911//40S RIBOSOMAL PROTEIN S28.//1.0:33:36//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P34789

30

F-OVARC1001916//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN).//0.00082:114:27//HOMO SAPIENS (HUMAN).//P98174

35

F-OVARC1001928//FERREDOXIN III (FDIII).//1.0:64:29//ANABAENA VARIABILIS.//P46050

40

F-OVARC1001942//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMINO, ACETYLTRANSFERASE 1).//3.0e-07:93:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P12945

45

F-OVARC1001943//HYPOTHETICAL 62.2 KD PROTEIN ZK652.6 IN CHROMOSOME III.//1.7e-23:147:43//CAENORHABDITIS ELEGANS.//P34664

50

F-OVARC1001949//ZINC FINGER PROTEIN 177.//2.0e-23:56:66//HOMO SAPIENS (HUMAN).//Q13360

55

F-OVARC1001950//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.011:57:47//HOMO SAPIENS (HUMAN).//P39188

F-OVARC1001987//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//0.39:14:64//MUS MUSCULUS (MOUSE).//P02319

F-OVARC1001989//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.4e-13:55:72//HOMO SAPIENS (HUMAN).//P39188

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F-OVARC1002044

5 F-OVARC1002050//UTROPHIN (DYSTROPHIN-RELATED PROTEIN 1) (DRP1) (DRP).//3.6e-12:221:25//HOMO SAPIENS (HUMAN).//P46939

F-OVARC1002066

10 F-OVARC1002082

15 F-OVARC1002107//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.99:149:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25386

F-OVARC1002112//HISTONE MACRO-H2A.1.//2.8e-64:133:98//RATTUS NORVEGICUS (RAT).//Q02874

20 F-OVARC1002127//60S RIBOSOMAL PROTEIN L22.//0.0023:95:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//P50887

25 F-OVARC1002138//PROBABLE 26S PROTEASE SUBUNIT YTA6 (TAT-BINDING HOMOLOG 6).//6.4e-51:198:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40328

F-OVARC1002143

30 F-OVARC1002156//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//0.00010:64:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53915

35 F-OVARC1002158//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//8.2e-07:119:35//AUTOGRAPHAL CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479

40 F-OVARC1002165//EBNA-6 NUCLEAR PROTEIN (EBNA-3C) (EBNA-4B).//0.00023:90:45//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03204

45 F-OVARC1002182//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II.//1.3e-34:165:35//CAENORHABDITIS ELEGANS.//Q18964

F-PLACE1000004//HYPOTHETICAL 180.2 KD PROTEIN C31A2.05C IN CHROMOSOME I.//8.8e-05:148:25//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09725

50 F-PLACE1000005//PROTEIN Q300.//0.30:10:100//MUS MUSCULUS (MOUSE).//Q02722

55 F-PLACE1000007//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//2.3e-39:134:62//CAENORHABDITIS ELEGANS.//P34547

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F-PLACE1000014//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A))
 (RO(SS-A)).//0.00036:63:39//HOMO SAPIENS (HUMAN).//P19474
 5 F-PLACE1000031
 F-PLACE1000040//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//4.4e-12:97:41//HOMO
 10 SAPIENS (HUMAN).//P39194
 F-PLACE1000048//50S RIBOSOMAL PROTEIN L15 (FRAGMENT).//0.98:31:38//BACILLUS SP.
 (STRAIN C-125).//P38373
 15 F-PLACE1000050//COLLAGEN ALPHA 1(III) CHAIN.//0.00062:190:33//BOS TAURUS
 (BOVINE).//P04258
 20 F-PLACE1000061//60S RIBOSOMAL PROTEIN L37A.//6.4e-19:51:86//GALLUS GALLUS
 (CHICKEN).//P32046
 25 F-PLACE1000066//SSU72 PROTEIN.//2.3e-39:165:49//SACCHAROMYCES CEREVISIAE
 (BAKER'S YEAST).//P53538
 F-PLACE1000078//BAD PROTEIN (BCL-2 BINDING COMPONENT 6).//1.7e-06:21:95//HOMO
 SAPIENS (HUMAN).//Q92934
 30 F-PLACE1000081//HOMEBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3).//0.0053:146:33//MUS
 MUSCULUS (MOUSE).//P06798
 35 F-PLACE1000094
 F-PLACE1000133//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B
 TRANSCRIPTION FACTOR 3).//1.8e-62:158:81//HOMO SAPIENS (HUMAN).//P20290
 40 F-PLACE1000142//ENOYL-COA HYDRATASE, MITOCHONDRIAL PRECURSOR (EC
 4.2.1.17) (SHORT CHAIN ENOYL-COA HYDRATASE) (SCEH) (ENOYL-COA HYDRATASE 1)
 .//9.8e-12:104:34//HOMO SAPIENS (HUMAN).//P30084
 45 F-PLACE1000184//AC PROTEIN.//0.44:31:29//BACTERIOPHAGE T4.//P18924
 F-PLACE1000185//HYPOTHETICAL GLYCINE-RICH 49.6 KD PROTEIN CY130.10C
 50 PRECURSOR.//0.11:48:33//MYCOBACTERIUM TUBERCULOSIS.//Q10637
 F-PLACE1000213//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-
 ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//3.4e-05:194:
 55 26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640
 F-PLACE1000214

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F-PLACE1000236//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//0.027:63:34//GALLUS
 GALLUS (CHICKEN).//P02457
 5
 F-PLACE1000246//TEGUMENT PROTEIN (GENE 11 PROTEIN).//0.78:100:26//EQUINE
 HERPESVIRUS TYPE 4 (STRAIN 1942) (EHV-4) (EQUINE HERPESVIRUS TYPE 1 SUBTYPE
 2).//Q00039
 10
 F-PLACE1000292
 F-PLACE1000308//EARLY NODULIN 75 (N-75) (NGM-75) (FRAGMENT).//0.049:28:
 15 42//MEDICAGO SATIVA (ALFALFA).//P11728
 F-PLACE1000332
 20 F-PLACE1000347//HYPOTHETICAL PROTEIN TP0420.//0.15:24:54//TREPONEMA
 PALLIDUM.//O83435
 F-PLACE1000374//LYSOZYME C (EC 3.2.1.17) (1,4-BETA-N-ACETYLMURAMIDASE C).//1.0:
 25 63:25//ORYCTOLAGUS CUNICULUS (RABBIT).//P16973
 F-PLACE1000380//MATING PROCESS PROTEIN MID2 (SERINE-RICH PROTEIN SMS1)
 (PROTEIN KINASE A INTERFERENCE PROTEIN).//0.018:169:28//SACCHAROMYCES
 30 CEREVISIAE (BAKER'S YEAST).//P36027
 F-PLACE1000383//MYOTUBULARIN.//1.2e-65:215:57//HOMO SAPIENS (HUMAN).//Q13496
 35 F-PLACE1000401//ELASTIN PRECURSOR (TROPOELASTIN).//0.00023:145:30//MUS
 MUSCULUS (MOUSE).//P54320
 F-PLACE1000406//54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)).//3.4e-27:90:
 40 63//HOMO SAPIENS (HUMAN).//Q15233
 F-PLACE1000420//7,8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-) (8-OXO-
 45 DGTPASE).//4.7e-07:134:29//MUS MUSCULUS (MOUSE).//P53368
 F-PLACE1000421//HYPOTHETICAL 8.8 KD PROTEIN C11D3.01C IN CHROMOSOME I.//0.48:
 72:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10080
 50 F-PLACE1000424
 F-PLACE1000435
 55 F-PLACE1000444//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.0e-31:129:63//HOMO
 SAPIENS (HUMAN).//P39195

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F-PLACE1000453//PROTEIN Q300.//0.013:16:68//MUS MUSCULUS (MOUSE).//Q02722

5 F-PLACE1000481//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.14:63:36//HOMO
SAPIENS (HUMAN).//P08547

F-PLACE1000492//BASP1 PROTEIN.//0.17:114:28//HOMO SAPIENS (HUMAN).//P80723

10 F-PLACE1000540

F-PLACE1000547//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-
MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE
15 PYROPHOSPHORYLASE).//1.8e-21:87:56//SACCHAROMYCES CEREVISIAE (BAKER'S
YEAST).//P41940

20 F-PLACE1000562//HYPOTHETICAL PROTEIN MJ0562.//1.0:35:34//METHANOCOCCUS
JANNASCHII.//Q57982

F-PLACE1000564//ADRENAL SPECIFIC 30 KD PROTEIN (CLONE PG2).//0.13:66:37//HOMO
25 SAPIENS (HUMAN).//P15803

F-PLACE1000583//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.0e-45:
192:47//HOMO SAPIENS (HUMAN).//P51522

30 F-PLACE1000588//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE
NUCLEOTIDE- BINDING PROTEIN 1).//5.3e-63:122:88//HOMO SAPIENS (HUMAN).//P32455

35 F-PLACE1000596//RING CANAL PROTEIN (KELCH PROTEIN).//2.6e-12:120:
38//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-PLACE1000599//EARLY E3B 12.7 KD PROTEIN PRECURSOR.//0.83:53:32//HUMAN
40 ADENOVIRUS TYPE 12.//P36707

F-PLACE1000610

45 F-PLACE1000611//HYPOTHETICAL 33.6 KD PROTEIN IN MCK1-RPS19B INTERGENIC
REGION.//9.4e-07:64:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48558

F-PLACE1000636//MALE STERILITY PROTEIN 2.//3.7e-09:83:43//ARABIDOPSIS THALIANA
50 (MOUSE-EAR CRESS).//Q08891

F-PLACE1000653//PUTATIVE PHOSPHOACETYLGLUCOSAMINE MUTASE (EC 5.4.2.3)
(ACETYLGLUCOSAMINE PHOSPHOMUTASE) (N-ACETYLGLUCOSAMINE-PHOSPHATE
55 MUTASE).//1.9e-30:203:41//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09687

F-PLACE1000656//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH
GLYCOPROTEIN).//0.0029:75:33//NICOTIANA TABACUM (COMMON TOBACCO).//P13983

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- 5 F-PLACE1000706//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR
COREPRESSOR KAP-1) (KRAB-ASSOCIATED PROTEIN 1).//1.1e-38:180:42//HOMO SAPIENS
(HUMAN).//Q13263
- 10 F-PLACE1000712//VERY HYPOTHETICAL 8.9 KD PROTEIN CY441.05 PRECURSOR.//0.93:
49:34//MYCOBACTERIUM TUBERCULOSIS.//P71934
- F-PLACE1000716
- 15 F-PLACE1000748//HYPOTHETICAL 10.4 KD PROTEIN IN SPAT 3'REGION (ORF-11).//0.90:
53:37//SHIGELLA FLEXNERI.//P55794
- 20 F-PLACE1000749//HYPOTHETICAL PROTEIN MG148.//0.0014:142:27//MYCOPLASMA
GENITALIUM.//P47394
- F-PLACE1000755//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III.//1.1e-15:98:
48//CAENORHABDITIS ELEGANS.//P34529
- 25 F-PLACE1000769//VIGILIN.//0.51:60:33//GALLUS GALLUS (CHICKEN).//P81021
- F-PLACE1000785//PROBABLE COLD SHOCK PROTEIN CY15C10.04.//1.0:22:
45//MYCOBACTERIUM TUBERCULOSIS.//O06360
- 30 F-PLACE1000786//HYPOTHETICAL 30.2 KD PROTEIN ZK632.12 IN CHROMOSOME
III.//2.6e-38:159:51//CAENORHABDITIS ELEGANS.//P34657
- 35 F-PLACE1000793//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//0.0097:128:
30//HOMO SAPIENS (HUMAN).//P50552
- 40 F-PLACE1000798//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//9.4e-07:47:61//HOMO
SAPIENS (HUMAN).//P39188
- F-PLACE1000841
- 45 F-PLACE1000849//ELAV PROTEIN.//3.5e-05:140:35//DROSOPHILA VIRILIS (FRUIT FLY)
//P23241
- 50 F-PLACE1000856//HYPOTHETICAL PROTEIN MJ0008.//0.95:100:23//METHANOCOCCUS
JANNASCHII.//Q60319
- 55 F-PLACE1000863//PUTATIVE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN
YHR148W.//2.3e-46:172:54//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32899
- F-PLACE1000909//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN)
//0.00022:105:35//HOMO SAPIENS (HUMAN).//P16157

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F-PLACE1000931//KILLER TOXIN HM-1.//0.95:24:33//WILLIOPSIS MRAKII (YEAST)
 (HANSENULA MRAKII).//P10410
 5
 F-PLACE1000948//SL CYTOKINE PRECURSOR (FLT3 LIGAND).//0.97:52:40//HOMO
 SAPIENS (HUMAN).//P49771
 10
 F-PLACE1000972//MYOSIN ID HEAVY CHAIN.//1.9e-06:79:43//DICTYOSTELIUM
 DISCOIDEUM (SLIME MOLD).//P34109
 F-PLACE1000977//HYPOTHETICAL 94.2 KD PROTEIN C38D4.5 IN CHROMOSOME III.//2.5e-
 15 23:105:41//CAENORHABDITIS ELEGANS.//P46941
 F-PLACE1000979//ZINC FINGER PROTEIN 7 (ZINC FINGER PROTEIN KOX4) (ZINC FINGER
 PROTEIN HF.16).//0.91:83:30//HOMO SAPIENS (HUMAN).//P17097
 20
 F-PLACE1000987//HYPOTHETICAL 111.5 KD PROTEIN C22G7.02 IN CHROMOSOME
 I.//0.10:128:24//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09796
 25
 F-PLACE1001000
 F-PLACE1001007//ZYXIN.//2.2e-05:135:30//GALLUS GALLUS (CHICKEN).//Q04584
 30
 F-PLACE1001010//BETA-1 BUNGAROTOXIN B CHAIN, MAJOR COMPONENT PRECURSOR
 (BUNGAROTOXIN, B1 CHAIN).//1.0:30:40//BUNGARUS MULTICINCTUS (MANY-BANDED
 KRAIT).//P00987
 35
 F-PLACE1001015
 F-PLACE1001024
 40
 F-PLACE1001036
 F-PLACE1001054//HOLOTRICIN 3 PRECURSOR.//0.0044:56:39//HOLOTRICHIA
 DIOMPHALIA.//Q25055
 45
 F-PLACE1001062//SACCHAROPINE DEHYDROGENASE [NADP+, L-GLUTAMATE FORMING]
 (EC 1.5.1.10).//0.0013:38:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38999
 50
 F-PLACE1001076
 F-PLACE1001088//EARLY NODULIN 75 (N-75) (NGM-75) (FRAGMENT).//0.95:32:
 50//MEDICAGO SATIVA (ALFALFA).//P11728
 55
 F-PLACE1001092//HYPOTHETICAL 49.0 KD PROTEIN IN NSP1-KAR2 INTERGENIC
 REGION.//0.0026:81:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47057

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F-PLACE1001104//HYPOTHETICAL 131.5 KD PROTEIN C02F12.7 IN CHROMOSOME
 X.//0.00063:125:32//CAENORHABDITIS ELEGANS.//Q11102
 5
 F-PLACE1001118//ZINC FINGER PROTEIN MLZ-4 (ZINC FINGER PROTEIN 46).//2.6e-77:
 209:63//MUS MUSCULUS (MOUSE).//Q03309
 10
 F-PLACE1001136//ALPHA-N-ACETYL GALACTOSAMINIDASE PRECURSOR (EC 3.2.1.49)
 (ALPHA- GALACTOSIDASE B).//0.99:107:30//HOMO SAPIENS (HUMAN).//P17050
 F-PLACE1001168
 15
 F-PLACE1001171//RETROVIRUS-RELATED POL POLYPROTEIN (FRAGMENT).//0.00012:37:
 59//HOMO SAPIENS (HUMAN).//P12895
 20
 F-PLACE1001185//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC
 REGION.//3.6e-12:88:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53867
 F-PLACE1001238
 25
 F-PLACE1001241//METALLOTHIONEIN B (MTB) (FRAGMENT).//0.13:30:53//COLINUS
 VIRGINIANUS (BOBWHITE QUAIL) (COMMON BOBWHITE).//P27087
 30
 F-PLACE1001257//RING CANAL PROTEIN (KELCH PROTEIN).//4.1e-24:125:
 46//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
 F-PLACE1001272//HYPOTHETICAL PROTEIN IN KSGA 3'REGION (ORF L5) (FRAGMENT)
 35
 .//1.0:24:45//MYCOPLASMA CAPRICOLUM.//P43040
 F-PLACE1001279//CYTOTOXIN 3 (CYTOTOXIN V-II-3).//0.98:31:41//NAJA MOSSAMBICA
 (MOZAMBIQUE COBRA).//P01470
 40
 F-PLACE1001280//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS:
 CHONDROCALCIN].//0.0051:156:32//MUS MUSCULUS (MOUSE).//P28481
 45
 F-PLACE1001294//GAMETOGENESIS EXPRESSED PROTEIN GEG-154.//3.7e-56:109:
 93//MUS MUSCULUS (MOUSE).//P50636
 F-PLACE1001304//ZINC FINGER PROTEIN 35 (ZFP-35).//3.2e-30:75:57//MUS MUSCULUS
 50
 (MOUSE).//P15620
 F-PLACE1001311//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.7e-31:66:66//HOMO
 SAPIENS (HUMAN).//P39189
 55
 F-PLACE1001323

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- F-PLACE1001351//REV PROTEIN (ANTI-REPRESSION TRANSACTIVATOR PROTEIN)
(ART/TRS).//0.11:66:27//SIMIAN IMMUNODEFICIENCY VIRUS (AGM155 ISOLATE) (SIV-AGM)
./P27971
- 5 F-PLACE1001366//SHORT NEUROTOXIN 2 (TOXIN CM-14) (TOXIN V-N-I2).//0.070:18:
33//NAJA HAJE ANNULIFERA (BANDED EGYPTIAN COBRA).//P01422
- 10 F-PLACE1001377//DISINTEGRIN TRIGRAMIN BETA (PLATELET AGGREGATION
ACTIVATION INHIBITOR).//4.9e-06:50:46//TRIMERESURUS GRAMINEUS (INDIAN GREEN
TREE VIPER) (GREEN HABU SNAKE).//P17495
- 15 F-PLACE1001383//M PROTEIN, SEROTYPE 49 PRECURSOR.//0.080:136:
24//STREPTOCOCCUS PYOGENES.//P16947
- F-PLACE1001384
- 20 F-PLACE1001387//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE
EPS8.//1.9e-22:142:39//HOMO SAPIENS (HUMAN).//Q12929
- 25 F-PLACE1001395//HYPOTHETICAL 8.5 KD PROTEIN IN ASIA-MOTA INTERGENIC
REGION.//0.98:67:34//BACTERIOPHAGE T4.//P22917
- F-PLACE1001399//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.1e-32:47:74//HOMO
30 SAPIENS (HUMAN).//P39194
- F-PLACE1001412//GLYCOPHORIN C (PAS-2') (GLYCOPROTEIN BETA) (GLPC)
(GLYCOCONNECTIN) (SIALOGLYCOPROTEIN D) (GLYCOPHORIN D) (GPD).//0.00021:125:
35 36//HOMO SAPIENS (HUMAN).//P04921
- F-PLACE1001414//CHYMOTRYPSIN/ELASTASE ISOINHIBITORS 2 TO 5.//0.99:37:
35//ASCARIS SUUM (PIG ROUNDWORM) (ASCARIS LUMBRICOIDES).//P07852
- 40 F-PLACE1001440//PROLINE-RICH PEPTIDE P-B.//0.35:16:50//HOMO SAPIENS (HUMAN)
./P02814
- 45 F-PLACE1001456//RELAXIN.//0.48:38:36//BALAENOPTERA ACUTOROSTRATA (MINKE
WHALE) (LESSER RORQUAL).//P11184
- F-PLACE1001468//HYPOTHETICAL PROTEIN MJ0602.//0.10:86:32//METHANOCOCCUS
50 JANNASCHII.//Q58019
- F-PLACE1001484//HYPOTHETICAL 7.5 KD PROTEIN IN DNAC-RPLI INTERGENIC
REGION.//1.0:47:34//BACILLUS SUBTILIS.//P37480
- 55 F-PLACE1001502//COLLAGEN 1(X) CHAIN PRECURSOR.//0.00029:118:34//BOS TAURUS
(BOVINE).//P23206

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F-PLACE1001503//HYPOTHETICAL 77.3 KD PROTEIN T05G5.8 IN CHROMOSOME III.//2.2e-07:107:30//CAENORHABDITIS ELEGANS.//P34561
 5
 F-PLACE1001517//SMALL PROTEIN INHIBITOR OF INSECT ALPHA-AMYLASES 2 (SI ALPHA-2).//0.56:22:45//SORGHUM BICOLOR MILO (SORGHUM).//P21924
 10
 F-PLACE1001534//PUTATIVE GENE PROTEIN 54.//0.43:44:40//BACTERIOPHAGE SP01.//O48408
 15
 F-PLACE1001545//HYPOTHETICAL 7.9 KD PROTEIN IN CELF-KATE INTERGENIC REGION.//0.99:70:32//ESCHERICHIA COLI.//P37795
 20
 F-PLACE1001551//CHLOROPLAST 50S RIBOSOMAL PROTEIN L32.//1.0:66:28//MARCHANTIA POLYMORPHA (LIVERWORT).//P12196
 25
 F-PLACE1001570//SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN).//0.024:120:27//HOMO SAPIENS (HUMAN).//Q15431
 30
 F-PLACE1001602//CCR4-ASSOCIATED FACTOR 1 (CAF1).//1.1e-30:90:78//MUS MUSCULUS (MOUSE).//Q60809
 F-PLACE1001603//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT).//0.054:77:33//RATTUS NORVEGICUS (RAT).//P10164
 F-PLACE1001608
 35
 F-PLACE1001610//PROBABLE E4 PROTEIN.//0.90:58:29//HUMAN PAPILLOMAVIRUS TYPE 28.//P51896
 40
 F-PLACE1001611//METALLOTHIONEIN-IG (MT-1G).//0.35:30:40//HOMO SAPIENS (HUMAN).//P13640
 45
 F-PLACE1001632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.6e-28:144:43//HOMO SAPIENS (HUMAN).//P51523
 50
 F-PLACE1001634//PHOTOSYSTEM II REACTION CENTRE N PROTEIN.//1.0:36:41//CYANIDIUM CALDARIUM (GALDIERIA SULPHURARIA).//O19926
 55
 F-PLACE1001640//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.24:47:38//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1).//P18804
 F-PLACE1001672//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.0:27:66//HOMO SAPIENS (HUMAN).//P39188
 F-PLACE1001691//HYPOTHETICAL 15.5 KD PROTEIN IN PIK1-POL2 INTERGENIC

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REGION.//0.40:81:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53842

5 F-PLACE1001692//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE II).//8.3e-41:103:55//RATTUS NORVEGICUS (RAT).//P08635

F-PLACE1001705

10 F-PLACE1001716//HYPOTHETICAL 138.5 KD PROTEIN C17H9.01 IN CHROMOSOME L//6.1e-07:157:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O13798

F-PLACE1001720

15 F-PLACE1001729//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//6.5e-05:196:32//MUS MUSCULUS (MOUSE).//P05143

20 F-PLACE1001739//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//0.00050:213:23//RATTUS NORVEGICUS (RAT).//P12839

25 F-PLACE1001740//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.4e-17:90:56//HOMO SAPIENS (HUMAN).//P39188

F-PLACE1001745//HYPOTHETICAL PROTEIN KIAA0125.//0.96:38:36//HOMO SAPIENS (HUMAN).//Q14138

30 F-PLACE1001746//CONGLUTIN DELTA-2 SMALL CHAIN.//0.98:23:43//LUPINUS ANGSTIFOLIUS (NARROW-LEAVED BLUE LUPINE).//P09930

35 F-PLACE1001748//HYPOTHETICAL 99.0 KD PROTEIN SPBC119.17.//2.9e-28:167:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O42908

40 F-PLACE1001756//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//9.2e-43:126:77//HOMO SAPIENS (HUMAN).//P39189

45 F-PLACE1001761//50S RIBOSOMAL PROTEIN L35.//0.26:42:38//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//P56057

F-PLACE1001771//TRANSIENT-RECEPTOR-POTENTIAL LIKE PROTEIN.//4.8e-35:223:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//P48994

50 F-PLACE1001781//HYPOTHETICAL 71.1 KD PROTEIN IN DSK2-CAT8 INTERGENIC REGION.//9.5e-41:194:46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q03262

55 F-PLACE1001799

F-PLACE1001810

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F-PLACE1001817//SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR
(EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA).//2.8e-40:115:
61//NEOCALLIMASTIX FRONTALIS (RUMEN FUNGUS).//P53587

5

F-PLACE1001821

10

F-PLACE1001844//IG KAPPA CHAIN V-I REGION (HAU).//0.59:89:35//HOMO SAPIENS
(HUMAN).//P01600

F-PLACE1001845

15

F-PLACE1001869//MPA43 PROTEIN.//3.5e-14:153:33//SACCHAROMYCES CEREVISIAE
(BAKER'S YEAST).//P53583

20

F-PLACE1001897//LIGATOXIN A.//1.0:43:27//PHORADENDRON LIGA (ARGENTINE
MISTLETOE).//P01540

25

F-PLACE1001912//LONG NEUROTOXIN 2 (TOXIN C).//0.57:44:45//ASTROTIA STOKESI
(STOKES'S SEA SNAKE) (DSTEIRA STOKESI).//P01381

F-PLACE1001920//LATE GENES ACTIVATOR (EARLY PROTEIN GP4) (GPF).//0.89:75:
29//BACTERIOPHAGE NF.//P09877

30

F-PLACE1001928

35

F-PLACE1001983//IMMEDIATE-EARLY PROTEIN IE180.//0.0049:51:45//PSEUDORABIES
VIRUS (STRAIN KAPLAN) (PRV).//P33479

F-PLACE1001989//PUTATIVE AMIDASE (EC 3.5.1.4).//8.9e-08:125:36//MORAXELLA
CATARRHALIS.//Q49091

40

F-PLACE1002004

45

F-PLACE1002046//LIGATIN (FRAGMENT).//1.6e-84:191:84//MUS MUSCULUS (MOUSE)
.//Q61211

F-PLACE1002052

50

F-PLACE1002066

F-PLACE1002072//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.//0.16:
77:31//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P40602

55

F-PLACE1002073//HYPOTHETICAL 118.2 KD PROTEIN F43C1.1 IN CHROMOSOME
III.//4.0e-11:174:28//CAENORHABDITIS ELEGANS.//Q09564

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F-PLACE1002090//SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72).//2.8e-57:
112:99//HOMO SAPIENS (HUMAN).//O76094

5 F-PLACE1002115//P8 MTCP-1 PROTEIN (MATURE T-CELL PROLIFERATION-1 TYPE A)
(MTCP-1 TYPE A) (P8MTCP1).//1.0:49:30//MUS MUSCULUS (MOUSE).//Q61908

10 F-PLACE1002119//T-LYMPHOCYTE ACTIVATED PROTEIN (CYCLOHEXIMIDE-INDUCED)
(CHX1) (IMMEDIATE EARLY RESPONSE 2 PROTEIN).//2.7e-11:118:36//MUS MUSCULUS
(MOUSE).//P17950

15 F-PLACE1002140//HYPOTHETICAL 12.3 KD PROTEIN IN MOBL 3'REGION (ORF 4).//0.0086:
39:46//THIOBACILLUS FERROOXIDANS.//P20088

F-PLACE1002150

20 F-PLACE1002157//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.4e-34:56:82//HOMO
SAPIENS (HUMAN).//P39189

25 F-PLACE1002163//NEUROTOXIN 1.//1.0:17:52//CENTRUROIDES SCULPTURATUS (BARK
SCORPION).//P01492

F-PLACE1002170

30 F-PLACE1002171//TRANSCRIPTION REGULATORY PROTEIN SWI3 (SWI/SNF COMPLEX
COMPONENT SWI3) (TRANSCRIPTION FACTOR

35 TYE2).//0.00023:179:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32591

F-PLACE1002205//HYPOTHETICAL 13.5 KD PROTEIN IN MOB1-SGA1 INTERGENIC
REGION.//0.77:21:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40490

40 F-PLACE1002213//HISTONE H4 (FRAGMENT).//0.62:31:32//BLEPHARISMA
JAPONICUM.//P80738

45 F-PLACE1002227//HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5'REGION.//0.41:49:
36//RHIZOBIUM LEGUMINOSARUM.//P14310

50 F-PLACE1002256//CYTOCHROME B (EC 1.10.2.2).//0.61:95:29//CAENORHABDITIS
ELEGANS.//P24890

F-PLACE1002259//HYPOTHETICAL 9.2 KD PROTEIN IN SPS1-QCR7 INTERGENIC
REGION.//0.99:22:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P56508

55 F-PLACE1002319//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC
REGION.//0.91:18:72//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53867

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F-PLACE1002342//HYPOTHETICAL PROTEIN C16.//1.0:53:32//SWINEPOX VIRUS (STRAIN KASZA) (SPV).//P32219

5 F-PLACE1002395//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//6.4e-05:127:37//PLASMODIUM VIVAX.//P08677

F-PLACE1002399

10

F-PLACE1002433//DYNACTIN, 150 KD ISOFORM (150 KD DYNEIN-ASSOCIATED POLYPEPTIDE) (DP-150) (DAP-150) (P150-GLUED).//0.00094:182:25//RATTUS NORVEGICUS (RAT).//P28023

15

F-PLACE1002437//ATP-BINDING CASSETTE TRANSPORTER 1.//4.5e-19:62:77//MUS MUSCULUS (MOUSE).//P41233

20

F-PLACE1002438//HYPOTHETICAL 141.5 KD ZINC FINGER PROTEIN IN TUB1-CPR3 INTERGENIC REGION.//0.014:63:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04545

25

F-PLACE1002450//OOCYTE ZINC FINGER PROTEIN XLCOF6 (FRAGMENT).//3.9e-28:159:38//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P18749

30

F-PLACE1002465//LARIAT DEBRANCHING ENZYME (EC 3.1.-.-).//0.0014:148:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O13765

F-PLACE1002474//FIBRILLIN 2 PRECURSOR.//2.1e-24:203:33//MUS MUSCULUS (MOUSE).//Q61555

35

F-PLACE1002477//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//0.15:65:41//HOMO SAPIENS (HUMAN).//P39193

40

F-PLACE1002493//SEMENOGELIN II PRECURSOR (SGII).//1.0:72:31//MACACA MULATTA (RHESUS MACAQUE).//Q95196

45

F-PLACE1002499//HYPOTHETICAL 39.3 KD PROTEIN C02B8.6 IN CHROMOSOME X.//2.9e-11:67:35//CAENORHABDITIS ELEGANS.//Q11096

50

F-PLACE1002500//COBALT-ZINC-CADMIUM RESISTANCE PROTEIN CZCD (CATION EFFLUX SYSTEM PROTEIN CZCD).//8.4e-11:143:32//ALCALIGENES EUTROPHUS.//P13512

F-PLACE1002514//HYPOTHETICAL 8.1 KD PROTEIN IN SPEA-METK INTERGENIC REGION (O71).//1.0:15:60//ESCHERICHIA COLI.//P46878

55

F-PLACE1002529

F-PLACE1002532//HOMEBOX PROTEIN DLX-5.//1.1e-76:183:81//MUS MUSCULUS

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(MOUSE).//P70396

5 F-PLACE1002537//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.6e-18:51:86//HOMO
SAPIENS (HUMAN).//P39195

10 F-PLACE1002571//ACTIN-LIKE PROTEIN 13E./6.0e-56:140:47//DROSOPHILA
MELANOGASTER (FRUIT FLY).//P45890

F-PLACE1002578

15 F-PLACE1002583

F-PLACE1002591//CORONIN-LIKE PROTEIN P57./5.5e-26:78:69//BOS TAURUS (BOVINE)
.//Q92176

20 F-PLACE1002598

F-PLACE1002604

25 F-PLACE1002625//HYPOTHETICAL 180.2 KD PROTEIN IN FAA4-HOR7 INTERGENIC
REGION./6.4e-08:193:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04781

30 F-PLACE1002655//ADSEVERIN (GELSOLIN-LIKE PROTEIN).//7.1e-100:210:89//MUS
MUSCULUS (MOUSE).//Q60604

35 F-PLACE1002665//MOBILIZATION PROTEIN MOBS./0.35:60:30//THIOBACILLUS
FERROOXIDANS.//P20086

F-PLACE1002685//ACTIN BINDING PROTEIN./0.052:115:29//SACCHAROMYCES EXIGUUS
(YEAST).//P38479

40 F-PLACE1002714//CIS-GOLGI MATRIX PROTEIN GM130./1.8e-06:214:30//RATTUS
NORVEGICUS (RAT).//Q62839

45 F-PLACE1002722//THROMBIN RECEPTOR PRECURSOR./2.0e-19:134:38//XENOPUS
LAEVIS (AFRICAN CLAWED FROG).//P47749

50 F-PLACE1002768//FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R)
(FOLLITROPIN RECEPTOR) (FRAGMENT)./0.43:40:35//MUS MUSCULUS (MOUSE).//P35378

F-PLACE1002772

55 F-PLACE1002775//CENTROMERE/MICROTUBULE BINDING PROTEIN CBF5
(CENTROMERE-BINDING FACTOR 5) (NUCLEOLAR PROTEIN CBF5)./4.8e-07:96:
29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14007

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F-PLACE1002782//COBALT-ZINC-CADMIUM RESISTANCE PROTEIN CZCD (CATION EFFLUX SYSTEM PROTEIN CZCD)//1.1e-07:114:35//ALCALIGENES EUTROPHUS//P13512

5 F-PLACE1002794//CUTICLE COLLAGEN 12 PRECURSOR//0.0068:98:39//CAENORHABDITIS ELEGANS//P20630

10 F-PLACE1002811//CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT KINASE 4 INHIBITOR C) (P18-INK4C)//1.1e-09:137:34//MUS MUSCULUS (MOUSE)//Q60772

15 F-PLACE1002815//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT)//0.46:35:42//HORDEUM VULGARE (BARLEY)//P17991

20 F-PLACE1002816//HYPOTHETICAL PROTEIN KIAA0288 (HA6116)//1.0e-86:201:74//HOMO SAPIENS (HUMAN)//P56524

F-PLACE1002834//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1)//1.6e-30:54:96//HOMO SAPIENS (HUMAN)//P51522

25 F-PLACE1002839//METALLOTHIONEIN-I (MT-I)//1.0:43:37//MUS MUSCULUS (MOUSE)//P02802

30 F-PLACE1002851//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR (VAI)//0.77:35:37//VICIA ANGUSTIFOLIA (COMMON VETCH)//P01065

35 F-PLACE1002853//HYPOTHETICAL 7.9 KD PROTEIN IN PE 5'REGION (ORF1)//1.0:18:55//LYMANTRIA DISPAR MULTICAPSID NUCLEAR POLYHEDROSIS VIRUS (LDMNPV)//P36866

40 F-PLACE1002881//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.1e-27:91:70//HOMO SAPIENS (HUMAN)//P39188

F-PLACE1002908//HYPOTHETICAL 33.8 KD PROTEIN R10E11.4 IN CHROMOSOME III//2.0e-31:148:46//CAENORHABDITIS ELEGANS//P34548

45 F-PLACE1002941//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.6e-11:40:85//HOMO SAPIENS (HUMAN)//P39195

50 F-PLACE1002962//ENDOTHELIN-1 PRECURSOR (ET-1) (FRAGMENT)//0.90:38:36//CANIS FAMILIARIS (DOG)//P13206

55 F-PLACE1002968//TOXIN IV-5 PRECURSOR (TITYUSTOXIN) (FRAGMENT)//0.97:26:38//TITYUS SERRULATUS (BRAZILIAN SCORPION)//P01496

F-PLACE1002991//PUTATIVE AMIDASE (EC 3.5.1.4)//3.3e-20:120:41//METHANOCOCCUS JANNASCHII//Q58560

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F-PLACE1002993//HYPOTHETICAL 17.8 KD PROTEIN IN SMPA-SMPB INTERGENIC
 REGION (F158).//0.00045:93:23//ESCHERICHIA COLI.//P52121
 5 F-PLACE1002996//PUTATIVE REGULATORY PROTEIN TSC-22 (TGFB STIMULATED CLONE
 22 HOMOLOG).//0.17:91:29//GALLUS GALLUS (CHICKEN).//Q91012
 10 F-PLACE1003025//SUPPRESSOR PROTEIN SRP40.//0.0079:214:24//SACCHAROMYCES
 CEREVISIAE (BAKER'S YEAST).//P32583
 15 F-PLACE1003027//HYPOTHETICAL 128.6 KD PROTEIN ZK1098.10 IN CHROMOSOME
 III.//1.3e-49:167:63//CAENORHABDITIS ELEGANS.//P34609
 F-PLACE1003044//SPORE COAT PROTEIN D.//0.97:24:45//BACILLUS SUBTILIS.//P07791
 20 F-PLACE1003045
 F-PLACE1003092
 25 F-PLACE1003100//HEP27 PROTEIN (PROTEIN D).//3.9e-51:188:57//HOMO SAPIENS
 (HUMAN).//Q13268
 F-PLACE1003108
 30 F-PLACE1003136
 F-PLACE1003145//BUTYROPHILIN PRECURSOR (BT).//0.00024:170:24//BOS TAURUS
 35 (BOVINE).//P18892
 F-PLACE1003153//HUNCHBACK PROTEIN (FRAGMENT).//1.0:32:37//LOCUSTA
 40 MIGRATORIA (MIGRATORY LOCUST).//Q01777
 F-PLACE1003174//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN-
 PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//6.3e-05:54:38//ARABIDOPSIS
 45 THALIANA (MOUSE-EAR CRESS).//P42743
 F-PLACE1003176//HYPOTHETICAL 62.3 KD PROTEIN IN PCS60-ABD1 INTERGENIC
 REGION.//0.24:74:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38319
 50 F-PLACE1003190//SOF1 PROTEIN.//1.0e-52:158:41//SACCHAROMYCES CEREVISIAE
 (BAKER'S YEAST).//P33750
 F-PLACE1003200
 55 F-PLACE1003205//SPERM PROTAMINE P1.//0.074:20:45//CAENOLESTES
 FULIGINOSUS.//P42131

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F-PLACE1003238//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//0.013:20:
 55//HOMO SAPIENS (HUMAN).//Q15391
 5
 F-PLACE1003249//HYPOTHETICAL PROTEIN KIAA0125.//0.98:48:37//HOMO SAPIENS
 (HUMAN).//Q14138
 10
 F-PLACE1003256//OMEGA-CONOTOXINS GVIA, GVIB AND GVIC PRECURSOR (SHAKER
 PEPTIDE).//0.84:53:30//CONUS GEOGRAPHUS (GEOGRAPHY CONE).//P01522
 15
 F-PLACE1003258//EARLY EMBRYOGENESIS ZYG-11 PROTEIN.//4.1e-18:70:
 47//CAENORHABDITIS ELEGANS.//P21541
 F-PLACE1003296//SPECTRIN BETA CHAIN, ERYTHROCYTE.//0.063:160:24//HOMO
 SAPIENS (HUMAN).//P11277
 20
 F-PLACE1003302//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//9.4e-69:84:
 94//HOMO SAPIENS (HUMAN).//P51522
 25
 F-PLACE1003334//NUCLEOBINDIN PRECURSOR (NUCB1) (BONE 63 KD CALCIUM-
 BINDING PROTEIN).//0.029:125:24//RATTUS NORVEGICUS (RAT).//Q63083
 30
 F-PLACE1003342//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.97:44:40//DROSOPHILA
 MELANOGASTER (FRUIT FLY).//Q01643
 F-PLACE1003343//GENE 11 PROTEIN.//1.0:37:37//SPIROPLASMA VIRUS SPV1-R8A2
 B.//P15902
 35
 F-PLACE1003353//SH2/SH3 ADAPTOR CRK (ADAPTER MOLECULE CRK) (CRK2).//6.4e-05:
 69:40//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P87378
 40
 F-PLACE1003361//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.6e-23:66:75//HOMO
 SAPIENS (HUMAN).//P39192
 F-PLACE1003366//SMALL PROLINE-RICH PROTEIN 2-1.//0.62:19:57//HOMO SAPIENS
 45 (HUMAN).//P35326
 F-PLACE1003369//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//4.3e-06:102:
 42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323
 50
 F-PLACE1003373//PROTEIN Q300.//0.042:29:37//MUS MUSCULUS (MOUSE).//Q02722
 55
 F-PLACE1003375//OLFACTORY RECEPTOR 11 (M49) (FRAGMENT).//0.99:46:34//MUS
 MUSCULUS (MOUSE).//Q60890
 F-PLACE1003383

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5 F-PLACE1003394//RAS-RELATED PROTEIN RAB-14.//2.8e-80:166:89//RATTUS
NORVEGICUS (RAT).//P35287

F-PLACE1003401

10 F-PLACE1003420//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//8.1e-17:138:
37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40556

F-PLACE1003454

15 F-PLACE1003478

F-PLACE1003493//ENDOTHELIAL CELL MULTIMERIN PRECURSOR.//3.4e-11:123:
20 32//HOMO SAPIENS (HUMAN).//Q13201

F-PLACE1003516//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.0e-32:68:76//HOMO
SAPIENS (HUMAN).//P08547

25 F-PLACE1003519//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//9.2e-17:77:50//HOMO
SAPIENS (HUMAN).//P39188

30 F-PLACE1003521//HYPOTHETICAL BAMHI-ORF9 PROTEIN.//1.0:38:42//FOWLPOX VIRUS
(ISOLATE HP-438[MUNICH]).//P14366

F-PLACE1003528//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.96:32:40//XENOPUS
35 LAEVIS (AFRICAN CLAWED FROG).//P03931

F-PLACE1003537//CEF PROTEIN.//0.92:47:29//BACTERIOPHAGE T4.//Q01436

40 F-PLACE1003553

F-PLACE1003566//HYPOTHETICAL BAMHI-ORF9 PROTEIN.//1.0:32:34//FOWLPOX VIRUS
(ISOLATE HP-438[MUNICH]).//P14366

45 F-PLACE1003575

F-PLACE1003583//PROBABLE E5 PROTEIN.//0.16:64:31//HUMAN PAPILLOMAVIRUS TYPE
50 35.//P27226

F-PLACE1003584

55 F-PLACE1003592//EXCISIONASE.//0.26:19:52//BACTERIOPHAGE PHI-80.//P05998

F-PLACE1003593//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:42:30//OVIS ARIES
(SHEEP).//O78751

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- 5 F-PLACE1003596//OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG.//6.3e-87:238:67//CAENORHABDITIS ELEGANS.//P46975
- 10 F-PLACE1003602//HYPOTHETICAL 11.0 KD PROTEIN IN FAA3-MAS3 INTERGENIC REGION.//8.4e-17:98:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40554
- 15 F-PLACE1003605//HAP5 TRANSCRIPTIONAL ACTIVATOR.//2.0e-09:82:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q02516
- 20 F-PLACE1003611//PANCREATIC SECRETORY TRYPSIN INHIBITOR.//0.99:32:43//CANIS FAMILIARIS (DOG).//P04542
- 25 F-PLACE1003618//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.7e-65:229:58//HOMO SAPIENS (HUMAN).//P08547
- 30 F-PLACE1003625//30S RIBOSOMAL PROTEIN S20 (FRAGMENT).//1.0:56:26//PROTEUS MIRABILIS.//P42275
- 35 F-PLACE1003638//PROTEIN Q300.//0.079:41:39//MUS MUSCULUS (MOUSE).//Q02722
- 40 F-PLACE1003669//TRICHOHYALIN.//2.9e-07:180:30//OVIS ARIES (SHEEP).//P22793
- 45 F-PLACE1003704//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//3.3e-16:98:40//HOMO SAPIENS (HUMAN).//Q08170
- 50 F-PLACE1003709//HYPOTHETICAL 59.5 KD PROTEIN IN CCT3-CCT8 INTERGENIC REGION.//2.8e-07:128:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47074
- 55 F-PLACE1003711//ALPHA/BETA-GLIADIN PRECURSOR (PROLAMIN) (CLASS A-IV).//5.0e-05:88:30//TRITICUM AESTIVUM (WHEAT).//P04724
- F-PLACE1003723//TYROSINE-PROTEIN KINASE SRM (EC 2.7.1.112) (PTK70).//6.0e-06:98:36//MUS MUSCULUS (MOUSE).//Q62270
- F-PLACE1003738//OOCYTE ZINC FINGER PROTEIN XLCOF6 (FRAGMENT).//2.5e-45:147:46//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P18749
- F-PLACE1003760//CYTOCHROME B (EC 1.10.2.2).//0.91:49:34//TRYPANOSOMA BRUCEI BRUCEI.//P00164
- F-PLACE1003762//METALLOTHIONEIN-LIKE PROTEIN TYPE 2.//0.98:28:32//MALUS DOMESTICA (APPLE) (MALUS SYLVESTRIS).//O24058
- F-PLACE1003768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//8.5e-19:123:37//HOMO SAPIENS (HUMAN).//P08547

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F-PLACE1003771

5 F-PLACE1003783//SRY-RELATED PROTEIN ADW2 (FRAGMENT)//1.0:29:37//ALLIGATOR
MISSISSIPPIENSIS (AMERICAN ALLIGATOR)//P40634

10 F-PLACE1003784//HYPOTHETICAL 98.1 KD PROTEIN IN SPX19-GCR2 INTERGENIC
REGION//1.2e-13:199:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40164

15 F-PLACE1003795//EC PROTEIN I/II (ZINC-METALLOTHIONEIN CLASS II)//0.67:53:
30//TRITICUM AESTIVUM (WHEAT)//P30569

F-PLACE1003833//METHIONYL-TRNA FORMYLTRANSFERASE (EC 2.1.2.9)//0.99:158:
28//THERMUS AQUATICUS (SUBSP. THERMOPHILUS)//P43523

20 F-PLACE1003850

F-PLACE1003858//HUNCHBACK PROTEIN (FRAGMENT)//0.37:28:42//LITHOBIUS
FORFICATUS//Q02030

25 F-PLACE1003864//OUTER MEMBRANE LIPOPROTEIN LOLB PRECURSOR//0.0046:116:
31//ACTINOBACILLUS ACTINOMYCETEMCOMITANS (HAEMOPHILUS
ACTINOMYCETEMCOMITANS)//O52727

30 F-PLACE1003870

35 F-PLACE1003885//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE
ADENYLYLTRANSFERASE) (FRAGMENT)//1.6e-92:166:75//HOMO SAPIENS (HUMAN)
//P51003

40 F-PLACE1003886//IMMEDIATE-EARLY PROTEIN IE180//0.54:96:34//PSEUDORABIES VIRUS
(STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV)//P11675

45 F-PLACE1003888//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE
PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-
DELTA-1) (PLC-III) (FRAGMENT)//8.8e-54:260:46//BOS TAURUS (BOVINE)//P10895

50 F-PLACE1003892//PROBABLE E5 PROTEIN//1.0:13:61//HUMAN PAPILLOMAVIRUS TYPE
18//P06792

55 F-PLACE1003900//BETA-FRUCTOFURANOSIDASE, SOLUBLE ISOENZYME I (EC 3.2.1.26)
(SUCROSE-6- PHOSPHATE HYDROLASE) (INVERTASE) (FRAGMENTS)//0.58:49:
36//DAUCUS CAROTA (CARROT)//P80065

F-PLACE1003903//CTP SYNTHASE (EC 6.3.4.2) (UTP-AMMONIA LIGASE) (CTP
SYNTHETASE)//3.8e-52:92:85//HOMO SAPIENS (HUMAN)//P17812

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- 5 F-PLACE1003915//PROBABLE ARGINYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.19)
(ARGININE- TRNA LIGASE) (ARGRS).//2.6e-26:202:36//SACCHAROMYCES CEREVISIAE
(BAKER'S YEAST).//Q05506
- 10 F-PLACE1003923//HISTIDYL-TRNA SYNTHETASE (EC 6.1.1.21) (HISTIDINE-TRNA LIGASE)
(HISRS).//0.94:65:29//STREPTOCOCCUS EQUISIMILIS.//P30053
- 15 F-PLACE1003932//HYPOTHETICAL 17.3 KD PROTEIN IN SEC15-SAP4 INTERGENIC
REGION.//0.098:79:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53074
- 20 F-PLACE1003936
- F-PLACE1003968//5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK
GAMMA-1 CHAIN).//4.7e-68:164:78//RATTUS NORVEGICUS (RAT).//P80385
- 25 F-PLACE1004103///// ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.9e-14:60:73//HOMO
SAPIENS (HUMAN).//P39192
- 30 F-PLACE1004104//EXOCYST COMPLEX COMPONENT SEC5.//0.020:202:
20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P89102
- F-PLACE1004114///// ALU SUBFAMILY J WARNING ENTRY !!!!!/2.1e-15:69:60//HOMO
SAPIENS (HUMAN).//P39188
- 35 F-PLACE1004118//REGULATORY PROTEIN E2.//0.73:58:36//CANINE ORAL
PAPILLOMAVIRUS (COPV).//Q89420
- F-PLACE1004128//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4
(TRANSDUCIN BETA CHAIN 4).//7.7e-62:108:100//MUS MUSCULUS (MOUSE).//P29387
- 40 F-PLACE1004149//PROBABLE NUCLEAR ANTIGEN.//0.0011:73:42//PSEUDORABIES VIRUS
(STRAIN KAPLAN) (PRV).//P33485
- 45 F-PLACE1004156//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//0.00061:39:
48//OWENIA FUSIFORMIS.//P21260
- 50 F-PLACE1004161//PLASMINOGEN-BINDING PROTEIN PAM PRECURSOR (FRAGMENT)
.//0.033:108:27//STREPTOCOCCUS PYOGENES.//P49054
- 55 F-PLACE1004183//HYPOTHETICAL 64.3 KD PROTEIN IN CDC12-ERP5 INTERGENIC
REGION.//4.0e-07:146:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38817
- F-PLACE1004197//BUTYROPHILIN PRECURSOR (BT).//5.9e-11:208:27//MUS MUSCULUS
(MOUSE).//Q62556

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- F-PLACE1004203//PROTEIN A39.//8.5e-18:139:33//VACCINIA VIRUS (STRAIN COPENHAGEN).//P21062
- 5 F-PLACE1004242//PHOTOSYSTEM II REACTION CENTRE J PROTEIN.//1.0:28:42//PISUM SATIVUM (GARDEN PEA).//P13555
- 10 F-PLACE1004256//MYOSIN HEAVY CHAIN D (MHC D).//0.73:134:25//CAENORHABDITIS ELEGANS.//P02567
- 15 F-PLACE1004257//HYPOTHETICAL PROTEIN HI0490.//0.13:75:29//HAEMOPHILUS INFLUENZAE.//P44006
- F-PLACE1004258//COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGEN) (FRAGMENT).//0.027:128:35//HOMO SAPIENS (HUMAN).//P25067
- 20 F-PLACE1004270//LARGE TEGUMENT PROTEIN.//1.8e-10:100:44//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03186
- 25 F-PLACE1004274//HYPOTHETICAL PROTEIN E-95.//0.44:61:42//HUMAN ADENOVIRUS TYPE 2.//P03286
- 30 F-PLACE1004277//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.0013:55:38//BOS TAURUS (BOVINE).//P25508
- F-PLACE1004284//7 KD PROTEIN (ORF 4).//1.0:63:23//CHRYSANTHEMUM VIRUS B (CVB) .//P37990
- 35 F-PLACE1004289//SPERM PROTAMINE P3.//0.00057:22:77//MUS MUSCULUS (MOUSE) .//Q62100
- 40 F-PLACE1004302//SERINE/THREONINE PROTEIN KINASE AFSK (EC 2.7.1.-).//0.0065:148:29//STREPTOMYCES COELICOLOR.//P54741
- 45 F-PLACE1004316//AUTOPHAGY PROTEIN APG5.//8.8e-06:117:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12380
- F-PLACE1004336//COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR.//0.0027:83:36//HOMO SAPIENS (HUMAN).//P53420
- 50 F-PLACE1004358//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//2.9e-05:200:33//GALLUS GALLUS (CHICKEN).//P02457
- 55 F-PLACE1004376//AXONEME-ASSOCIATED PROTEIN MST101(2).//2.4e-05:179:29//DROSOPHILA HYDEI (FRUIT FLY).//Q08696
- F-PLACE1004384//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!1.6e-28:46:76//HOMO

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SAPIENS (HUMAN).//P39194

5 F-PLACE1004388//HYPOTHETICAL 75.2 KD PROTEIN IN ACS1-GCV3 INTERGENIC
REGION.//5.7e-34:202:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39722

10 F-PLACE1004405//NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ (N-
ACETYLNEURAMINYLLACTOSE- BINDING FIBRILLAR HEMAGGLUTININ RECEPTOR-
BINDING SUBUNIT) (NLBH) (FLAGELLAR SHEATH ADHESIN) (ADHESIN A) (FRAGMENT)
.//0.93:74:33//HELICOBACTER ACINONYX.//Q47947

15 F-PLACE1004425//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.81:70:42//HOMO SAPIENS
(HUMAN).//P39195

20 F-PLACE1004428//PRISTANOYL-COA OXIDASE (EC 1.3.3.-)//1.9e-31:203:39//RATTUS
NORVEGICUS (RAT).//Q63448

25 F-PLACE1004437//ISOCITRATE DEHYDROGENASE [NAD], MITOCHONDRIAL SUBUNIT
BETA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+-SPECIFIC ICDH)
(FRAGMENT).//4.2e-93:140:100//MACACA FASCICULARIS (CRAB EATING MACAQUE)
(CYNOMOLGUS MONKEY).//Q28479

30 F-PLACE1004451//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.00013:40:62//HOMO
SAPIENS (HUMAN).//P39188

F-PLACE1004460//MATERNAL TUDOR PROTEIN.//0.0066:218:23//DROSOPHILA
MELANOGASTER (FRUIT FLY).//P25823

35 F-PLACE1004467//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//7.8e-10:33:87//HOMO
SAPIENS (HUMAN).//P39193

40 F-PLACE1004471//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.0e-56:92:
58//HOMO SAPIENS (HUMAN).//P51522

45 F-PLACE1004473//HYPOTHETICAL 54.3 KD PROTEIN C23D3.03C IN CHROMOSOME
I.//0.019:136:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09844

F-PLACE1004491//LYSIS PROTEIN.//0.95:53:30//BACTERIOPHAGE FR.//P19903

50 F-PLACE1004506//AUTOIMMUNOGENIC CANCER/TESTIS ANTIGEN NY-ESO-1 (LAGE-1)
.//0.58:66:34//HOMO SAPIENS (HUMAN).//P78358

55 F-PLACE1004510//TRANSCRIPTION INITIATION FACTOR TFIID 150 KD SUBUNIT (TAFII-
150) (TAFII150).//3.0e-07:63:46//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24325

F-PLACE1004516//HYPOTHETICAL PROTEIN 5' TO ASP-RICH AND HIS-RICH PROTEINS
(FRAGMENT).//0.95:62:29//PLASMODIUM FALCIPARUM (ISOLATE FCM17 / SENEGAL)

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./P14587

5 F-PLACE1004518//METALLOTHIONEIN 10-III (MT-10-III).//0.91:28:42//MYTILUS EDULIS
(BLUE MUSSEL).//P80248

10 F-PLACE1004548//DIHYDROPYRIDINE-SENSITIVE L-TYPE, SKELETAL MUSCLE CALCIUM
CHANNEL GAMMA SUBUNIT.//0.94:75:32//ORYCTOLAGUS CUNICULUS (RABBIT).//P19518

F-PLACE1004550//CUTICLE COLLAGEN 2.//0.90:155:31//CAENORHABDITIS
ELEGANS.//P17656

15 F-PLACE1004564//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD
SUBUNIT (CPSF 100 KD SUBUNIT).//3.2e-70:121:100//BOS TAURUS (BOVINE).//Q10568

20 F-PLACE1004629//PROTEIN OS-9 PRECURSOR.//1.7e-10:132:36//HOMO SAPIENS
(HUMAN).//Q13438

F-PLACE1004645//TRANSCRIPTION INITIATION FACTOR IIB HOMOLOG (TFIIB).//0.00036:
100:30//PYROCOCCUS FURIOSUS.//Q51731

25 F-PLACE1004646//PROBABLE UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9).//0.91:58:
29//KLEBSIELLA PNEUMONIAE.//Q48481

30 F-PLACE1004658//GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 4 PRECURSOR
(N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2D) (NR2D) (NMDAR2D).//0.031:134:
32//MUS MUSCULUS (MOUSE).//Q03391

35 F-PLACE1004664//HYPOTHETICAL 180.2 KD PROTEIN IN FAA4-HOR7 INTERGENIC
REGION.//0.025:125:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04781

40 F-PLACE1004672//HYPOTHETICAL 36.7 KD PROTEIN C2F7:14C IN CHROMOSOME I.//7.6e-
52:158:56//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09704

F-PLACE1004674//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257)
./1.4e-88:144:93//MUS MUSCULUS (MOUSE).//P12815

45 F-PLACE1004681//CCR4-ASSOCIATED FACTOR 1 (CAF1).//1.0e-34:70:100//MUS
MUSCULUS (MOUSE).//Q60809

50 F-PLACE1004686//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//3.4e-08:48:62//HOMO
SAPIENS (HUMAN).//P39192

55 F-PLACE1004691//METALLOTHIONEIN (MT).//0.064:24:45//ARIANTA
ARBUSTORUM.//P55946

F-PLACE1004693

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F-PLACE1004716//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//1.0.27:37//PAN
 PANISCUS (PYGMY CHIMPANZEE) (BONOBO)//Q35587
 5
 F-PLACE1004722//HYPOTHETICAL 61.5 KD PROTEIN IN CLA4-MID1 INTERGENIC
 REGION//0.95:53:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P48565
 10
 F-PLACE1004736//NEURONAL AXONAL MEMBRANE PROTEIN NAP-22//0.014:163:
 30//RATTUS NORVEGICUS (RAT)//Q05175
 F-PLACE1004740//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.9e-09:37:70//HOMO
 15 SAPIENS (HUMAN)//P39194
 F-PLACE1004743//HYPOTHETICAL 12.6 KD PROTEIN IN ALGR3 3'REGION//0.99:72:
 33//PSEUDOMONAS AERUGINOSA//P21484
 20
 F-PLACE1004751//CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-
 SIALYLTRANSFERASE (EC 2.4.99.-) (BETA-GALACTOSIDE ALPHA-2,3-
 SIALYLTRANSFERASE) (ST3GALIII) (ALPHA 2,3-ST) (GAL-NAC6S) (STZ) (SIAT4-C) (SAT-3)
 25 (ST-4)//2.2e-08:90:38//HOMO SAPIENS (HUMAN)//Q11206
 F-PLACE1004773//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN)//3.2e-
 25:233:32//HOMO SAPIENS (HUMAN)//P16157
 30
 F-PLACE1004777//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN)
 //8.1e-26:210:30//RATTUS NORVEGICUS (RAT)//P30337
 F-PLACE1004793//ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN
 35 GP36]//0.00062:106:25//MOUSE MAMMARY TUMOR VIRUS (STRAIN BR6)//P10259
 F-PLACE1004804
 40
 F-PLACE1004813//HYPOTHETICAL PROTEIN UL12//1.0.22:40//HUMAN
 CYTOMEGALOVIRUS (STRAIN AD169)//P16777
 F-PLACE1004814//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II//2.8e-
 45 06:136:25//CAENORHABDITIS ELEGANS//Q09217
 F-PLACE1004815
 50
 F-PLACE1004824//HYPOTHETICAL 106.7 KD PROTEIN IN MUP1-SPR3 INTERGENIC
 REGION//2.3e-09:70:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53236
 F-PLACE1004827//HYPOTHETICAL 9.4 KD PROTEIN IN FLAL 3'REGION (ORF3)//0.54:25:
 55 56//BACILLUS LICHENIFORMIS//P22754

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F-PLACE1004836//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.0066:12:66//BOS TAURUS (BOVINE).//P20072

5 F-PLACE1004838

F-PLACE1004840

10 F-PLACE1004868//MALE STERILITY PROTEIN 2.//4.0e-16:172:30//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q08891

F-PLACE1004885

15

F-PLACE1004900//MAST CELL DEGRANULATING PEPTIDE PRECURSOR (MCDP) (MCD) (PEPTIDE 401).//1.0:23:47//APIS MELLIFERA (HONEYBEE).//P01499

20 F-PLACE1004902//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//7.3e-15:94:47//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O42643

25 F-PLACE1004913//HYPOTHETICAL 7.2 KD PROTEIN IN BCSA-DEGR INTERGENIC REGION.//1.0:42:33//BACILLUS SUBTILIS.//P54165

30 F-PLACE1004918//HYPOTHETICAL 12.4 KD PROTEIN IN RPS21B-MRS3 INTERGENIC REGION.//0.98:50:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47012

F-PLACE1004930//HYPOTHETICAL PROTEIN MJ0562.//0.82:44:36//METHANOCOCCUS JANNASCHII.//Q57982

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F-PLACE1004934

40 F-PLACE1004937//HYPOTHETICAL 67.1 KD TRP-ASP REPEATS CONTAINING PROTEIN C57A10.05C IN CHROMOSOME I.//9.0e-10:87:33//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87053

45 F-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//4.0e-14:184:25//CAENORHABDITIS ELEGANS.//Q11073

F-PLACE1004972//BROMELAIN INHIBITOR 2 (BI-II) (BROMELAIN INHIBITOR VI) (BI-VI).//1.0:35:37//ANANAS COMOSUS (PINEAPPLE).//P27478

50

F-PLACE1004979//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//5.3e-30:55:72//HOMO SAPIENS (HUMAN).//P39192

55 F-PLACE1004982//M PROTEIN, SEROTYPE 12 PRECURSOR (FRAGMENT).//0.00049:124:27//STREPTOCOCCUS PYOGENES.//P19401

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F-PLACE1004985//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//1.0:26:34//LUMBRICUS TERRESTRIS (COMMON EARTHWORM)//Q34942

5 F-PLACE1005026//TELOMERE-BINDING PROTEIN HOMOLOG//0.0011:179:27//EUPLOTES CRASSUS//Q06183

F-PLACE1005027

10

F-PLACE1005046//ANNEXIN VII (SYNEXIN) (FRAGMENT)//0.082:44:36//BOS TAURUS (BOVINE)//P20072

15 F-PLACE1005052//MALE SPECIFIC SPERM PROTEIN MST84DD//0.38:36:44//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01645

F-PLACE1005055

20

F-PLACE1005066//RING CANAL PROTEIN (KELCH PROTEIN)//2.9e-38:194:39//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q04652

25 F-PLACE1005077

F-PLACE1005085//INSECT TOXIN 1 (BOT IT1)//0.85:36:33//BUTHUS OCCITANUS TUNETANUS (COMMON EUROPEAN SCORPION)//P55902

30

F-PLACE1005086//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/8.5e-38:93:76//HOMO SAPIENS (HUMAN)//P39194

35 F-PLACE1005101//HYPOTHETICAL PROTEIN ZAP128 (FRAGMENT)//1.6e-11:35:100//HOMO SAPIENS (HUMAN)//P49753

40 F-PLACE1005102//ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING PROTEIN) (LP-1) (ZINC FINGER PROTEIN Z13)//3.0e-14:110:38//MUS MUSCULUS (MOUSE)//Q60821

45 F-PLACE1005108//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF) //0.41:35:34//BOS TAURUS (BOVINE)//P37359

F-PLACE1005111//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L) (CHARGERIN II)//1.0:29:41//RATTUS NORVEGICUS (RAT)//P11608

50

F-PLACE1005128//RABPHILIN-3A (FRAGMENT)//5.9e-05:95:36//MUS MUSCULUS (MOUSE) //P47708

55 F-PLACE1005146//FIBROBLAST GROWTH FACTOR INDUCIBLE PROTEIN 15 (FIN15)//0.17:48:35//MUS MUSCULUS (MOUSE)//Q61075

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F-PLACE1005162//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.0e-31:60:76//HOMO SAPIENS (HUMAN).//P39189

5 F-PLACE1005176

F-PLACE1005181//HYPOTHETICAL 7 KD PROTEIN.//1.0:31:45//MEASLES VIRUS (STRAIN HALLE) (SUBACUTE SCLEROSE PANENCEPHALITIS VIRUS).//P06831

10

F-PLACE1005187//GLUCAN SYNTHASE-1 (EC 2.4.1.34) (1,3-BETA-GLUCAN SYNTHASE) (UDP-GLUCOSE-1,3-BETA-D-GLUCAN GLUCOSYLTRANSFERASE).//0.0025:58:34//NEUROSPORA CRASSA.//P38678

15

F-PLACE1005206//HYPOTHETICAL 10.7 KD PROTEIN.//0.34:57:42//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20511

20

F-PLACE1005232//AMELOGENIN, Y ISOFORM PRECURSOR.//0.70:60:35//HOMO SAPIENS (HUMAN).//Q99218

25

F-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//0.0017:114:27//PHYCOMYCES BLAKESLEEANUS.//Q01577

30

F-PLACE1005261//HYPOTHETICAL 90.8 KD PROTEIN T05H10.7 IN CHROMOSOME II.//1.2e-38:206:41//CAENORHABDITIS ELEGANS.//Q10003

F-PLACE1005266

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F-PLACE1005277//PROTEIN GURKEN PRECURSOR.//0.58:95:29//DROSOPHILA MELANOGASTER (FRUIT FLY).//P42287

40

F-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP).//2.0e-12:211:29//GALLUS GALLUS (CHICKEN).//P53352

F-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//1.8e-78:205:78//BOS TAURUS (BOVINE).//P08760

45

F-PLACE1005308//WOUND-INDUCED BASIC PROTEIN.//0.99:40:40//PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN).//Q09020

50

F-PLACE1005313//HYPOTHETICAL 8.7 KD PROTEIN IN LEUX-FECE INTERGENIC REGION (O67).//0.15:36:41//ESCHERICHIA COLI.//P39355

55

F-PLACE1005327//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS) .//1.0:19:52//HOMO SAPIENS (HUMAN).//P30808

F-PLACE1005331//BREAKPOINT CLUSTER REGION PROTEIN.//0.00021:98:35//HOMO SAPIENS (HUMAN).//P11274

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F-PLACE1005335//IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-3.//0.37:98:33//MUS
MUSCULUS (MOUSE).//P81067

5

F-PLACE1005373//PSEUDOURIDYLATE SYNTHASE 4 (EC 4.2.1.70) (PSEUDOURIDINE
SYNTHASE 4) (TRNA PSEUDOURIDINE 55 SYNTHASE) (PSI55 SYNTHASE)
(PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//0.010:96:
10 28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48567

F-PLACE1005374

15 F-PLACE1005409

F-PLACE1005453//LICHENASE PRECURSOR (EC 3.2.1.73) (ENDO-BETA-1,3-1,4
GLUCANASE).//1.0:50:32//NICOTIANA PLUMBAGINIFOLIA (LEADWORT-LEAVED TOBACCO)
20 .//P07979

F-PLACE1005467//KERATIN, FEATHER (F-KER).//0.0095:42:35//LARUS NOVAE-
HOLLANDIAE (SILVER GULL).//P02451

25

F-PLACE1005471//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.23:
49:32//PHYTOPHTHORA INFESTANS (POTATO LATE BLIGHT FUNGUS).//Q37598

30 F-PLACE1005477//HYPOTHETICAL PROTEIN ORF-1137.//9.6e-13:115:38//MUS MUSCULUS
(MOUSE).//P11260

F-PLACE1005480//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT).//0.97:33:30//HORDEUM
35 VULGARE (BARLEY).//P17991

F-PLACE1005481//HUNCHBACK PROTEIN (FRAGMENT).//0.30:52:38//APIS MELLIFERA
(HONEYBEE).//P31504

40

F-PLACE1005494//TRANSIENT-RECEPTOR-POTENTIAL PROTEIN.//3.9e-05:87:
33//DROSOPHILA MELANOGASTER (FRUIT FLY).//P19334

45 F-PLACE1005502

F-PLACE1005526//IMMEDIATE-EARLY PROTEIN IE180.//4.6e-05:132:32//PSEUDORABIES
VIRUS (STRAIN KAPLAN) (PRV).//P33479

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F-PLACE1005528//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//3.4e-09:31:74//HOMO
SAPIENS (HUMAN).//P39195

55 F-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME
III.//9.7e-50:148:58//CAENORHABDITIS ELEGANS.//Q09251

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F-PLACE1005550//HYPOTHETICAL 40.2 KD PROTEIN K12H4.3 IN CHROMOSOME III.//3.0e-21:127:37//CAENORHABDITIS ELEGANS.//P34524

5 F-PLACE1005554//CYTOCHROME B (EC 1.10.2.2) (FRAGMENT).//0.84:38:31//DIPODOMYS CALIFORNICUS (KANGAROO RAT).//P16359

10 F-PLACE1005557//60S RIBOSOMAL PROTEIN L27.//4.8e-09:60:48//CRYPTOCOCCUS NEOFORMANS (FILOBASIDIELLA NEOFORMANS).//P46288

F-PLACE1005574//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.89:44:29//BOS TAURUS (BOVINE).//P03929

15 F-PLACE1005584//MALE SPECIFIC SPERM PROTEIN MST87F.//0.00030:33:48//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175

20 F-PLACE1005595//IMMEDIATE-EARLY PROTEIN IE180.//0.00048:162:30//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675

25 F-PLACE1005603//HIGH-MOBILITY-GROUP PROTEIN (NONHISTONE CHROMOSOMAL PROTEIN).//0.00034:83:30//TETRAHYMENA PYRIFORMIS.//P40625

F-PLACE1005611//DNAJ PROTEIN.//8.6e-20:108:48//CLOSTRIDIUM ACETOBUTYLICUM.//P30725

30 F-PLACE1005623//EXTRACELLULAR SIGNAL-REGULATED KINASE 5 (EC 2.7.1.-) (ERK5) (ERK4) (BMK1 KINASE).//0.80:116:31//HOMO SAPIENS (HUMAN).//Q13164

35 F-PLACE1005630//INTERLEUKIN-14 PRECURSOR (IL-14) (HIGH MOLECULAR WEIGHT B-CELL GROWTH FACTOR) (HMW-BCGF).//0.0024:74:39//HOMO SAPIENS (HUMAN).//P40222

40 F-PLACE1005639//EXTRACELLULAR MATRIX PROTEIN 1 (SECRETORY COMPONENT P85) (FRAGMENT).//0.72:18:61//RATTUS NORVEGICUS (RAT).//Q62894

45 F-PLACE1005646//RNA HELICASE-LIKE PROTEIN DB10.//4.8e-29:172:45//NICOTIANA SYLVESTRIS (WOOD TOBACCO).//P46942

F-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE).//3.7e-64:133:75//MESOCRICETUS AURATUS (GOLDEN HAMSTER).//Q60561

50 F-PLACE1005666//CHLOROPLAST 50S RIBOSOMAL PROTEIN L28.//0.57:36.41//PORPHYRA PURPUREA.//P51224

55 F-PLACE1005698//HYPOTHETICAL PROTEIN IN SIGD 3'REGION (ORFC) (FRAGMENT).//0.50:61:29//BACILLUS SUBTILIS.//P40405

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F-PLACE1005727//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
(FRAGMENT).//0.46:27:51//BRASSICA NAPUS (RAPE).//P40603

5 F-PLACE1005730//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT).//0.95:21:
52//ORYCTOLAGUS CUNICULUS (RABBIT).//P02456

10 F-PLACE1005739//INTERFERON-GAMMA INDUCIBLE PROTEIN MG11.//3.4e-46:111:
53//MUS MUSCULUS (MOUSE).//Q60710

15 F-PLACE1005755//HYPOTHETICAL 70.2 KD PROTEIN IN GSH1-CHS6 INTERGENIC
REGION.//2.6e-12:66:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P42951

F-PLACE1005763//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC
3.1.2.14) (THIOESTERASE II).//1.5e-26:69:57//RATTUS NORVEGICUS (RAT).//P08635

20 F-PLACE1005799//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN)
.//0.028:96:32//HOMO SAPIENS (HUMAN).//P26371

25 F-PLACE1005802//PROTEIN PROSPERO.//0.86:64:42//DROSOPHILA MELANOGASTER
(FRUIT FLY).//P29617

30 F-PLACE1005803//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN
MYD116.//1.0:95:25//MUS MUSCULUS (MOUSE).//P17564

F-PLACE1005804//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-
MANNOSIDASE 1B).//2.8e-73:198:73//MUS MUSCULUS (MOUSE).//P39098

35 F-PLACE1005813//HYPOTHETICAL 49.0 KD PROTEIN IN NSP1-KAR2 INTERGENIC
REGION.//0.022:78:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47057

40 F-PLACE1005828//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.8e-23:56:76//HOMO
SAPIENS (HUMAN).//P39195

45 F-PLACE1005834//LATE CONTROL GENE B PROTEIN (GPB).//0.97:33:
39//BACTERIOPHAGE 186.//P08711

F-PLACE1005845

50 F-PLACE1005850//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//5.5e-28:96:73//HOMO
SAPIENS (HUMAN).//P39194

F-PLACE1005851

55 F-PLACE1005876//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD
SUBUNIT (CPSF 100 KD SUBUNIT).//2.2e-99:155:95//BOS TAURUS (BOVINE).//Q10568

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F-PLACE1005884

5 F-PLACE1005890//BEM46 PROTEIN (FRAGMENT)//1.8e-33:137:
49//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//P54069

10 F-PLACE1005898//NADH-UBIQUINONE OXIDOREDUCTASE MLRQ SUBUNIT (EC 1.6.5.3)
(EC 1.6.99.3) (COMPLEX I-MLRQ) (CI-MLRQ)//0.77:58:34//HOMO SAPIENS (HUMAN)
//O00483

15 F-PLACE1005921//AIG1 PROTEIN//1.4e-23:165:38//ARABIDOPSIS THALIANA (MOUSE-EAR
CRESS)//P54120

F-PLACE1005923//HYPOTHETICAL 22.4 KD PROTEIN (ORF16)//0.90:118:28//PARAMECIUM
TETRAURELIA//P15617

20 F-PLACE1005925//HYPOTHETICAL GENE 30 PROTEIN//0.94:57:29//HERPESVIRUS
SAIMIRI (STRAIN 11)//Q01010

25 F-PLACE1005932//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH
GLYCOPROTEIN)//0.42:128:32//NICOTIANA TABACUM (COMMON TOBACCO)//P13983

30 F-PLACE1005934//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6)
(RPB1) (FRAGMENT)//0.40:76:35//CRICETULUS GRISEUS (CHINESE HAMSTER)//P11414

F-PLACE1005936//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN)//0.50:15:
66//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CLONE 12) (HIV-1)//P04326

35 F-PLACE1005951//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH
GLYCOPROTEIN)//0.0025:135:32//NICOTIANA TABACUM (COMMON TOBACCO)//P13983

40 F-PLACE1005953//HIGH POTENTIAL IRON-SULFUR PROTEIN (HIIP)//0.64:57:
33//RHODOFERAX FERMENTANS//P80882

45 F-PLACE1005955//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC
REGION//1.0e-32:110:50//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38821

F-PLACE1005966//TACHYPLESIN II PRECURSOR//0.97:31:35//TACHYPLEUS
TRIDENTATUS (JAPANESE HORSESHOE CRAB)//P14214

50 F-PLACE1005968//GATA FACTOR SREP//0.17:52:40//PENICILLIUM
CHRYSOGENUM//Q92259

55 F-PLACE1005990//CELL PATTERN FORMATION-ASSOCIATED PROTEIN//0.36:55:
36//EMERICELLA NIDULANS (ASPERGILLUS NIDULANS)//P36011

F-PLACE1006002//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.5e-36:102:75//HOMO

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SAPIENS (HUMAN).//P39192

5 F-PLACE1006003//HYPOTHETICAL 6.8 KD PROTEIN IN COX3-NAD1 INTERGENIC REGION
(ORF 61).//1.0:22:40//MARCHANTIA POLYMORPHA (LIVERWORT).//P38473

10 F-PLACE1006011//POLY [ADP-RIBOSE] POLYMERASE (EC 2.4.2.30) (PARP) (ADPRT)
(NAD(+)) ADP- RIBOSYLTRANSFERASE) (POLY[ADP-RIBOSE] SYNTHETASE).//2.8e-21:163:
36//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q11207

15 F-PLACE1006017//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.1e-10:43:67//HOMO
SAPIENS (HUMAN).//P39192

20 F-PLACE1006037//VITELLOGENIN I PRECURSOR (VTG I) [CONTAINS: LIPOVITELLIN 1
(LV1); PHOSVITIN (PV); LIPOVITELLIN 2 (LV2)].//0.00019:123:37//FUNDULUS
HETEROCLITUS (KILLIFISH) (MUMMICHOG).//Q90508

F-PLACE1006040//CAMP-REGULATED PHOSPHOPROTEIN 19 (ARPP-19).//3.2e-40:110:
76//HOMO SAPIENS (HUMAN).//P56211

25 F-PLACE1006076//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR A-II.//0.99:30:
40//ARACHIS HYPOGAEA (PEANUT).//P01066

30 F-PLACE1006119//IMPORTIN BETA-3 SUBUNIT (KARYOPHERIN BETA-3 SUBUNIT) (RAN-
BINDING PROTEIN 5).//8.8e-94:218:76//HOMO SAPIENS (HUMAN).//O00410

35 F-PLACE1006129//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.00092:228:
26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323

F-PLACE1006139//HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC
REGION.//5.9e-55:128:50//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43616

40 F-PLACE1006143//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.4e-25:107:63//HOMO
SAPIENS (HUMAN).//P39194

45 F-PLACE1006157//E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION
MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2)
(LECAM2) (CD62E).//1.3e-21:168:32//SUS SCROFA (PIG).//P98110

50 F-PLACE1006159//COLD SHOCK INDUCED PROTEIN TIR1 PRECURSOR (SERINE-RICH
PROTEIN 1).//0.46:98:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P10863

F-PLACE1006164//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0:70:
28:42//ARTEMIA SALINA (BRINE SHRIMP).//P19049

55 F-PLACE1006167//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-
ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//8.9e-05:167:

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32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640

5 F-PLACE1006170//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2
ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE
ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT).//1.1e-67:157:88//MUS MUSCULUS
(MOUSE).//P17427

10 F-PLACE1006187//G1/S-SPECIFIC CYCLIN E.//5.6e-75:224:62//HOMO SAPIENS (HUMAN)
.//P24864

15 F-PLACE1006195//T-RELATED PROTEIN (TRP) (BRACHYENTERON PROTEIN).//0.99:177:
29//DROSOPHILA MELANOGASTER (FRUIT FLY).//P55965

F-PLACE1006196//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//2.0e-33:183:
46//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09747

20 F-PLACE1006205

F-PLACE1006223//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.00015:
22:50//MUS MUSCULUS (MOUSE).//P15265

F-PLACE1006225//VIRION INFECTIVITY FACTOR (SOR PROTEIN).//1.0:63:34//HUMAN
IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1).//P18805

30 F-PLACE1006236

F-PLACE1006239//60S ACIDIC RIBOSOMAL PROTEIN P2 (FRAGMENT).//0.48:23:
35 52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P51407

F-PLACE1006246//CMP-SIALIC ACID TRANSPORTER (CMP-SIA-TR).//0.012:84:30//MUS
MUSCULUS (MOUSE).//Q61420

40 F-PLACE1006248//140 KD NUCLEOLAR PHOSPHOPROTEIN (NOPP140).//0.017:203:
22//RATTUS NORVEGICUS (RAT).//P41777

45 F-PLACE1006262//L-FUCULOSE PHOSPHATE ALDOLASE (EC 4.1.2.17).//0.84:25:
52//HAEMOPHILUS INFLUENZAE.//P44777

50 F-PLACE1006288

F-PLACE1006318//CYSTEINE-RICH ANTIFUNGAL PROTEIN 1 (AFP1) (M1).//1.0:29:
48//SINAPIS ALBA (WHITE MUSTARD) (BRASSICA HIRTA).//P30231

55 F-PLACE1006325//CYCLIN-DEPENDENT KINASE INHIBITOR 1C (CYCLIN-DEPENDENT
KINASE INHIBITOR P57) (P57KIP2).//0.99:97:32//HOMO SAPIENS (HUMAN).//P49918

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- F-PLACE1006335//PROLINE-RICH PEPTIDE P-B.//0.56:19:52//HOMO SAPIENS (HUMAN)
//P02814
- 5 F-PLACE1006357
- F-PLACE1006360
- 10 F-PLACE1006368//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110)
//0.0057:122:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32380
- F-PLACE1006371//ARS BINDING PROTEIN 1.//0.00030:142:30//SCHIZOSACCHAROMYCES
15 POMBE (FISSION YEAST).//P49777
- F-PLACE1006382//NEUROTOXIN V.//0.85:28:39//ANDROCTONUS MAURETANICUS
MAURETANICUS (SCORPION).//P01482
- 20 F-PLACE1006385//HYPOTHETICAL 45.1 KD PROTEIN IN RPS5-ZMS1 INTERGENIC
REGION.//3.1e-35:165:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47160
- 25 F-PLACE1006412//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.3e-08:40:47//HOMO
SAPIENS (HUMAN).//P08547
- F-PLACE1006414//FORKHEAD-RELATED TRANSCRIPTION FACTOR 4 (FREAC-4).//3.8e-05:
30 123:39//HOMO SAPIENS (HUMAN).//Q16676
- F-PLACE1006438//ZINC FINGER PROTEIN 165.//2.8e-21:76:64//HOMO SAPIENS (HUMAN)
//P49910
- 35 F-PLACE1006445//SUPPRESSOR OF HAIRY WING PROTEIN.//0.058:99:29//DROSOPHILA
VIRILIS (FRUIT FLY).//Q08876
- 40 F-PLACE1006469//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA
LIGASE) (ACYL- ACTIVATING ENZYME).//1.8e-64:177:50//ESCHERICHIA COLI.//P27550
- F-PLACE1006470
- 45 F-PLACE1006482//TRANSCRIPTION FACTOR MAFF.//2.0e-47:120:85//GALLUS GALLUS
(CHICKEN).//Q90595
- 50 F-PLACE1006488//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.8e-85:
173:95//CANIS FAMILIARIS (DOG).//Q00004
- F-PLACE1006492//VERY HYPOTHETICAL 11.2 KD PROTEIN C56F8.13 IN CHROMOSOME
55 I.//0.75:32:56//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10261
- F-PLACE1006506

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F-PLACE1006521

5 F-PLACE1006531//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME
III.//1.3e-53:167:61//CAENORHABDITIS ELEGANS.//P34681

F-PLACE1006534

10 F-PLACE1006540

15 F-PLACE1006552//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT).//1.3e-07:242:
23//HYDRA ATTENUATA (HYDRA) (HYDRA VULGARIS).//P39922

F-PLACE1006598//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!!//0.17:43:51//HOMO
SAPIENS (HUMAN).//P39190

20 F-PLACE1006615//ACROSIN PRECURSOR (EC 3.4.21.10).//3.6e-05:66:43//ORYCTOLAGUS
CUNICULUS (RABBIT).//P48038

25 F-PLACE1006617//HYPOTHETICAL 14.6 KD PROTEIN (READING FRAME C) (REPUCATION)
./1.0:74:29//STAPHYLOCOCCUS AUREUS.//P03861

30 F-PLACE1006626//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III.//2.9e-10:73:
46//CAENORHABDITIS ELEGANS.//P34529

F-PLACE1006629//HYPOTHETICAL PROTEIN BB0410.//1.0:23:43//BORRELIA
BURGDORFERI (LYME DISEASE SPIROCHETE).//O51371

35 F-PLACE1006640

F-PLACE1006673

40 F-PLACE1006678//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT).//1.0:36:41//ORYCTOLAGUS
CUNICULUS (RABBIT).//P02456

45 F-PLACE1006704//BROAD-COMPLEX CORE-TNT1-Q1-Z1 PROTEIN (BRCORE-TNT1-Q1-
Z1) [CONTAINS: BROAD-COMPLEX CORE-Q1-Z1

50 PROTEIN].//0.00062:157:26//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01295

F-PLACE1006731//RIBOFLAVIN KINASE (EC 2.7.1.26) (FLAVOKINASE) / FMN
ADENYLYLTRANSFERASE (EC 2.7.7.2) (FAD PYROPHOSPHORYLASE) (FAD SYNTHETASE)
./1.3e-07:127:36//CORYNEBACTERIUM AMMONIAGENES (BREVIBACTERIUM
55 AMMONIAGENES).//Q59263

F-PLACE1006754//CARCINOEMBRYONIC ANTIGEN CGM1 PRECURSOR (CD66D

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ANTIGEN).//1.9e-19:78:53//HOMO SAPIENS (HUMAN).//P40198

5 F-PLACE1006760//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT).//0.21:107:30//RATTUS NORVEGICUS (RAT).//P13941

10 F-PLACE1006779//CYTOTOXIN 5 (CTX V).//1.0:20:30//NAJA MOSSAMBICA (MOZAMBIQUE COBRA).//P25517

F-PLACE1006782//ZINC FINGER PROTEIN 1.//0.00052:178:28//CANDIDA ALBICANS (YEAST).//P28875

15 F-PLACE1006792

20 F-PLACE1006795//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN SHAW (SHAW2).//1:0:80:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//P17972

F-PLACE1006800//HYPOTHETICAL 9.4 KD PROTEIN.//0.99:62:33//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20569

25 F-PLACE1006805

30 F-PLACE1006815//HYPOTHETICAL PROTEIN UL61.//0.038:146:32//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16818

F-PLACE1006819//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.3e-98:239:76//HOMO SAPIENS (HUMAN).//P08547

35 F-PLACE1006829//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 8 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 8) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUITINATING ENZYME 8).//0.061:34:58//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P50102

40 F-PLACE1006860

45 F-PLACE1006867

F-PLACE1006878//HYPOTHETICAL 8.2 KD PROTEIN IN MOBL 3'REGION (ORF 3).//0.85:27:37//THIOBACILLUS FERROOXIDANS.//P20087

50 F-PLACE1006883//VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).//0.78:51:37//MUS MUSCULUS (MOUSE).//P48281

55 F-PLACE1006901//HYPOTHETICAL 8.1 KD PROTEIN.//0.99:55:23//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20567

F-PLACE1006904//MATING-TYPE LOCUS ALLELE B1 PROTEIN.//0.95:86:26//USTILAGO

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MAYDIS (SMUT FUNGUS).//P22015

- 5 F-PLACE1006917//HYPOTHETICAL 40.9 KD PROTEIN C08B11.5 IN CHROMOSOME II.//6.9e-15:101:45//CAENORHABDITIS ELEGANS.//Q09442
- 10 F-PLACE1006932//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE.//0.089:28:39//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//Q48251
- 15 F-PLACE1006935//HYPOTHETICAL 95.2 KD PROTEIN R144.6 IN CHROMOSOME III.//0.93:35:48//CAENORHABDITIS ELEGANS.//Q10000
- 20 F-PLACE1006956//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//0.00079:122:36//HOMO SAPIENS (HUMAN).//O00268
- 20 F-PLACE1006958//OSMOTIC STRESS PROTEIN 94 (HEAT SHOCK 70-RELATED PROTEIN APG-1).//8.8e-70:140:98//MUS MUSCULUS (MOUSE).//P48722
- F-PLACE1006961
- 25 F-PLACE1006962//APOLIPOPROTEIN C-I PRECURSOR (APO-C1).//1.0:25:40//PAPIO HAMADRYAS (HAMADRYAS BABOON).//P34929
- 30 F-PLACE1006966//HYPOTHETICAL 49.1 KD PROTEIN IN SSB2-SPX18 INTERGENIC REGION.//1.6e-47:221:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40160
- 35 F-PLACE1006989//HYPOTHETICAL 13.1 KD HIT-LIKE PROTEIN IN P37 5'REGION.//0.15:46:32//MYCOPLASMA HYORHINIS.//P32083
- 40 F-PLACE1007014//36 KD NUCLEOLAR PROTEIN HNP36 (DELAYED-EARLY RESPONSE PROTEIN 12) (DER12).//3.4e-09:120:29//HOMO SAPIENS (HUMAN).//Q14542
- 40 F-PLACE1007021//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.00046:42:59//HOMO SAPIENS (HUMAN).//P39188
- 45 F-PLACE1007045//HYPOTHETICAL PROTEIN ORF-1137.//8.1e-14:115:35//MUS MUSCULUS (MOUSE).//P11260
- 50 F-PLACE1007053//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.038:48:39//HOMO SAPIENS (HUMAN).//P22531
- 50 F-PLACE1007068//PROTEIN-LYSINE 6-OXIDASE PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE).//0.0040:113:39//GALLUS GALLUS (CHICKEN).//Q05063
- 55 F-PLACE1007097//HYPOTHETICAL 6.8 KD PROTEIN IN HE65-PK2 INTERGENIC REGION.//0.97:47:29//AUTOGRAPHIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41663

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F-PLACE1007105//HYPOTHETICAL 83.6 KD PROTEIN C15A10.10 IN CHROMOSOME
 L//2.9e-33:219:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//O13730
 5 F-PLACE1007111
 F-PLACE1007112//HYPOTHETICAL 9.2 KD PROTEIN//0.47:75:28//ESCHERICHIA
 10 COLI//P03853
 F-PLACE1007132//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.8e-11:56:57//HOMO
 SAPIENS (HUMAN)//P39188
 15 F-PLACE1007140//GAR2 PROTEIN//0.72:185:24//SCHIZOSACCHAROMYCES POMBE
 (FISSION YEAST)//P41891
 20 F-PLACE1007178//HYPOTHETICAL 8.5 KD PROTEIN CY274.40C//0.97:79:
 30//MYCOBACTERIUM TUBERCULOSIS//Q10826
 F-PLACE1007226//HYPOTHETICAL 42.6 KD PROTEIN IN GSHB-ANSB INTERGENIC
 25 REGION (O378)//1.9e-15:123:32//ESCHERICHIA COLI//P52062
 F-PLACE1007238//MYOSIN HEAVY CHAIN IB (MYOSIN HEAVY CHAIN IL)//5.5e-10:98:
 44//ACANTHAMOEBA CASTELLANII (AMOEBA)//P19706
 30 F-PLACE1007239//TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION
 ELONGATION FACTOR A)//3.9e-19:96:57//HOMO SAPIENS (HUMAN)//P23193
 35 F-PLACE1007242//GUANINE NUCLEOTIDE DISSOCIATION STIMULATOR RALGDS FORM B
 (RALGEF)//1.0:132:30//RATTUS NORVEGICUS (RAT)//Q03386
 F-PLACE1007243//HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC
 40 REGION//0.041:114:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P39981
 F-PLACE1007257//DIAPHANOUS PROTEIN//1.3e-42:205:46//DROSOPHILA
 MELANOGASTER (FRUIT FLY)//P48608
 45 F-PLACE1007274//CADMIUM-METALLOTHIONEIN (CD-MT)//0.054:60:30//HELIX POMATIA
 (ROMAN SNAIL) (EDIBLE SNAIL)//P33187
 50 F-PLACE1007276//BETA-DEFENSIN 1 PRECURSOR (RHBD-1) (DEFENSIN, BETA 1)//1.0:
 42:28//SUS SCROFA (PIG)//O62697
 55 F-PLACE1007282//OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER
 PROTEIN VP4) [CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP8]//0.070:126:
 27//HUMAN ROTAVIRUS (SEROTYPE 4 / STRAIN ST. THOMAS 3)//P11200

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F-PLACE1007286

5 F-PLACE1007301//HYPOTHETICAL PROTEIN KIAA0168.//0.042:61:39//HOMO SAPIENS (HUMAN).//P50749

F-PLACE1007317

10 F-PLACE1007342//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1).//1.7e-06:77:36//DROSOPHILA MELANOGASTER (FRUIT FLY).//P13002

15 F-PLACE1007346//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (KRAB-A INTERACTING PROTEIN) (KRIP-1).//0.0026:147:27//MUS MUSCULUS (MOUSE).//Q62318

20 F-PLACE1007367//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!1.3e-37:110:76//HOMO SAPIENS (HUMAN).//P39189

25 F-PLACE1007375//PHORBOL ESTER/DIACYLGLYCEROL-BINDING PROTEIN UNC-13.//4.7e-07:71:39//CAENORHABDITIS ELEGANS.//P27715

F-PLACE1007386//HYPOTHETICAL 7.6 KD PROTEIN IN FLO1-PHO11 INTERGENIC REGION.//0.74:48:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39561

30 F-PLACE1007402//TRANSCRIPTIONAL REGULATORY PROTEIN ENTR (ENTERICIDIN R).//0.99:63:36//CITROBACTER FREUNDII.//O69280

35 F-PLACE1007409//WHITE PROTEIN.//7.9e-38:179:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//P10090

40 F-PLACE1007416//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL ACTIVATION ANTIGEN CD26) (TP103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN-2) (ADABP).//0.031:159:23//HOMO SAPIENS (HUMAN).//P27487

45 F-PLACE1007450//ZINC FINGER PROTEIN 39 (ZINC FINGER PROTEIN KOX27) (FRAGMENT).//0.023:36:50//HOMO SAPIENS (HUMAN).//P17038

F-PLACE1007452//HYPOTHETICAL 22.1 KD PROTEIN IN CCP1-MET1 INTERGENIC REGION.//2.2e-18:85:54//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36149

50 F-PLACE1007454//PHOTOSYSTEM II REACTION CENTRE N PROTEIN.//0.66:13:53//CHLAMYDOMONAS REINHARDTII.//Q06480

55 F-PLACE1007460//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.93:45:33//SUS SCROFA (PIG).//Q35914

F-PLACE1007478//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE

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TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//5.3e-08:50:56//MUS MUSCULUS (MOUSE).//P11369

5 F-PLACE1007484//HYPOTHETICAL 6.8 KD PROTEIN IN REPLICATION ORIGIN REGION.//0.87:43:37//ESCHERICHIA COLI.//P03849

10 F-PLACE1007488//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN).//1.2e-25:202:31//HOMO SAPIENS (HUMAN).//P98174

15 F-PLACE1007507//HYPOTHETICAL 16.0 KD PROTEIN IN TAF60-G4P1 INTERGENIC REGION.//0.12:128:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53139

20 F-PLACE1007511//KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (CK 19) .//2.1e-45:209:48//BOS TAURUS (BOVINE).//P08728

F-PLACE1007524//HYPOTHETICAL 9.2 KD PROTEIN.//0.74:80:30//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20550

25 F-PLACE1007525

F-PLACE1007537//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN).//0.045:92:30//MUS MUSCULUS (MOUSE), AND RATTUS NORVEGICUS (RAT) .//P80144

35 F-PLACE1007544//IMMEDIATE-EARLY PROTEIN IE180.//1.5e-07:59:50//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479

F-PLACE1007547//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//2.5e-16:188:34//CAENORHABDITIS ELEGANS.//P34537

40 F-PLACE1007557

F-PLACE1007583//PROLINE RICH 33 KD EXTENSIN-RELATED PROTEIN PRECURSOR (FRAGMENT).//0.98:72:33//DAUCUS CAROTA (CARROT) .//P06600

45 F-PLACE1007598//ZINC FINGER PROTEIN 92 (ZINC FINGER PROTEIN HTF12) (FRAGMENT).//1.7e-11:88:43//HOMO SAPIENS (HUMAN).//Q03936

50 F-PLACE1007618//ANION EXCHANGE PROTEIN 2 (NON-ERYTHROID BAND 3-LIKE PROTEIN) (B3RP).//0.19:109:27//MUS MUSCULUS (MOUSE).//P13808

55 F-PLACE1007621//PHOSPHATE REGULON SENSOR PROTEIN PHOR (EC 2.7.3.-) (FRAGMENT).//0.98:34:41//PSEUDOMONAS AERUGINOSA.//P23621

F-PLACE1007632//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT).//0.70:110:34//BOS TAURUS

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(BOVINE).//P02465

5 F-PLACE1007645//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.99:20:45//STRUTHIO
CAMELUS (OSTRICH).//O21401

10 F-PLACE1007649//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-
ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//8.1e-06:197:
26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640

15 F-PLACE1007677//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.0:47:46//HOMO SAPIENS
(HUMAN).//P39192

F-PLACE1007688//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN
HOMOLOG).//2.7e-06:116:28//AEDES ALBOPICTUS (FOREST DAY MOSQUITO).//Q26457

20 F-PLACE1007690//SPERM PROTAMINE P1.//0.12:26:50//TACHYGLOSSUS ACULEATUS
ACULEATUS (AUSTRALIAN ECHIDNA).//P35311

25 F-PLACE1007697//SPERM PROTAMINE P1.//0.19:34:52//DIDELPHIS MARSUPIALIS
VIRGINIANA (NORTH AMERICAN OPOSSUM), AND MONODELPHIS DOMESTICA (SHORT-
TAILED GREY OPOSSUM).//P35305

30 F-PLACE1007705//BIOH PROTEIN.//0.015:97:29//ESCHERICHIA COLI.//P13001

F-PLACE1007706//HYPOTHETICAL 112.2 KD PROTEIN IN TIF35-NPL3 INTERGENIC
REGION (ORF1).//5.3e-55:190:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)
.//P32898

35 F-PLACE1007725

40 F-PLACE1007729//PROTEASE (EC 3.4.23.-).//1.8e-21:136:42//MOUSE MAMMARY TUMOR
VIRUS (STRAIN BR6).//P10271

45 F-PLACE1007730//SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT).//0.0031:77:
40//HOMO SAPIENS (HUMAN).//P81489

F-PLACE1007737//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.78:39:56//HOMO SAPIENS
(HUMAN).//P39195

50 F-PLACE1007743

55 F-PLACE1007746//RRP5 PROTEIN HOMOLOG (KIAA0185) (FRAGMENT).//0.0066:168:
25//HOMO SAPIENS (HUMAN).//Q14690

F-PLACE1007791//KRUEPPEL PROTEIN (FRAGMENT).//0.62:17:41//LITHOBIUS
FORFICATUS.//Q01872

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- 5 F-PLACE1007807//HYPOTHETICAL 6.4 KD PROTEIN IN BLTR-SPOIIC INTERGENIC
REGION.//1.0:40:30//BACILLUS SUBTILIS.//P54446
- F-PLACE1007810//ANTHOPLEURIN A (TOXIN AP-A).//0.79:28:46//ANTHOPLEURA
XANTHOGRAMMICA (GIANT GREEN SEA ANEMONE).//P01530
- 10 F-PLACE1007829//SPORE COAT PROTEIN G.//1.0:65:38//BACILLUS SUBTILIS.//P39801
- F-PLACE1007843
- 15 F-PLACE1007846//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.5e-32:37:94//HOMO
SAPIENS (HUMAN).//P08547
- F-PLACE1007852//RHO-RELATED GTP-BINDING PROTEIN RHOH (GTP-BINDING PROTEIN
20 TTF).//8.7e-05:138:30//HOMO SAPIENS (HUMAN).//Q15669
- F-PLACE1007858//ANAPHASE SPINDLE ELONGATION PROTEIN.//0.0039:127:
25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P50275
- F-PLACE1007866
- F-PLACE1007877
- 30 F-PLACE1007897//CD44 ANTIGEN PRECURSOR (PHAGOCYTIC GLYCOPROTEIN I) (PGP-
1) (HUTCH-I) (EXTRACELLULAR MATRIX RECEPTOR-III) (ECMR-III) (GP90 LYMPHOCYTE
HOMING/ADHESION RECEPTOR) (HERMES ANTIGEN) (HYALURONATE RECEPTOR)
35 (HEPARAN SULFATE PROTEOGLYCAN) (HAM1 ANTIGEN).//0.44:128:28//MESOCRICETUS
AURATUS (GOLDEN HAMSTER).//Q60522
- F-PLACE1007908//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//5.5e-28:61:65//HOMO
40 SAPIENS (HUMAN).//P39192
- F-PLACE1007946//HYPOTHETICAL MERCURIC RESISTANCE PROTEIN MERC.//0.84:48:
37//PSEUDOMONAS AERUGINOSA.//P04139
- 45 F-PLACE1007954//HYPOTHETICAL 45.5 KD PROTEIN IN FIG1-GIP1 INTERGENIC
REGION.//0.00070:96:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38226
- 50 F-PLACE1007955//HYPOTHETICAL 84.3 KD PROTEIN ZK945.10 IN CHROMOSOME
II.//0.00027:255:23//CAENORHABDITIS ELEGANS.//Q09625
- F-PLACE1007958//HIGH-AFFINITY CAMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE
55 (EC 3.1.4.17).//1.7e-09:127:30//MUS MUSCULUS (MOUSE).//P70453
- F-PLACE1007969//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC

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REGION.//2.4e-05:104:37//AUTOGRAPHICA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479

5 F-PLACE1007990//SPERM PROTAMINE P1.//0.78:36:47//ORNITHORHYNCHUS ANATINUS (DUCKBILL PLATYPUS).//P35307

10 F-PLACE1008000//CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSYN-110) (SYNAPTIC DENSITY PROTEIN PSD-93).//1.2e-16:128:39//RATTUS NORVEGICUS (RAT).//Q63622

15 F-PLACE1008002

F-PLACE1008044//NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN NUP107) (107 KD NUCLEOPORIN) (P105).//3.9e-106:208:93//RATTUS NORVEGICUS (RAT).//P52590

20 F-PLACE1008045//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//3.9e-09:49:53//BOS TAURUS (BOVINE).//P25508

25 F-PLACE1008080//RNA REPLICASE POLYPROTEIN (EC 2.7.7.48).//0.00025:100:27//EGGPLANT MOSAIC VIRUS.//P20126

30 F-PLACE1008095//PROTOPORPHYRINOGEN OXIDASE (EC 1.3.3.4) (PPO).//0.90:74:25//MYCOBACTERIUM TUBERCULOSIS.//O53230

35 F-PLACE1008111//HYPOTHETICAL PROTEIN MJEC512.//0.30:38:42//METHANOCOCCUS JANNASCHII.//Q60311

F-PLACE1008122//PEA2 PROTEIN (PPF2 PROTEIN).//0.0085:117:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40091

40 F-PLACE1008129//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (FRAGMENTS).//1.8e-06:154:36//GALLUS GALLUS (CHICKEN).//P02467

45 F-PLACE1008132//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//1.4e-13:227:36//CAENORHABDITIS ELEGANS.//Q09531

F-PLACE1008177//TRICHOHYALIN.//2.7e-10:230:26//OVIS ARIES (SHEEP).//P22793

50 F-PLACE1008181

F-PLACE1008198//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//0.00044:121:34//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437

55 F-PLACE1008201//ZINC FINGER PROTEIN ZFMSA12A.//3.0e-05:82:37//MICROPTERUS SALMOIDES (LARGEMOUTH BASS).//P38621

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- 5 F-PLACE1008209//METALLOTHIONEIN-I (MT-I)//0.95:39:35//CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET)//P02797
- 10 F-PLACE1008231//PROCYCLIC FORM SPECIFIC POLYPEPTIDE B1-ALPHA PRECURSOR (PROCYCLIN) (PARP)//0.028:23:52//TRYPANOSOMA BRUCEI BRUCEI//P08469
- 15 F-PLACE1008244//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1//2.2e-23:148:38//PODOSPORA ANSERINA//Q00808
- 20 F-PLACE1008273//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP) //1.1e-97:222:81//BOS TAURUS (BOVINE)//P53620
- 25 F-PLACE1008275//DNA REPAIR PROTEIN REV1 (EC 2.7.7.-)//5.8e-20:161:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P12689
- 30 F-PLACE1008280//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//6.1e-23:124:42//HOMO SAPIENS (HUMAN)//P08547
- 35 F-PLACE1008309//HYPOTHETICAL 98.3 KD PROTEIN C9G1.06C IN CHROMOSOME I//0.47:99:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//O14302
- 40 F-PLACE1008329//PUTATIVE Z PROTEIN//0.73:52:28//OVIS ARIES (SHEEP)//P08105
- 45 F-PLACE1008330//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//9.0e-37:75:81//HOMO SAPIENS (HUMAN)//P39194
- 50 F-PLACE1008331//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.1e-08:70:50//HOMO SAPIENS (HUMAN)//P39188
- 55 F-PLACE1008356//FRUIT PROTEIN PKIW1501//0.0037:148:29//ACTINIDIA CHINENSIS (KIWI) (YANGTAO)//P43393
- F-PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN)//3.5e-18:205:30//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q04652
- F-PLACE1008369
- F-PLACE1008392
- F-PLACE1008398//GENE 33 POLYPEPTIDE//1.5e-102:225:84//RATTUS NORVEGICUS (RAT)//P05432
- F-PLACE1008401//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//2.9e-08:186:34//MUS MUSCULUS (MOUSE)//P05143

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F-PLACE1008402//GENERAL VESICULAR TRANSPORT FACTOR P115 (TRANSCYTOSIS ASSOCIATED PROTEIN) (TAP).//9.4e-105:207:98//BOS TAURUS (BOVINE).//P41541

5 F-PLACE1008405

F-PLACE1008424//PROTEIN UL56.//1.0:65:33//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN HFEM).//P36297

10

F-PLACE1008426//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).//4.4e-05:185:28//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q99323

15 F-PLACE1008429//NEURONAL AXONAL MEMBRANE PROTEIN NAP-22.//0.00054:172:25//RATTUS NORVEGICUS (RAT).//Q05175

20 F-PLACE1008437//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III.//1.9e-23:226:34//CAENORHABDITIS ELEGANS.//P34681

F-PLACE1008455//DNA-BINDING PROTEIN (AGNOPROTEIN).//0.97:23:52//BUDGERIGAR FLEDGLING DISEASE VIRUS (BFDV).//P13893

25

F-PLACE1008457//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.1e-12:89:47//HOMO SAPIENS (HUMAN).//P39188

30 F-PLACE1008465//ZINC FINGER PROTEIN 31 (ZINC FINGER PROTEIN KOX29) (FRAGMENT).//0.00017:23:43//HOMO SAPIENS (HUMAN).//P17040

35 F-PLACE1008488//HYPOTHETICAL PROTEIN UL61.//9.1e-05:204:30//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16818

40 F-PLACE1008524//HOMEBOX PROTEIN HLX1 (HOMEBOX PROTEIN HB24).//0.95:74:36//HOMO SAPIENS (HUMAN).//Q14774

F-PLACE1008531//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//3.1e-05:86:45//HOMO SAPIENS (HUMAN).//P39192

45 F-PLACE1008532//HYPOTHETICAL 36.4 KD PROTEIN IN SMP1-MBA1 INTERGENIC REGION.//3.9e-21:62:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38298

50 F-PLACE1008533//HYPOTHETICAL 86.2 KD PROTEIN C4G8.04 IN CHROMOSOME I.//3.5e-06:118:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09830

F-PLACE1008568//NEURONATIN.//0.046:34:52//HOMO SAPIENS (HUMAN).//Q16517

55 F-PLACE1008584//HUNCHBACK PROTEIN (FRAGMENT).//0.94:30:43//LITHOBIUS FORFICATUS.//Q02030

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F-PLACE1008603//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NUCLEOPORIN) (P140).//3.9e-123:224:96//RATTUS NORVEGICUS (RAT) .//P37199

5

F-PLACE1008621//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//5.0e-05:31:67//HOMO SAPIENS (HUMAN).//P20931

10

F-PLACE1008625//DISAGREGIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).//0.87:17:52//ORNITHODOROS MOUBATA (SOFT TICK).//P36235

15

F-PLACE1008626//METALLOTHIONEIN-I (MT-I).//0.77:33:36//SCYLLA SERRATA (MUD CRAB) .//P02805

20

F-PLACE1008627//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF) (GIFB).//0.14:44:31//HOMO SAPIENS (HUMAN).//P25713

F-PLACE1008629

25

F-PLACE1008630//PROTAMINE Z3 (SCYLLIORHININE Z3).//0.78:33:36//SCYLLIORHINUS CANICULA (SPOTTED DOGFISH) (SPOTTED CATSHARK).//P30258

30

F-PLACE1008643//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H4 PRECURSOR (ITI HEAVY CHAIN H4) (INTER-ALPHA-TRYPSIN INHIBITOR FAMILY HEAVY CHAIN-RELATED PROTEIN) (PLASMA KALLIKREIN SENSITIVE GLYCOPROTEIN 120) (PK-120).//1.7e-30:220:41//HOMO SAPIENS (HUMAN).//Q14624

35

F-PLACE1008650//PP1/PP2A PHOSPHATASES PLEIOTROPIC REGULATOR PRL1.//2.5e-10:106:31//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q42384

40

F-PLACE1008693//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR (MSTI).//1.0:36:38//MEDICAGO SCUTELLATA (SNAIL MEDIC).//P80321

45

F-PLACE1008696//NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-23KD) (CI-23KD) (TYKY SUBUNIT).//4.8e-14:47:80//HOMO SAPIENS (HUMAN).//O00217

50

F-PLACE1008715//HYPOTHETICAL 13.4 KD PROTEIN IN ACT5-YCK1 INTERGENIC REGION.//0.66:105:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38834

F-PLACE1008748//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.10:178:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214

55

F-PLACE1008757//HYPOTHETICAL 10.1 KD PROTEIN IN RHSD-GCL INTERGENIC REGION (ORFD3).//0.60:44:34//ESCHERICHIA COLI.//P33669

F-PLACE1008790//IMPORTIN ALPHA-6 SUBUNIT (KARYOPHERIN ALPHA-6 SUBUNIT)

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(IMPORTIN ALPHA S2).//3.0e-69:191:80//MUS MUSCULUS (MOUSE).//O35345

5 F-PLACE1008798//BACTERIOCIN LACTOBIN A.//1.0:34:41//LACTOBACILLUS AMYLOVORUS
//P80696

F-PLACE1008807//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.91:77:36//HOMO
10 SAPIENS (HUMAN).//P08547

F-PLACE1008808//REC1 PROTEIN.//0.45:39:30//USTILAGO MAYDIS (SMUT FUNGUS)
//P14746

15 F-PLACE1008813

F-PLACE1008851//VERY HYPOTHETICAL 11.8 KD PROTEIN IN KTR3-DUR1,2 INTERGENIC
20 REGION.//1.0:62:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38309

F-PLACE1008854//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC
REGION.//1.0:82:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47170

25 F-PLACE1008867//PATATIN T5 PRECURSOR (POTATO TUBER PROTEIN).//0.65:61:
36//SOLANUM TUBEROSUM (POTATO).//P15478

F-PLACE1008887//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.5e-56:180:
30 54//NYCTICEBUS COUCANG (SLOW LORIS).//P08548

F-PLACE1008902

35 F-PLACE1008920

F-PLACE1008925//HYPOTHETICAL 41.2 KD PROTEIN IN GAPA-RND INTERGENIC
40 REGION.//0.90:77:33//ESCHERICHIA COLI.//P76242

F-PLACE1008934//HYPOTHETICAL PROTEIN IN ADHS 5'REGION (ORF3) (FRAGMENT)
//0.14:77:45//GLUCONOBACTER SUBOXYDANS.//O05543

45 F-PLACE1008941//ZINC FINGER PROTEIN 141.//1.1e-17:45:95//HOMO SAPIENS (HUMAN)
//Q15928

F-PLACE1008947//MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B)
50 (CENP-B).//4.1e-14:136:39//MUS MUSCULUS (MOUSE).//P27790

F-PLACE1009020//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.74:37:48//BOS TAURUS
55 (BOVINE).//P20072

F-PLACE1009027//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.39:
57:36//BALAENOPTERA MUSCULUS (BLUE WHALE).//P41301

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F-PLACE1009039

5 F-PLACE1009045//HYPOTHETICAL 9.5 KD PROTEIN IN SPEA-METK INTERGENIC REGION
(F83).//0.48:32:43//ESCHERICHIA COLI.//P46879

F-PLACE1009048

10 F-PLACE1009050

F-PLACE1009060//HYPOTHETICAL 98.3 KD PROTEIN R10E12.1 IN CHROMOSOME
15 III.//4.9e-23:244:31//CAENORHABDITIS ELEGANS.//P34552

F-PLACE1009090//50S RIBOSOMAL PROTEIN L35.//1.0:27:51//MYCOPLASMA
20 GENITALIUM.//P47439

F-PLACE1009091

F-PLACE1009094//NEL-LIKE PROTEIN (FRAGMENT).//3.6e-15:180:30//HOMO SAPIENS
25 (HUMAN).//Q92832

F-PLACE1009099//ZINC FINGER PROTEIN 27 (ZFP-27) (MKR4 PROTEIN) (FRAGMENT)
30 .//1.4e-94:228:71//MUS MUSCULUS (MOUSE).//P10077

F-PLACE1009110//HIRUDIN HV1 (BUFRUDIN).//1.0:49:34//HIRUDINARIA MANILLENSIS
(BUFFALO LEECH).//P81492

35 F-PLACE1009111//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.4e-05:30:83//HOMO
SAPIENS (HUMAN).//P39195

F-PLACE1009113//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.032:40:52//BOS TAURUS
40 (BOVINE).//P20072

F-PLACE1009130//HYPOTHETICAL PROTEIN KIAA0032.//3.3e-37:214:38//HOMO SAPIENS
45 (HUMAN).//Q15034

F-PLACE1009150//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.6e-32:56:76//HOMO
SAPIENS (HUMAN).//P39195

50 F-PLACE1009155//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.2e-17:101:57//HOMO
SAPIENS (HUMAN).//P39194

F-PLACE1009158//HYPOTHETICAL PROTEIN HKRFX (J1I).//0.0058:73:42//HUMAN
55 CYTOMEGALOVIRUS (STRAIN AD169).//P09711

F-PLACE1009166//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//0.0086:96:

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30//HOMO SAPIENS (HUMAN).//P49902

5 F-PLACE1009172//HYPOTHETICAL 8.7 KD PROTEIN IN GAPA-RND INTERGENIC REGION.//1.0:19:52//ESCHERICHIA COLI.//P76246

10 F-PLACE1009174//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.1e-17:47:82//HOMO SAPIENS (HUMAN).//P39194

F-PLACE1009183

15 F-PLACE1009186//HYPOTHETICAL 11.4 KD PROTEIN C13G6.04 IN CHROMOSOME I.//0.019:62:24//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09783

20 F-PLACE1009190//PALMITOYL-COA HYDROLASE (EC 3.1.2.2) (LONG-CHAIN FATTY-ACYL-COA HYDROLASE) (FRAGMENT).//0.027:53:28//RATTUS NORVEGICUS (RAT).//P80250

F-PLACE1009200//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/5.4e-28:84:71//HOMO SAPIENS (HUMAN).//P39194

25 F-PLACE1009230//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.8e-12:50:74//HOMO SAPIENS (HUMAN).//P39189

30 F-PLACE1009246//UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.8 KD PROTEIN (EC 1.10.2.2) (MITOCHONDRIAL HINGE PROTEIN) (CR7).//1.0:17:52//SOLANUM TUBEROSUM (POTATO).//P48504

35 F-PLACE1009298//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//6.6e-41:177:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P34110

40 F-PLACE1009308//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//0.00034:108:33//HOMO SAPIENS (HUMAN).//P26371

F-PLACE1009319//PRESYNAPTIC DENSITY PROTEIN 95 (PSD-95).//5.3e-16:84:50//HOMO SAPIENS (HUMAN).//P78352

45 F-PLACE1009328//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.9e-82:263:67//HOMO SAPIENS (HUMAN).//P08547

50 F-PLACE1009335//60S RIBOSOMAL PROTEIN L32.//0.95:71:36//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), AND RATTUS NORVEGICUS (RAT).//P02433

55 F-PLACE1009338//TRANSCRIPTION FACTOR HES-5 (HAIRY AND ENHANCER OF SPLIT 5).//0.90:42:40//MUS MUSCULUS (MOUSE).//P70120

F-PLACE1009368//BASIC PROLINE-RICH PEPTIDE IB-1.//0.013:33:48//HOMO SAPIENS (HUMAN).//P04281

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- 5 F-PLACE1009375//HYPOTHETICAL 88.1 KD PROTEIN K02D10.1 IN CHROMOSOME
III.//0.0022:135:21//CAENORHABDITIS ELEGANS.//P34492
- F-PLACE1009388//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/4.8e-22:73:65//HOMO
SAPIENS (HUMAN).//P39195
- 10 F-PLACE1009398//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//8.1e-83:
223:65//HOMO SAPIENS (HUMAN).//P51523
- 15 F-PLACE1009404//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT PW212
PRECURSOR.//0.047:145:29//TRITICUM AESTIVUM (WHEAT).//P08489
- 20 F-PLACE1009410//TOXIN C13S1C1 PRECURSOR.//0.22:21:47//DENDROASPIS
ANGUSTICEPS (EASTERN GREEN MAMBA).//P18329
- F-PLACE1009434//NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT K (EC 1.6.5.3)
(FRAGMENT).//0.81:61:29//ANTHOCEROS FORMOSAE.//Q31791
- 25 F-PLACE1009443//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//9.1e-05:
93:32//MUS MUSCULUS (MOUSE).//Q62203
- 30 F-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE)
(PTDINS-4-KINASE) (PI4K-ALPHA).//6.4e-15:41:97//HOMO SAPIENS (HUMAN).//P42356
- 35 F-PLACE1009459//HYPOTHETICAL 42.3 KD PROTEIN C12G12.11C IN CHROMOSOME
I.//0.0011:119:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09874
- F-PLACE1009468//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//4.2e-34:101:
75//RATTUS NORVEGICUS (RAT).//P54319
- 40 F-PLACE1009476//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)
.//0.086:21:52//HOMO SAPIENS (HUMAN).//P30808
- 45 F-PLACE1009477
- F-PLACE1009493//HYPOTHETICAL 127.3 KD PROTEIN B0416.1 IN CHROMOSOME X.//1.4e-
18:138:39//CAENORHABDITIS ELEGANS.//Q11069
- 50 F-PLACE1009524//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN) (ARF
EXCHANGE FACTOR).//9.4e-80:155:85//HOMO SAPIENS (HUMAN).//Q99418
- 55 F-PLACE1009539//GTP-BINDING NUCLEAR PROTEIN RAN/TC4.//1.0:76:26//GIARDIA
LAMBLIA (GIARDIA INTESTINALIS).//P38543
- F-PLACE1009542//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00016:31:77//HOMO

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SAPIENS (HUMAN).//P39188

5 F-PLACE1009571//ATP SYNTHASE B CHAIN (EC 3.6.1.34) (SUBUNIT I).//0.88:116:29//STREPTOCOCCUS PNEUMONIAE.//Q59952

10 F-PLACE1009581//50S RIBOSOMAL PROTEIN L32.//0.00023:37:51//RHODOBACTER CAPSULATUS (RHODOPSEUDOMONAS CAPSULATA).//P30788

F-PLACE1009595

15 F-PLACE1009596//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN C14B1.4 IN CHROMOSOME III.//2.1e-36:116:49//CAENORHABDITIS ELEGANS.//Q17963

20 F-PLACE1009607//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.8e-43:73:69//HOMO SAPIENS (HUMAN).//P39188

F-PLACE1009613

25 F-PLACE1009621//TRANSCRIPTION FACTOR BTF3 HOMOLOG 2.//0.91:29:44//HOMO SAPIENS (HUMAN).//Q13891

30 F-PLACE1009622//MATERNAL EFFECT PROTEIN STAUFEN.//1.3e-22:132:47//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25159

F-PLACE1009637//HYPOTHETICAL 18.1 KD PROTEIN IN CFXA 3'REGION.//0.30:28:57//BACTEROIDES VULGATUS.//P30905

35 F-PLACE1009639//LIPASE MODULATOR PRECURSOR (LIPASE HELPER PROTEIN).//0.23:79:31//PSEUDOMONAS AERUGINOSA.//Q04591

40 F-PLACE1009659//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (BRAIN PROTEIN H19) (MH19) (FRAGMENT).//3.9e-126:227:96//MUS MUSCULUS (MOUSE).//P28660

45 F-PLACE1009665//IG KAPPA CHAIN V-I REGION (HAU).//0.52:89:35//HOMO SAPIENS (HUMAN).//P01600

50 F-PLACE1009670//CYCLOMALTODEXTRIN GLUCANOTRANSFERASE PRECURSOR (EC 2.4.1.19) (CYCLODEXTRIN-GLYCOSYLTRANSFERASE) (CGTASE).//0.16:114:29//PAENIBACILLUS MACERANS (BACILLUS MACERANS).//P31835

55 F-PLACE1009708//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN C12G12.13C IN CHROMOSOME I.//9.6e-19:156:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09876

F-PLACE1009721//MSF1 PROTEIN.//7.7e-23:176:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P35200

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- 5 F-PLACE1009731//AIG1 PROTEIN.//1.1e-09:91:43//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P54120
- F-PLACE1009763//HYPOTHETICAL 48.9 KD PROTEIN C24H6.12C IN CHROMOSOME I.//8.3e-42:171:51//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09765
- 10 F-PLACE1009794//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT).//0.99:36:33//HORDEUM VULGARE (BARLEY).//P17991
- 15 F-PLACE1009798//HYPOTHETICAL PROTEIN C22F3.14C IN CHROMOSOME I (FRAGMENT) .//2.6e-34:191:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09779
- F-PLACE1009845//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31).//2.2e-19: 190:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38968
- 20 F-PLACE1009861//CATHEPSIN B PRECURSOR (EC 3.4.22.1).//4.4e-20:171:33//BOS TAURUS (BOVINE).//P07688
- 25 F-PLACE1009879//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGENIC REGION (ORF70).//0.99:30:33//ASTASIA LONGA (EUGLENOPHYCEAN ALGA).//P34779
- F-PLACE1009886
- 30 F-PLACE1009888//NONSTRUCTURAL POLYPROTEIN [CONTAINS: NONSTRUCTURAL PROTEIN NSP4] (FRAGMENT).//1.0:33:42//WESTERN EQUINE ENCEPHALITIS VIRUS.//P13896
- 35 F-PLACE1009908//HYPOTHETICAL GTP-BINDING PROTEIN C3F10.16C IN CHROMOSOME I.//3.1e-42:205:46//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10190
- 40 F-PLACE1009921
- F-PLACE1009924//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.70:128: 29//TRYPANOSOMA BRUCEI BRUCEI.//P24499
- 45 F-PLACE1009925//ATP SYNTHASE D CHAIN, MITOCHONDRIAL (EC 3.6.1.34).//0.99:111: 27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P30902
- 50 F-PLACE1009935//HYPOTHETICAL PROTEIN MJ0258.//0.063:75:32//METHANOCOCCUS JANNASCHII.//Q57706
- 55 F-PLACE1009947//NEUROGRANIN (NG) (P17) (B-50 IMMUNOREACTIVE C-KINASE SUBSTRATE) (BICKS) (FRAGMENT).//0.33:51:45//BOS TAURUS (BOVINE).//P35722
- F-PLACE1009971//MIPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED

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PROTEIN).//0.022:84:27//MUS MUSCULUS (MOUSE).//P28575

5 F-PLACE1009992//BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1).//0.00011:35:51//HOMO SAPIENS (HUMAN).//P13497

10 F-PLACE1009995//TROPOMYOSIN, SMOOTH MUSCLE/FIBROBLAST CTM1.//0.052:185:22//CICUTA INTESTINALIS.//Q07068

15 F-PLACE1009997//TRANSCRIPTION ELONGATION FACTOR S-II (RNA POLYMERASE II ELONGATION FACTOR DMS-II) (TFIIS).//0.68:98:28//DROSOPHILA MELANOGASTER (FRUIT FLY).//P20232

F-PLACE1010023//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III.//6.6e-06:111:32//CAENORHABDITIS ELEGANS.//Q18262

20 F-PLACE1010031//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//0.0024:72:33//AUTOGRAPHIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479

25 F-PLACE1010053//HYPOTHETICAL PROTEIN HI0593.//0.83:24:45//HAEMOPHILUS INFLUENZAE.//P44022

30 F-PLACE1010069

F-PLACE1010074//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS5.//0.00027:192:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q92331

35 F-PLACE1010076//HUNCHBACK PROTEIN (FRAGMENT).//0.80:39:30//SCIARA COPROPHILA (FUNGUS GNAT).//Q01790

40 F-PLACE1010083//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//2.7e-48:177:46//HOMO SAPIENS (HUMAN).//P98171

45 F-PLACE1010089//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 13) (DEUBIQUITINATING ENZYME 11) (KIAA0055).//7.9e-07:55:43//HOMO SAPIENS (HUMAN).//P40818

50 F-PLACE1010096//100 KD PROTEIN (EC 6.3.2.-).//1.0e-107:232:90//RATTUS NORVEGICUS (RAT).//Q62671

55 F-PLACE1010102//DNA-DIRECTED RNA POLYMERASE SUBUNIT N (EC 2.7.7.6).//1.0:33:45//METHANOCOCCUS JANNASCHII.//Q57649

F-PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-47:200:46//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

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- 5 F-PLACE1010106//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE]//1.2e-14:94:41//MUS MUSCULUS (MOUSE)//P11369
- 10 F-PLACE1010134//HYPOTHETICAL 171.5 KD HELICASE IN NUT1-ARO2 INTERGENIC REGION//4.0e-28:78:76//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53115
- 15 F-PLACE1010148//GAR2 PROTEIN//2.6e-05:180:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//P41891
- 20 F-PLACE1010152//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E)//2.1e-59:227:54//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q24574
- 25 F-PLACE1010181//MALE SPECIFIC SPERM PROTEIN MST87F//0.39:12:58//DROSOPHILA MELANOGASTER (FRUIT FLY)//P08175
- 30 F-PLACE1010194//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN)//1.4e-07:95:43//GALLUS GALLUS (CHICKEN)//P30352
- 35 F-PLACE1010202//TRISTETRAPROLINE (TTP) (TIS11A) (TIS11) (ZFP-36)//0.094:109:29//RATTUS NORVEGICUS (RAT)//P47973
- 40 F-PLACE1010231//LANTIBIOTIC NISIN A PRECURSOR//0.99:42:35//LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS)//P13068
- 45 F-PLACE1010261//SEGREGATION DISTORTER PROTEIN//6.0e-71:201:62//DROSOPHILA MELANOGASTER (FRUIT FLY)//P25722
- 50 F-PLACE1010270
- 55 F-PLACE1010274//HYPOTHETICAL 16.2 KD PROTEIN C4F8.01 IN CHROMOSOME I//4.4e-08:100:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//O14177
- 60 F-PLACE1010293//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.9e-26:94:64//HOMO SAPIENS (HUMAN)//P39188
- 65 F-PLACE1010310//SYNAPSINS IA AND IB//5.7e-09:89:37//RATTUS NORVEGICUS (RAT) //P09951
- 70 F-PLACE1010321//IMMEDIATE-EARLY PROTEIN IE180//0.033:145:31//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV)//P33479